



GRAND ROUNDS CALL With Dr. Nalini Chilkov

July 10th, 2019

5:30 PM Pacific / 6:30 PM Mountain / 7:30 PM Central / 8:30 PM Eastern

Agenda

- Clinical Pearl:
 - Why Liquid Biopsies? When To Assay Circulating Tumor Cells and Cell Free Tumor DNA
- Clinical Questions:
 - Does Resveratrol Fuel her2neu breast cancer?
 - Review of Resveratrol and Cancer
 - How to safely manage hypercoagulation and risk of thrombus formation
 - Interactions with anti coagulant pharmaceuticals
 - Nutriceutical and Botanical Interventions
 - Basic Biomarkers for Monitoring
 - Is there lecture material available on this topic?
 - Should Girls Be Getting the HPV Vaccine?
 - Overview of HPV infections
 - Overview of 10 years of vaccination in first world countries vs no vaccination in 3rd world countries
 - Naturopathic Approach to HPV infection
 - Melatonin Enhances HPV vaccine efficacy in mice
 - Research
 - The Importance of assessing PERCEIVED STRESS in cancer patients

Clinical Pearl: Why Liquid Biopsies? When to Assay Circulating Tumor Cells and Cell Free Tumor DNA

Slides and References are found in Resource Library

Case Study:

Submitted by: No Case Study Submitted

Overview:

Core Questions:

Recommendations:

Questions & Answers

Jaclyn Tolentino, D.O.: Looking for a better understanding, your reflections and opinion on the article *Resveratrol fuels HER2 and ERα-positive breast cancer behaving as proteasome inhibitor* (<u>https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5361678/</u>)</u> 2016

IN VIVO MURINE and IN VITRO CELL CULTURE

Our results demonstrate that resveratrol, acting as a proteasome inhibitor, leads to Δ 16HER2 accumulation which favors the formation of Δ 16HER2/HER3 heterodimers. The consequential activation of downstream mTORC1/p70S6K/4EBP1 pathway triggers cancer growth and proliferation. This study provides evidence that resveratrol mechanism of action (and hence its effects) depends on the intrinsic molecular properties of the cancer model under investigation, exerting a tumor-promoting effect in luminal B breast cancer subtype models.

Curr Protein Pept Sci. 2018;19(3):311-322. doi: 10.2174/1389203718666170111115914.

******* "might resveratrol be protective against breast cancer or does it rather fuel it?".******

Walking a Tightrope: A Perspective of Resveratrol Effects on Breast Cancer. <u>Bartolacci C</u>1, <u>Andreani</u> <u>C</u>1, <u>Amici A</u>1, <u>Marchini C</u>1.

Abstract

It is an acknowledged fact that health benefits are derived from fruit- and vegetables-enriched diets. In particular, polyphenols, compounds bearing one or more hydroxyl groups attached to an aromatic ring, are ascribed for most of such beneficial effects. Among them, resveratrol, a phytoalexin found in numerous plant species, and more notably in grapes, has widely piqued the interest of the scientific community by virtue of its anti-aging, anti-inflammatory and anti-oxidant properties. Moreover, evidence claiming resveratrol ability to hinder processes underlying all the three steps of carcinogenesis (tumor initiation, progression and metastasization) has propelled an incredibly massive number of studies aimed at enquiring its eventual clinical potential in the fight against cancer. However, despite a large body of data pointing to the advantages of dietary resveratrol intake in respect of certain disease conditions, and cancer inter alia, its real position still remains quite ambiguous. In this uncertain scenario, the present review focuses its attention on the highly entangled relationship between resveratrol and breast cancer, attempting to shape the plethora of controversial results stemming from studies carried out on several in vitro and in vivo breast cancer models. Coping with such a tricky matter, there are so many variabilities concerning both resveratrol itself (dosage, administration, bioavailabilty, among others) and the unique molecular traits of each specific breast cancer subtype that must be taken into account when facing the dilemma: "might resveratrol be protective against breast cancer or does it rather fuel it?".

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Breast Cancer Res Treat. 2013 Aug;141(1):55-65.

Immunoliposome encapsulation increases cytotoxic activity and selectivity of curcumin and resveratrol against HER2 overexpressing human breast cancer cells.<u>Catania A1, Barrajón-Catalán E, Nicolosi S, Cicirata F, Micol V</u>.

Abstract

Natural compounds have been studied as a source of countless bioactive compounds with diverse activities. Among them, many dietary phytochemicals have been thoroughly studied for their cytotoxic or apoptotic effects in several cellular models in order to explain their anticancer capacity. Curcumin and resveratrol are two natural compounds with a large body of evidence showing their cytotoxic activity against a wide variety of cancer cells; however, their poor absorption, bioavailability, and low selectivity have limited their clinical use. With the aim of improving bioavailability and selectivity, the antiproliferative effects of free-, liposomed-, and immunoliposomed-curcumin and/or resveratrol formulations have been compared in two human breast cancer cell lines with different HER2 expression levels. The results demonstrate that when HER2-targeted immunoliposomes are coupled to trastuzumab there is a dramatic increase in the antiproliferative effects of curcumin and resveratrol in HER2 positive human breast cancer cells in comparison to regular liposomed or free forms, indicating an increase of its therapeutic effect. The enhancement of the cytotoxic effects was also correlated to the uptake of curcumin at intracellular level, as shown by using ImageStream technique. The striking efficacy of the immunoliposomed formulation containing both resveratrol and curcumin suggests a multitargeted mechanism of action that deserves further study. These findings show the potential of HER2-targeted nanovesicles to develop new drug delivery systems for cancer therapy based on these compounds and justify further preclinical trials. PMID: 23959397

DOI 10.1007/s10549-013-2667-y

<u>Cell Death Discov</u>. 2015; 1: 15061.

Published online 2015 Dec 7. doi: 10.1038/cddiscovery.2015.61

Resveratrol chemosensitizes HER-2-overexpressing breast cancer cells to docetaxel chemoresistance by inhibiting docetaxel-mediated activation of HER-2–Akt axis

<u>B S Vinod</u>,1,2 <u>H H Nair</u>,1,2 <u>V Vijayakurup</u>,1,2 <u>A Shabna</u>,1 <u>S Shah</u>,1 <u>A Krishna</u>,1 <u>K S Pillai</u>,1<u>S</u> <u>Thankachan</u>,1 and <u>R J Anto</u>1,*

Molecules. 2017 Jun; 22(6): 1014.

Published online 2017 Jun 18. doi: <u>10.3390/molecules22061014</u> PMID: <u>28629161</u>

Cancer Chemoprevention by Resveratrol: The p53 Tumor Suppressor Protein as a Promising Molecular Target

Danielly C. Ferraz da Costa,1 Eliane Fialho,2,* and Jerson L. Silva3,*

Norbert Latruffe, Academic Editor, Ole Vang, Academic Editor, and Dominique Vervandier-Fasseur, Academic Editor

Resveratrol regulates a variety of processes and signaling pathways that involves procarcinogen bioactivation and carcinogen detoxification [11,12]; reduction of oxidative stress [13] and inflammation [14]; apoptosis induction through the activation of both extrinsic and intrinsic pathways [15,16,17,18,19,20]; and other anticancer effects [21,22]. Resveratrol affects the three phases of carcinogenesis, tumor initiation, promotion and progression, and it also suppresses the final steps of carcinogenesis, e.g., angiogenesis and metastasis [11,23]. Resveratrol also impacts mitochondrial functions (the respiratory chain, oncoproteins, gene expression, among others), including those directly involving the p53 protein tumor suppressor protein [24]. Finally, in various cancer types, resveratrol behaves as a chemosensitizer that lowers the threshold of cell death induction by classical anticancer agents and counteracts tumor cell chemoresistance [25,26].

In vitro and in vivo studies have shown that resveratrol can act as a tumor-initiation suppressor by modulating phase I and phase II cytochrome P450 enzymes (CYPs) [5,12,27,28,29,30]. Resveratrol blocks the transcriptional activation of CYPs and inhibits the activity of CYP1A1, CYP1B1 and CYP1A2, which are phase I enzymes responsible for activating xenobiotics, thus halting the transformation of procarcinogen

agents into potential carcinogens [<u>12,27,28</u>]. Additionally, resveratrol enhances the expression and/or activity of phase II enzymes, including glutathione peroxidase, glutathione S-transferase, UDP-glucuronyltransferase, NAD(P)H:quinone oxidoreductase, and heme oxygenase, among others [<u>5,29,31</u>], subsequently stimulating carcinogen detoxification processes.

The role of resveratrol in the intracellular redox status has been described in many studies. Like other polyphenols, this microcomponent acts as an important cellular antioxidant, and its effects are dependent on the concentration tested and the cell type used. However, it has been proposed that resveratrol may also act as a pro-oxidant agent, representing one of the antineoplastic mechanisms of action involved in tumor cell death. Likewise, resveratrol has been shown to decrease the mitochondrial membrane potential and increase reactive oxygen species (ROS) generation, thus promoting apoptosis [32,33].

Some effects of resveratrol have been attributed to its estrogenic activity resulting from its structural similarity to diethylstilbestrol, a synthetic estrogen. Resveratrol can bind to estrogen receptors and may function as an agonist or antagonist, leading to opposite responses depending on the concentration, competition and expression of estrogen receptors in the cells. In MCF-7 human breast cancer cells, for example, which express these receptors, resveratrol may act as a superagonist [34].

Resveratrol is recognized as a potent tumor growth inhibitor in diverse experimental models. Previous studies have established its anticancer effects in a variety of cultured tumor cell lines, including colon [35,36,37], breast [19,38,39], prostate [40,41], pancreatic [42,43,44], lung [19,45,46], melanoma [47,48], glioma [49,50], and leukemia cells [51,52], among others. It has been suggested that the anti-proliferative properties of this microcomponent are related to its capacity to block DNA synthesis and to interfere with various stages of cell progression by regulating the machinery of proteins involved in cell cycle control. Hsieh and colleagues [53] first reported the ability of resveratrol to control growth and cell cycle transitions in human breast carcinoma cell lines with different metastatic potentials: highly invasive MDA-MB-435 and the minimally invasive MCF-7 cells. Resveratrol exerts a greater inhibitory effect on MDA-MB-435 cells, in which a reduction of the fraction of cells in the G1 phase and a corresponding accumulation of cells in S phase was observed. Since then, many other studies have reported that resveratrol at micromolar concentrations arrests the cell cycle of a variety of human cancer cell lines at the G1/S transition, in S phase or in the G2/M phase [5,54,55]. Although several studies have found that the induction of cell cycle arrest by resveratrol is a reversible process and does not trigger apoptosis, many other authors have reported that this process is often followed by apoptotic cell death [56].

Investigations regarding the effects of resveratrol on apoptosis induction in tumor cells have revealed that this compound can stimulate cell death by modulating proteins involved in both the intrinsic and extrinsic apoptotic pathways [56]. Numerous lines of evidence suggest that resveratrol affects the activation of pro-apoptotic and the inhibition of anti-apoptotic molecules. These mechanisms have been described in culture cells and in vivo in tumor models that have been chemically induced in animals and xenographic models in nude mice [55]. Studies suggest that resveratrol-mediated apoptosis includes the activation of death receptors such as Fas and TRAIL; the activation of Bax, Bak, PUMA, Noxa and Bim; and the inhibition of Bcl-2 and Bcl-XL. Some of these responses are mediated by the activation of the p53 tumor suppressor protein by resveratrol, as will be later discussed.

In addition, resveratrol demonstrates important anti-angiogenic effects, thus contributing to the reduction of the metastatic potential of tumor cells. The following mechanisms are involved in this process: the inhibition of extracellular matrix metalloproteinases gene expression, such as MMP-2 and MMP-9, which are involved in tumor invasiveness; and the inhibition of the expression of HIF-1 α and VEGF, factors that are directly related to new blood vessel formation [54,55].

Although some of the anti-carcinogenic effects of resveratrol have already been shown to be triggered by the activation of extracellular receptors [57], there is evidence that its internalization by cells is necessary for the activation of some specific intracellular targets. It has been demonstrated by multiphoton microscopy

(two-photon excitation) that resveratrol, but not its glycosylated or sulfated metabolites, is efficiently captured by neuroblastoma cells, allowing this molecule to exert its antitumor effects, unlike metabolites [58]. Additionally, the importance of cell membrane microdomains in the early biochemical events triggered by resveratrol resulting in cancer cell death, as well as in its absorption and distribution, has been previously described. Resveratrol accumulates in lipid rafts and is then taken up by cells through raft-dependent endocytosis. These events allow for the activation of kinase pathways and redistribution of cell death receptors within lipid microdomains, ultimately leading to apoptotic cell death [17].

Int J Mol Sci. 2018 Mar; 19(3): 652.

Published online 2018 Feb 26. doi: <u>10.3390/ijms19030652</u>

PMCID: PMC5877513

PMID: 29495357

Regulation of Cell Signaling Pathways and miRNAs by Resveratrol in Different Cancers

Ammad Ahmad Farooqi,1 Sumbul Khalid,2 and Aamir Ahmad3,*

Resveratrol has been shown to modulate key regulators of oncogenic signaling pathways. It strongly inhibits the TGF/SMAD pathway and reduces phosphorylated SMADs, resulting in the inhibition of cancer cell proliferation and metastasis. Resveratrol has shown experimentally verified activity against WNT signaling and can inhibit the translocation of β -catenin into the nucleus. Resveratrol, context-dependently, regulates the NOTCH pathway in cancer cells, all of which underlines its flexible and potent anticancer activity.

Reduced apoptosis is a hallmark of aggressive cancer cells, and resveratrol re-balances pro- and anti-apoptotic proteins to improve the efficacy of TRAIL-based therapeutics.

Resveratrol has been shown to efficiently upregulate various tumor suppressor miRNAs in different cancers, and its suppressive effects on oncogenic miRNAs have also been well documented.

Dr. Chilkov:

Few human studies. Most studies are murine or cell culture.

Susie Thomson:

- Please provide guidelines for a patient who is currently on anticoagulant medication who would like to take nutraceuticals and Phytochemicals as well.
 - More information is required including the age and medical hx of the patient, CVD history, Oncology hx, Diabetes?, Obesity? Levels of Inflammation?
 - Multiple factors can be co-morbid for risk of thrombus formation Name of anticoagulant medication is not given Other medications patient is taking is not given

PLEASE SUBMIT A FORMAL CASE STUDY NEXT MONTH --Our approach is HIGHLY INDIVIDUALIZED

• Please address interactions and safety guidelines for Tumeric, resveratrol, omega 3 FA.

- Most oral Rx anticoagulants are targeting larger fibrin clots. While phytochemical and nutriceuticals primarily inhibit platelet aggregation, a different mechanism and influencing smaller clot formation in capillaries not major blood vessels. There is generally not a lot of adverse interactions at conservative dosing (2 grams per day or less) Our non-pharmaceutical interventions are mild compared to pharmaceuticals
- Is this information within the course materials?
 Yes there is a Clinical Pearl 06-14-2017

Dr. Chilkov

Increased Risk of Hypercoagulation in Cancer Patients

Cancer patients overall have a 7 fold higher risk of venous thrombosis Patients with hematologic malignancies have a 28 fold higher risk of venous thrombosis Patients with distant metastases have a 20 fold higher risk of venous thrombosis

"the large proportion of terminal events in neoplastic diseases are thrombotic"

Risk Factors Include:

- · Age, Race, Gender
- Advanced Disease, Angiogenesis and Metastasis
- Recent Diagnosis or Recent Recurrence
- Surgery, Chemotherapy, Radiotherapy, Hormonal and Biological Therapies
- · Immobility, Sedentary, Dehydration

Primary BioMarkers

- · CBC + platelets + diff
- *D-dimer* < 0.4
- Fibrinogen < 375 (ideal 275-300)
- HS CRP < 1.0
- Homocysteine < 8.0
- · TGFb1 (varies)

Selected Interventions

Proteolytic Enzymes

Lumbrokinase & Nattokinase

PhytoChemicals & Botanicals

- · Curucminoids from Curcuma longa,
- · Resveratrol from Vitis vin. and Polygonum cuspidatum,
- · Berberine from Scutellaria baicalensis,
- Salvianolic Acids, Tanshinones, Cryptotanshinones from Salivia miltiorrhiza,
- · Ginsenosides from Panax Ginseng, ,
- Polysaccharides from Angelica sinensis and Astragalus,
- Quercitin from red onions and red apples

Nutraceuticals

· Omega 3 Fatty Acids, Ascorbic Acid. Nicotinic Acid,

Pharmaceuticals

- ORAL: ASA, Apixaban (Eliquis), Dabigatran etexilate (Pradaxa)
- Low Molecular Weight Heparin (injection)

Anti-Inflammatory Diet

Lifestyle Factors: Hydration, Movement



Published online 2016 May 26. doi: <u>10.1093/cid/ciw354</u>

PMCID: PMC4967609 PMID: <u>27230391</u>

REVIEW Impact and Effectiveness of the Quadrivalent Human Papillomavirus Vaccine: A Systematic Review of 10 Years of Real-world Experience

Suzanne M. Garland,1 Susanne K. Kjaer,2 Nubia Muñoz,3 Stan L. Block,4 Darron R. Brown,5 Mark J. DiNubile,6 Brianna R. Lindsay,6 Barbara J. Kuter,6 Gonzalo Perez,6,7 Geraldine Dominiak-Felden,8 Alfred J. Saah,6 Rosybel Drury,8 Rituparna Das,6 and Christine Velicer

Prophylactic human papillomavirus (HPV) vaccination programs constitute major public health initiatives worldwide. We assessed the global effect of quadrivalent HPV (4vHPV) vaccination on HPV infection and disease. PubMed and Embase were systematically searched for peer-reviewed articles from January 2007 through February 2016 to identify observational studies reporting the impact or effectiveness of 4vHPV vaccination on infection, anogenital warts, and cervical cancer or precancerous lesions. **Over the last** decade, the impact of HPV vaccination in real-world settings has become increasingly evident, especially among girls vaccinated before HPV exposure in countries with high vaccine uptake. Maximal reductions of approximately 90% for HPV 6/11/16/18 infection, approximately 90% for genital warts, approximately 45% for low-grade cytological cervical abnormalities, and approximately 85% for high-grade histologically proven cervical abnormalities have been reported. The full public health potential of HPV vaccination is not yet realized. HPV-related disease remains a significant source of morbidity and mortality in developing and developed nations, underscoring the need for HPV vaccination programs with high population coverage.

The review and meta-analysis included data from 65 articles from 14 high-income countries (most of which had girls/women-only programs), encompassing follow-up data from more than 60 million individuals over 8 years.

During that time, the prevalence of HPV 16 and 18 decreased by 83% among girls age 13 to 19 years old, and by 66% among women age 20 to 24 years. In addition, cross protection occurred, with the prevalence of HPV 31, 33, and 45 decreasing by 54% among girls age 13 to 19 years. There was also evidence of herd protection from the vaccine. Specifically, anogenital warts decreased by 67% among girls age 15 to 19 and by 54% among women age 20 to 24, but also by 31% among women age 25 to 29, 48% among boys age 15 to 19, and 32% in men age 20 to 24.

"Our results provide strong evidence of HPV vaccination working to prevent cervical cancer in real-world settings, as both the cause (high-risk HPV infection) and proximal disease endpoint (CIN2+) are significantly declining," wrote <u>Mélanie Drolet, PhD</u>, of Laval University in Quebec, and colleagues from the HPV Vaccination Impact Study Group. "In terms of global policy implications, these results reinforce the recently revised position of WHO recommending HPV vaccination of multiple age cohorts of girls, and provide **promising early signs that the WHO call for action on cervical cancer elimination might be possible if sufficient population-level vaccination coverage can be reached."**

https://www.cancernetwork.com/cervical-cancer/meta-analysis-shows-importance-hpv-vaccines

Front Oncol. 2019; 9: 355.

Published online 2019 May 8. doi: 10.3389/fonc.2019.00355 PMCID: PMC6517478 PMID: 31134154

Mucosal and Cutaneous Human Papillomavirus Infections and Cancer Biology

Tarik Gheit*

Mucosal HPV infections occur during the first sexual exposures in early adulthood (<u>30</u>), although non-sexual infection may also be possible (<u>31</u>).

Although a majority of sexually active women will acquire a genital HPV infection, most (>90%) cervical HPV infections are resolved by the host immune system within 1–2 years (32, 33) and give rise only to asymptomatic infections.

However, a minority of HPV infections become persistent. The risk of developing epithelial cell abnormalities and cancer is then increased (<u>32</u>).

Persistent infection may be explained by several factors.

- <u>Alcohol consumption</u> and the HR HPV load synergistically increased the risk of persistent HR HPV infection in women (<u>34</u>).
- <u>Cigarette smoking</u> alone also plays an important role in the acquisition of persistent HPV infections in women, by decreasing the probability of clearing oncogenic infections (<u>35</u>). Smoking is also a risk factor for a persistent oral HPV infection (<u>36</u>).
- <u>Host genetic risk factors may also predispose an individual to persistent HPV infection and developing cervical cancer, as supported by the high rate of heritability of cervical cancer (37–39).</u>
- <u>Defective immune response due to genetic variations (e.g., inflammasome genetics) has been associated with virus persistence and progression to cervical cancer (39–41).</u>
- Human leukocyte antigen (HLA) genes also play a key role in the persistence of HPV infections and progression to cervical cancer, depending on their ability to bind to HPV antigens (<u>39</u>, <u>42</u>).

The bacterial microbiome composition may also play a role in the outcome of mucosal HPV infection.

A chronic mycoplasma infection was shown to promote cervical dysplasia induced by HPV (<u>302</u>). Therefore, identifying the bacterial microbiome could allow the identification of patients at high risk for developing cervical cancer.

Prophylactic vaccines show a good efficiency in covering targeted HPVs, but they are inefficient in existing infections. Therefore, therapeutic vaccines are needed to fill this gap.

Arch Virol. 2018 Mar;163(3):587-597. doi: 10.1007/s00705-017-3647-z. Epub 2017 Nov 17.

Enhancement of therapeutic DNA vaccine potency by melatonin through inhibiting VEGF expression and induction of antitumor immunity mediated by CD8+ T cells.

Baghban Rahimi S1, Mohebbi A1,2, Vakilzadeh G3,4, Biglari P2, Razeghi Jahromi S5, Mohebi SR6, Shirian S7, Gorji A4,8, Ghaemi A9,10.

Abstract

To be effective, therapeutic cancer vaccines should stimulate both an effective cell-mediated and a robust cytotoxic CD8+ T-cell response against human papillomavirus (HPV)-infected cells to treat the

pre-existing tumors and prevent potential future tumors. In this study, the therapeutic experiments were designed in order to evaluate antitumor effect against the syngeneic TC-1 tumor model. The anti-tumor efficacy of a HPV-16 E7 DNA vaccine adjuvanted with melatonin (MLT) was evaluated in a C57BL/6 mouse tumor model by measuring tumor growth post vaccination and the survival rate of tumor-bearing mice, analyzing the specific lymphocyte proliferation responses in control and vaccinated mice by MTT assay. The E7-specific cytotoxic T cells (CTL) were analyzed by lymphocyte proliferation and lactate dehydrogenates (LDH) release assays. IFN-γ, IL-4 and TNF-α secretion in splenocyte cultures as well as vascular endothelial growth factor (VEGF) and IL-10 in the tumor microenvironment were assayed by ELISA. Our results demonstrated that subcutaneous administration of C57BL/6 mice with a DNA vaccine adjuvanted with MLT dose-dependently and significantly induced strong HPV16 E7-specific CD8+ cytotoxicity and IFN-y and TNF- α responses capable of reducing HPV-16 E7-expressing tumor volume. A significantly higher level of E7-specific T-cell proliferation was also found in the adjuvanted vaccine group. Furthermore, tumor growth was significantly inhibited when the DNA vaccine was combined with MLT and the survival time of TC-1 tumor bearing mice was also significantly prolonged. In vivo studies further demonstrated that MLT decreased the accumulation of IL-10 and VEGF in the tumor microenvironment of vaccinated mice. These data indicate that melatonin as an adjuvant augmented the cancer vaccine efficiency against HPV-associated tumors in a dose dependent manner.

PMID: 29149434 DOI: 10.1007/s00705-017-3647-z

Naturopathic Approaches to HPV infection

CONSIDER

Indole 3 Carbinol (I3C), Di Indole Methane (DIM), EGCG, Curcumin, Resveratrol, Lomatium, L-MTHF, VItamin A (not beta carotene), Zinc, Homeopathic Thuja

Escharotic Topical Cervical Treatment

Vaginal Suppositories; VITAMIN A, EGCG, Lomatium

Wise Woman Herbals VAG-PAK Suppositories

Each Vag Pack suppository contains:

- Magnesium sulfate
- Iron subsulfate
- Hydrastis
- Vitamin ATea Tree Essential Oil
- Bitter orange essential oil
- Bitter of ange essential
 Thuia essential oil
- In a base of cocoa butter

Immune Enhancement, Inflammation Control, Lifestyle factors, Acupuncture

Dr Tori Hudson ND Oral Protocol

1500 mg coriolus versicolor (make sure it is hot water extract) 2x daily

5 mg LMTHF methylated folate

200 mg selenium

200 mg DIM

Reference

TriCurin, a synergistic formulation of curcumin, resveratrol, and epicatechin gallate, repolarizes tumor-associated macrophages and triggers an immune response to cause suppression of HPV+ tumors.

Mukherjee S, Hussaini R, White R, Atwi D, Fried A, Sampat S, Piao L, Pan Q, Banerjee P. Cancer Immunol Immunother. 2018 May;67(5):761-774. doi: 10.1007/s00262-018-2130-3. Epub 2018 Feb 16.

PMID: 29453519

Research:

PERCEIVED STRESS SCALE:

Assessment. 2004 Sep; 11(3): 216-223.

doi: <u>10.1177/1073191104267398</u> PMCID: PMC2746492 NIHMSID: NIHMS122193 PMID: <u>15358877</u>

Assessing Stress in Cancer Patients A Second-Order Factor Analysis Model for the Perceived Stress Scale

The Perceived Stress Scale was developed to measure the degree to which situations in one's life are appraised as stressful.

Psychological stress has been defined as the extent to which persons perceive (appraise) that their demands exceed their ability to cope.

Even though perceived stress may decline with time, data suggest that clinical interventions remain necessary and beneficial (see <u>Andersen, 2002</u>, for a discussion).

For example, if quality of life outcomes are to be improved, **the best time to offer psychological/behavioral interventions should be when stress is high—at the time of initial diagnosis and treatment**.

Despite any decline that occurs with time, it is the **magnitude of initial stress that predicts later quality of life outcomes (increased negative affect**: <u>Varni & Katz, 1997</u>; lower self-esteem/self-efficacy: <u>Koopman et al., 2002</u>; <u>Varni, Katz, Colgrove, & Dolgin, 1994</u>; and poorer physical health and sleep quality: <u>Jacobsen et al., 1998</u>).

The PSS can provide clinical information regarding the degree to which cancer patients appraise

their lives, in general, as stressful.

When used within the context of a stress model, the measure has the potential to identify the role of perceived stress in important cancer outcomes, such as patients' quality of life and adherence to treatment.

Cohen, S., Kamarck, T., Mermelstein, R. (1983). A global measure of perceived stress. <u>Journal of Health and Social</u> <u>Behavior</u>, <u>24</u>, 385-396. <u>Link to full-text (pdf)</u>

Cohen, S., & Williamson, G. (1988). Perceived stress in a probability sample of the United States. In S. Spacapam & S. Oskamp (Eds.), <u>The social psychology of health: Claremont Symposium on applied social psychology.</u> Newbury Park, CA: Sage

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 (-)-Epigallocatechin-3-gallate inhibits human papillomavirus (HPV)-16 oncoprotein-induced

angiogenesis in non-small cell lung cancer cells by targeting HIF-1α. *Cancer Chemotherapy and Pharmacology*, *71*(3), 713-725. doi:10.1007/s00280-012-2063-z

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Introduction to Liquid Biopsies

Rationale and Indications Circulating Tumor Cells and Cell Free Tumor DNA

Dr. Nalini Chilkov, Founder



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Circulating Tumor Cells Tumor Cells CTC Circulating Tumor Cells (CTCs) are tumor cells that detach from the primary tumor and travel in the bloodstream, spreading from the original tumor to other locations, leading to cancer metastasis. These cells exist in peripheral blood of cancer patients and detection of CTCs can help to determine the process of metastasis. In contrast with other blood cells, the number of CTCs is very rare in blood which makes them difficult to detect. American Institute of © American Institute of Integrative Oncology. All rights reserved. B

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CTCs and ctDNA

- Circulating Tumor Cells (CTCs): whole cells shed from tumors and containing intact genomic material including DNA, RNA, protein
- Circulating tumor DNA (ctDNA): fragmented DNA shed into blood as cells die
- Capture and analysis of CTCs and ctDNA in blood, help guide treatment decisions and patient management



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Personalized Cancer Diagnostics

When tissue biopsy isn't an option, obtain actionable molecular information for your patient's cancer

When cancer metastasizes or spreads, it sheds tumor cells and cancer-causing DNA fragments into the blood.

Technologies have been developed with advanced methods for detecting and assessing tumor cells and cancer-causing DNA fragments in the blood.

You get the same information you would get from a tissue sample—from a simple blood test.

And because liquid biopsies use blood, you are informed about what's happening with your patients' cancer NOW—not weeks, months, or years ago.



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When Should You Consider A Liquid Biopsy?

•Not enough tissue was obtained from an initial biopsy.

- •Cancer starts in a place that is difficult to access for surgical biopsy.
- •Cancer recurs after the initial tumor tissue has been removed.
- •The patient is not responding to treatment as expected.
- •The patient wishes to avoid additional biopsies.
- •Monitoring for recurrence or progression



Circulating Tumor Cells	Cell Free Tumor DNA
CTC PLATFORM	ctDNA PLATFORM
Translocations	Single Nucleotide Variants (SNVs)
DNA Amplifications	Insertions
Protein Expression	Deletions
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BIOCEPT TARGET SELECTOR TEST MENU					
TEST MENU - TARGET SELECTOR	ארק ו	070 F			
Cancer Profiles					
Non-Small Cell Lung Cancer Profile A ALKA BRASA SCENART TOOLS A KRASS	Breast Cancer Profile • AR • EGFR Amp. • ER • FGFR1 • HER2 • PD-L1 • PR • PTEN	CTC Count*			
PD-L1 • ROS1		Individual Markers (Please check all that apply)			
 Non-Small Cell Lung Cancer Expanded Profile ALK + BRAF + EGFR Mutations + KRAS MET + PD-L1 + RET + ROS1 Squamous Cell Lung Cancer Profile ALK + BRAF + EGFR + FGFR1 + PD-L1 + ROS1 	Colorectal Cancer Profile • BRAF • KRAS	CTC (Circulating Tumor Cells)*	CtDNA (Circulating Tumor DNA)		
	Gastric Cancer Profile	Expression FISH AR ALK MYC	 Molecular EGFR (Mutations: L858R. 		
	Melanoma Cancer Profile	AR-V7 EGFR PTEN	Del 19, T790M)		
	• BRAF	PD-L1 HER2 ROS1	BRAF		
	Prostate Cancer Profile • AR • AR-V7 • EGFR Amp. • MET • MYC • PTEN	PR MET Validated tumor types: NSCLC, SCC, Breast, Colorectal, Prostate, Gastric, Ovarian, Pancreatic			
Repeat every 3-6 months. Covered by Medicare and most insurance plans Pathology Report and documentation of diagnosis required					
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Example Test for Receptor Expression

Targeted Therapies: Trastuzumab (Herceptin®), pertuzumab (Perjeta®), emtansine (Kadcyla®), and lapatinib (Tykerb®).

HER2

- The human epidermal growth factor receptor 2 (HER2, also called ERBB2 or NEU) is associated with several forms of cancer.
- Approximately 15–30% of breast cancer patients have tumors that overexpress *HER2*, and 7–34% of gastric cancers are *HER2* positive.
- HER2 overexpression is also associated with salivary duct carcinomas.

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	Example Test for Receptor Expression. PD_L1	Targeted Therapies: Pembrolizumab (Keytruda®), nivolumab (Opdivo®), and atezolizumab (Tecentriq®)	
•	Programmed death-1 (PD-1) is an immune checkpoint receptor expressed by T cells.		
•	Expression of <i>PD-L1</i> has been described for many tumor types, including melanoma, both squamous and non-squamous NSCLC, breast, ovarian, pancreatic, esophageal, kidney, bladder, and hematopoietic malignancies.		
•	Upregulation of <i>PD-1</i> plays a key role in T-cell exhaustion, which hampers the ability of the immune system to destroy cancer cells.		
•	When P <i>D-1</i> binds its ligand PD-L1 (programmed death ligand-1), a signal is transduced, telling the T-cell to leave other cells alone.		
•	This checkpoint is in place to protect normal cells from immune attack, but some cancer cells co-opted this system, expressing high levels of <i>PD-L1</i> to evade the immune system.		
•	Detecting PD-L1 in tumor cells identifies cancer patients that may benefit from treatment with immunotherapy agents. These agents, called <i>PD-1</i> or <i>PD-L1</i> inhibitors (or checkpoint inhibitors) have been shown to increase immune responses to cancers and improve patient survival.		
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The same specimen can also be microscopically analyzed for DNA and protein targets

All CTC Test are enumerated can be used for monitoring





ctDNA Tests

Performing PCR upfront and then sequencing delivers added confidence to final result.

Switch-Blocker technology enriches oncogene mutations and suppresses wild type DNA resulting in ultra-high sensitivity and specificity.

All ctDNA tests are quantitative and can be used to monitor mutation load.

NGS technology allows multiplexing capabilities and future panel development.

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- •Monitoring for recurrence or progression

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Resveratrol fuels HER2 and ERα-positive breast cancer behaving as proteasome inhibitor

Cristina Andreani^{1*}, Caterina Bartolacci^{1*}, Kathleen Wijnant¹, Rita Crinelli², Marzia Bianchi², Mauro Magnani², Albana Hysi³, Manuela Iezzi³, Augusto Amici^{1*}, Cristina Marchini^{1*}

 ¹School of Biosciences and Veterinary Medicine, University of Camerino, Camerino, 62032, Italy
 ²Department of Biomolecular Sciences, Section of Biochemistry and Molecular Biology, University of Urbino "Carlo Bo", Urbino, 61029, Italy
 ³Aging Research Centre, G. d'Annunzio University, Chieti, 66100, Italy

*Equal contribution

Correspondence to: Cristina Marchini , Augusto Amici; email: cristina.marchini@unicam.it , augusto.amici@unicam.itKeywords: breast cancer, Δ16HER2 mice, resveratrol, estrogen receptor, proteasomeReceived: October 7, 2016Accepted: February 11, 2017Published: February 26, 2017

ABSTRACT

The phytoestrogen resveratrol has been reported to possess cancer chemo-preventive activity on the basis of its effects on tumor cell lines and xenograft or carcinogen-inducible *in vivo* models. Here we investigated the effects of resveratrol on spontaneous mammary carcinogenesis using $\Delta 16$ HER2 mice as HER2+/ER α + breast cancer model. Instead of inhibiting tumor growth, resveratrol treatment (0.0001% in drinking water; daily intake of 4µg/mouse) shortened tumor latency and enhanced tumor multiplicity in $\Delta 16$ HER2 mice. This *in vivo* tumor-promoting effect of resveratrol was associated with up-regulation of $\Delta 16$ HER2 and down-regulation of ER α protein levels and was recapitulated *in vitro* by murine (CAM6) and human (BT474) tumor cell lines. Our results demonstrate that resveratrol, acting as a proteasome inhibitor, leads to $\Delta 16$ HER2 accumulation which favors the formation of $\Delta 16$ HER2/HER3 heterodimers. The consequential activation of downstream mTORC1/p70S6K/4EBP1 pathway triggers cancer growth and proliferation. This study provides evidence that resveratrol mechanism of action (and hence its effects) depends on the intrinsic molecular properties of the cancer model under investigation, exerting a tumor-promoting effect in luminal B breast cancer subtype models.

INTRODUCTION

Several natural compounds have recently gathered renewed interest as potential anti-tumor agents. Resveratrol (*trans* -3,4',5-trihydroxystilbene), a natural polyphenol found in grapes, peanuts, cocoa, berries, and red wine, has been described as a putative cancer chemo-preventive compound able to counteract breast cancer initiation, promotion and progression [1]. Although several *in vitro* studies have proposed resveratrol to exert an anti-tumor activity by inducing apoptosis and/or cell cycle arrest in various mammary cancer cell lines [2-4], investigations attempting to dissect the *in vivo* effects of resveratrol upon cancer onset and progression have led to contradictory results [5-7]. Such a controversial scenario can be explained recalling that resveratrol, as a phytoestrogen, possesses both estrogenic and anti-estrogenic activities on ERapositive breast cancer [8-10]. The devised experimental conditions -dose, timing, way of administrationinfluence the outcome of resveratrol-based studies as well [11]. Moreover, the experimental model taken into consideration is determinant: the majority of available data has been obtained using transplantable or carcinogen-inducible tumor models that, even if informative, fail to reproduce the complexity of spontaneous tumorigenesis [11]. To our knowledge, the solely in vivo study on a spontaneous mammary tumor model was reported by Provinciali et al. who claimed how resveratrol supplementation delays tumor onset, growth and metastases in HER2/neu transgenic female mice [12]. This research was performed *in vivo* on transgenic mice carrying the rat HER2/neu oncogene under the transcriptional control of MMTV promoter, and *in vitro* on human SKBR3 cell line, both models representing ER-negative (-) and HER2-positive (+) breast cancers [13]. They ascribed such protective effects to a decrease in HER2 gene expression and a promotion of *in situ* apoptosis observed inside mammary tumor tissues [12].

Even though HER2 over-expression is considered a hallmark of aggressive breast cancer subtypes, increasing evidence has pointed toward a major contribution of $\Delta 16$ HER2 splice variant (lacking exon-16), which is commonly co-expressed with wild-type HER2, in promoting cancer progression, metastasis and resistance to Trastuzumab [14, 15]. The relevance of $\Delta 16$ HER2 and the availability of $\Delta 16$ HER2 mice, transgenic for the human $\Delta 16$ HER2 oncogenic isoform, drove us to evaluate the effects of resveratrol intake on $\Delta 16$ HER2-driven mammary carcinogenesis [16]. Unexpectedly, we found resveratrol to promote $\Delta 16$ HER2 carcinogenesis by up-regulating $\Delta 16$ HER2 protein levels in both primary tumors and metastases and down-regulating ER α expression in tumors, thus recapitulating endocrine therapy resistance. Mechanistically, resveratrol partially inhibits proteasome activity and leads to $\Delta 16$ HER2 protein accumulation. Increased $\Delta 16$ HER2 levels, in turn, trigger the formation of $\Delta 16$ HER2/HER3 heterodimers and the consequent HER3 phosphorylation. The resulting activation of mTORC1/p70S6K pathway finally fuels cell proliferation and mammary tumor development in $\Delta 16$ HER2 mice.

RESULTS

Resveratrolsupplementationpromotesmammary tumor development in $\Delta 16$ HER2 mice

In $\triangle 16$ HER2 mice, the MMTV-driven expression of only five copies of the human $\triangle 16$ HER2 transgene triggers neoplastic transformation of mammary epithelial cells with a short latency time. Since all transgenic females develop multiple asynchronous mammary tumors on average at the 15th week of age, resveratrol treatment started when the animals were 8 week-old and proceeded up to 23 weeks of age (Figure



Figure 1. Resveratrol fuels mammary tumor formation in a luminal B breast cancer *in vivo* model. (a) Schematic representation of the experimental workflow used for the treatment of $\Delta 16$ HER2 mice with vehicle or resveratrol. (b) Kaplan-Meier disease-free survival plot for vehicle- (n=9) and resveratrol-treated (n=9) $\Delta 16$ HER2 mice. ** $p \le 0.01$, Log Rank test. (c) Tumor multiplicity in resveratrol-treated *vs* control mice; the number of palpable mammary tumors per mouse is represented as mean \pm SD. Statistical significance was assessed by two-way ANOVA test. (d) Left panel: Representative Hematoxyilin-Eosin (H&E) and PCNA stained sections of tumors from resveratrol and vehicle treated mice. Magnification 400 X. Right panel: Quantification of PCNA staining in tumors from resveratrol and vehicle treated mice. Data are expressed as mean \pm SEM. *p < 0.05; unpaired two-tailed student t test.

1a). As shown in Figure 1b, resveratrol-receiving mice displayed a significantly anticipated tumor onset developing the first tumor mass at only 9 weeks of age

(p=0.0099), while the first tumor appeared at 12 weeks of age in untreated females. In particular, 50% of resveratrol-treated mice presented at least one mammary



Figure 2. Resveratrol treatment induces HER2 over-expression and ER α down-regulation in HER2+/ER α + mammary carcinomas. (a) Representative western blot analysis of ER α and β -actin (loading control) in spontaneous mammary tumors from Δ 16HER2 mice supplemented or not with resveratrol (left panel), and relative densitometry quantification from three independent experiments (right panel). The significance was determined by unpaired two-tailed student t test, *p < 0.05. (b) Representative western blot analysis of HER2 and β -actin (loading control) in spontaneous mammary tumors from Δ 16HER2 mice, supplemented or not with resveratrol (left panel), and relative densitometry quantification from three independent experiments (right panel). The significance was determined by unpaired two-tailed student t test, *p < 0.05. (c) Left panel: representative immunofluorescence images of tumor sections from control and resveratrol supplemented mice stained with an antibody anti-HER2 (green) and DRAQ5 dye (red) for nuclei staining. Magnification 400 X. Right panel: quantification of HER2 staining in tumors from resveratrol treatment induces HER2 over-expression in lung metastases. Left panel: representative immunofluorescence images of lung metastasis sections from control and resveratrol supplemented mice stained with an antibody anti-HER2 (green) and DRAQ5 (red). Magnification 400 X. Right panel: quantification of HER2 staining in tumors from resveratrol treatment induces HER2 over-expression in lung metastases. Left panel: representative immunofluorescence images of lung metastasis sections from control and resveratrol supplemented mice stained with an antibody anti-HER2 (green) and DRAQ5 (red). Magnification 400 X. Right panel: quantification of HER2 staining in tumors from resveratrol treatment induces HER2 over-expression in lung metastases. Left panel: representative immunofluorescence images of lung metastasis sections from control and resveratrol supplemented mice stained with an antibody anti-HER2 (green) a

mammary tumor at 15 weeks of age, when 90% of the control littermates were still tumor-free, although all the animals eventually developed tumors within 20 weeks of age. Moreover, as shown in Figure 1c, mice supplemented with resveratrol suffered from a higher number of tumor masses than controls, with an average of 9 tumors/mouse and 6 tumors/mouse, respectively (p=0.044). The enhanced proliferation rate triggered by resveratrol correlates with an increased expression of proliferating cell nuclear antigen (PCNA) in tumors from treated animals as demonstrated by immuno-histochemical (IHC) analysis (Figure 1d).

Resveratrol triggers $\Delta 16HER2$ over-expression and ER α down-regulation

To investigate the molecular mechanisms underlying the boosted cancer growth induced by resveratrol, ER α and Δ 16HER2 protein levels were analyzed by western blot in tumors explanted from resveratrol-treated and control mice. We found that *in vivo* administration of resveratrol

caused a dramatic drop in the ER α expression (Figure 2a, p<0.05) and a concomitant increase in Δ 16HER2 protein level (Figure 2b, p<0.05) in tumors. Confocal microscopy analysis confirmed the significant higher abundance of Δ 16HER2 in both primary tumors (Figure 2c) and lung metastatic lesions (Figure 2d, p<0.05) from resveratrol-treated mice compared to controls. These data suggest that the effect of resveratrol on Δ 16HER2 protein accumulation is similar in primary tumors and metastases, although resveratrol supplementation did not seem to influence the number of lung metastases (3 out of 6 mice were found with pulmonary metastases in the vehicle group, 4 out of 7 mice in resveratrol-group, Fig. S1).

Resveratrol *in vitro* treatment of $\Delta 16HER2+/ER\alpha+$ breast cancer cell lines (luminal B subtype) recapitulates the *in vivo* outcomes

To confirm the pro-tumor effect of resveratrol in human $\Delta 16\text{HER2+/ERa+}$ breast cancer, we tested resveratrol *in vitro* on human BT474 and murine CAM6 cell lines.



Figure 3. Resveratrol triggers HER2 over-expression and ER α down-regulation in luminal B breast cancer cell lines. (a) CAM6 and (b) BT474 cells were incubated for 24 hours in the presence of vehicle or increasing concentrations of resveratrol and cell viability was determined by MTT assay. Results (including vehicle group treated with 0.02 % DMSO) are expressed as percentage (%) of cell viability relative to untreated controls. Columns, mean of three separate experiments wherein each treatment was repeated in 16 wells; bars, SE. **p \leq 0.01, ***p \leq 0.001, one-way ANOVA followed by Bonferroni's multiple comparison test. Representative western blot analysis of HER2, ER α and β -actin (loading control) in murine CAM6 cells (c) or human BT474 cells (d), treated with resveratrol or 17 β -estradiol or vehicle for 24 hours (upper panel), and relative densitometry quantification (lower panel). The significance was determined by one-way ANOVA (*p < 0.05, **p \leq 0.01).

CAM6 cells have been established from Δ 16HER2 mice and can be considered the in vitro counterpart of $\Delta 16$ HER2 mammary tumors [17]. After 24 hours' incubation, despite high resveratrol concentrations resulted in reduced cell viability, low-range resveratrol concentrations (20-30 µM) promoted cell proliferation of both CAM6 and BT474 cells (Figure 3a and 3b), mimicking the in vivo resveratrol effect. Consistently, western blot analysis revealed that treatment with 40 uM resveratrol for 24 hours induced HER2 upregulation and a concomitant ERa down-regulation in both CAM6 and BT474 cells, recapitulating the molecular events observed inside $\Delta 16$ HER2 tumors (Figure 3c and 3d). Since 10 nM 17β-estradiol treatment only partially reproduced the resveratrol effect in CAM6 cells, inducing reduction of ERa without enhancing HER2 protein levels, we suppose that resveratrol exerts a more complex action on $\Delta 16$ HER2+ cancer cells than the mere estrogen-like effect.

Resveratrol causes Δ **16HER2 protein accumulation** by partial inhibition of proteasome activity

To evaluate whether the resveratrol-induced $\Delta 16$ HER2 over-expression was due to transcriptional or posttranscriptional mechanisms, $\Delta 16$ HER2 mRNA levels were analyzed by qRT-PCR in mammary tumors from resveratrol-treated and control mice. Despite the significantly higher level of $\Delta 16$ HER2 protein detected in resveratrol-treated tumors in comparison with controls (Figure 2b and 2c), no differences in $\Delta 16$ HER2 mRNA levels were found between the two experimental groups (Figure 4a and 4b). By contrast, the activity of



Figure 4. Resveratrol inhibits the chymotrypsin-like activity of 20S proteasome and resulted in an increased accumulation of protein-ubiquitin conjugates. Δ 16HER2 and β -actin (internal control) mRNA levels were measured by semiquantitative RT-PCR (a) and qRT-PCR (b) analyses in spontaneous mammary tumors from Δ 16HER2 mice supplemented or not with resveratrol. (c) The chymotrypsin-like activity of the 20S proteasome was measured in tumor samples, from Δ 16HER2 mice treated or not with resveratrol, as described in Materials and Methods, and expressed as fluorimetric units (FU) min⁻¹ mg⁻¹. The significance was determined by unpaired two-tailed student t test, *p < 0.05. (d) Western blot analysis of 20S proteasome subunit content (upper panel) and ubiquitin-protein conjugates and free ubiquitin levels (lower panel) in tumor samples from Δ 16HER2 mice treated or not with resveratrol. β -actin was used as loading control. (e) Representative western blot analysis of p53 and β -actin (loading control) in spontaneous mammary tumors from Δ 16HER2 mice, supplemented or not with resveratrol, and (f) relative densitometric quantification from three independent experiments. The significance was determined by unpaired two-tailed student t test, *p < 0.05. the 20S proteasome, which is responsible for the degradation of the bulk of the cellular proteins, was significantly affected by *in vivo* supplementation of resveratrol, as determined by the 20S chymotrypsin-like activity assay in tumor extracts (Figure 4c). Noteworthy, no difference was found in the cellular levels of the 20S subunits, suggesting that resveratrol may exert a direct inhibitory effect on the proteasome

enzymatic activity (Figure 4d, upper panel). In agreement with a partial inhibition of the proteasome, tumor masses from resveratrol-treated mice displayed a higher extent of ubiquitin-conjugated proteins with respect to those obtained from mice receiving placebo (Figure 4d, lower panel). Consistently, western blot analysis also revealed a significant increase in the levels of p53 protein in mammary tumors from resveratrol-



Figure 5. Increased HER2 level induced by resveratrol results in a preferential activation of mTORC1/p70S6K pathway. Representative western blot analysis of HER2 and HER3 downstream signaling pathways in spontaneous mammary tumors from Δ 16HER2 mice, treated or not with resveratrol (left panels), and densitometry quantification from three independent experiments (right panels). (a) PI3K/AKT and (b) mTOR signaling pathways were analyzed. β -actin was used as loading control. The significance was determined by t-test (*p < 0.05; **p ≤ 0.01; ***p ≤ 0.001). (c) Resveratrol promotes the direct coupling of Δ 16HER2 to HER3 kinase in HER2+/ER α + breast cancer. Δ 16HER2 kinase co-immunoprecipitates with pHER3. Proteins were immunoprecipitated with anti-HER2 antibody and then probed by western blot for pHER3. Input represents 10% of the co-immunoprecipitation protein amount (30 µg).

receiving mice in comparison with controls (Figure 4e and 4f, p<0.05), giving further evidence of resveratrolmediated proteasome inhibition. Noteworthy, such p53 augmentation inside tumors of resveratrol group did not trigger a concomitant up-regulation in the apoptotic cell death, as indicated by IHC analysis of cleaved caspase 3 (Figure S2). Moreover, the ability of resveratrol to inhibit in a concentration-dependent manner the activity of the proteasome was confirmed in both BT474 and CAM6 cell extracts (Figure S3).

Δ16HER2 accumulation induced by resveratrol results in a preferential activation of mTORC1/ p70S6K/4EBP1 pathway

To identify the signaling cascades beneath the resveratrol-induced Δ 16HER2 accumulation, the main oncogenic pathways known to be involved in breast carcinogenesis were analyzed by western blot. As shown in Figure 5a, despite tumors from resveratroltreated mice expressed significantly higher $\Delta 16$ HER2 levels than vehicle counterparts, no relevant differences were detected in its phosphorylation status. Noteworthy, phosphorylated HER3 levels were significantly higher in tumor extracts from resveratrol-treated animals (Figure 5a). Consistent with the over-expression of $\Delta 16$ HER2 and increased HER3 phosphorylation, tumors displayed high levels of $\Delta 16HER2$ -HER3 heterodimer upon resveratrol treatment, as measured by co-immunoprecipitation assay (Figure 5c). This result suggests that resveratrol-induced accumulation of $\Delta 16$ HER2 leads to $\Delta 16$ HER2/HER3 heterodimer formation and consequently to HER3 transactivation. It is known that HER2/HER3 heterodimers are powerful oncogenic units, in part because phospho-HER3 boosts PI3K-AKT-mTOR signaling pathway [18].

Consistently, we found that resveratrol-induced $\Delta 16 HER2/HER3$ heterodimerization caused concomitant increase in the levels of PI3K p85 and PI3K p110\alpha (PI3K-p85, p<0.01 and PI3K-p110\alpha, p < 0.05) and the up-regulation of the mammalian target of rapamycin complex 1 (mTORC1). The mTOR Ser/Thr kinase is the catalytic component of two structurally and functionally distinct signaling complexes. The rictor-containing mTORC2 regulates the actin cytoskeleton and activates Akt [19]. The raptor-containing mTORC1 regulates cell growth and nutrient signaling [20]. In particular, mTORC1 phosphorylates p70 S6 kinase (S6K) and eukaryotic initiation factor 4E binding protein 1 (4EBP1), thereby regulating translation of proteins that are critical for progression from G1 into S phase [21]. Therefore, we examined levels of phospho-4EBP1 and phospho-S6K as readouts of mTORC1 activity. As shown in Figure 5b, resveratrol significantly increased both phospho-

4EBP1 (p<0.01) and phospho-S6K levels (p<0.05) relative to vehicle. The phosphorylation of these two par excellence mTORC1 downstream effectors positively correlated with the level of mTOR Ser(P)-2481, while lower rictor and mTOR Ser(P)-2448 pointed toward inhibition of mTORC2. Interestingly, although resveratrol supplementation promoted the PTEN inhibiting phoshorylation of (pPTEN ser380/thr382/383) [22], no differences in terms of AKT activation (pAKT) were observed between resveratrol and control groups: this may be due to feedback loops that compensate PI3K-mediated AKT activation. Interestingly, other pathways known to be activated downstream $\Delta 16$ HER2, such as the Δ 16HER2/Src/STAT3 axis, did not vary significantly between the two experimental groups (Figure S4). It is worth to note that the levels of unphosphorylated proteins other than HER2, like mTOR (Figure 5b), Src and Erk1,2 (Figure S4) increased in tumor extracts from resveratrol group. This observation is consistent with the ubiquitin-proteasome system (UPS)-dependent degradation of these proteins [23-26] and supports our evidence about resveratrol acting as proteasome inhibitor.

DISCUSSION

The need for safe and low-toxic preventive and therapeutic strategies against cancer is still unmet. In this scenario phytoestrogens like resveratrol have received growing attention as valuable chemopreventive tools. Contrarily to previously published results [12], describing an antitumor effect of resveratrol in a HER2+/ERabreast cancer experimental model, here we have found that resveratrol, given at the same reported dose, regimen and administration way, did not prevent nor delay tumor onset: instead, significantly accelerated cancer development in Δ 16HER2 females that spontaneously develop HER2+/ER α + mammary carcinomas.

In $\Delta 16$ HER2 mice, resveratrol intake not only anticipated the tumor onset, but significantly augmented tumor multiplicity, promoting the growth of a higher number of tumor masses per mouse. Moreover, consistently with its pro-proliferative effect, we provide evidence that resveratrol treatment induced a strong increase in $\Delta 16$ HER2 expression, associated with a significant reduction of ER α protein level. In contrast to the observation by Provinciali et al., resveratrol did not affect $\Delta 16$ HER2 mRNA levels, suggesting that $\Delta 16$ HER2 protein accumulation was the consequence of a reduced degradation rather than an increased transcription. Indeed, it has been demonstrated that resveratrol can act as a potent proteasome inhibitor [27, 28]. In our experimental settings, resveratrol treatment partially inhibited the chymotrypsin-like proteasome activity, which may elicit the observed accumulation of $\Delta 16$ HER2 protein in mammary tumors, that in turn fuels cancer growth. Noteworthy, the same result was obtained in vitro using murine and human luminal B breast cancer cell lines (CAM6 and BT474 cells, respectively). Indeed, adding resveratrol to cell-free extracts of CAM6 and BT474 resulted in a concentration-dependent proteasome inhibition. On the whole, the in vivo and in vitro evidence we gathered suggests that resveratrol can act as a proteasome inhibitor as Oureshi et al. claimed [26]. Nonetheless, we cannot exclude that additional effects of resveratrol on signaling cascades might eventually mediate an indirect proteasome inhibition as well. Anyhow, the ability of resveratrol to inhibit the proteasome can be considered a double-edged sword. On one side, resveratrol has been reported to exert anti-inflammatory effects partially by counteracting the proteasome-mediated activation of NF-kB, thereby suppressing activation of proinflammatory cytokines and iNOS genes [26]. Since inflammation is a hallmark of neurodegenerative disorders and aging [29, 30], proteasome inhibition triggered by resveratrol might provide additional insights

into its anti-aging properties as well. On the other side, as our evidence has demonstrated, proteasome impairment and the consequent HER2 accumulation can promote breast cancer development. Strikingly, this resveratrol-induced $\Delta 16$ HER2 increase was associated with a concomitant ER α diminution. ER α is of critical importance in mammary cancer initiation and progression, having become an ideal target for anticancer therapies. However, expression of ERa in tumors is dynamic and can change during the course of tumor progression and following therapy [31, 32]. Loss of ER α represents a crucial mechanism for the acquisition of endocrine resistance [33-35]. Several clinical and preclinical studies have confirmed the existence of a remarkable crosstalk between HER2 and ER α that usually leads them to be inversely expressed inside breast cancer. Strikingly, such bidirectional fluctuations dictate the responsiveness to HER2- and/or ER-targeted therapies [36-38]. Accordingly, it has been shown that resistant breast cancer cells have higher HER2 expression than endocrine therapy-sensitive cells [39]. Our data perfectly fit in this scenario, suggesting that resveratrol treatment mirrors endocrine resistance acquirement, triggering HER2 up-regulation and ERa



Protein synthesis and cell growth

Figure 6. Proposed resveratrol's mechanism of action in a luminal B breast cancer model. Our data show that resveratrol down-regulates ERq and lowers the chymotrypsin-like activity of the 20S proteasome in HER2+/ERq+ breast cancer. leading to an increased accumulation of Δ16HER2, which efficiently couples to HER3 and activates the PI3K-AKT-mTOR pathway. In particular, Δ16HER2/HER3 heterodimers trigger the mTORC1/p70S6K/4EBP1 signaling axis inducing an upregulation of protein synthesis and cell growth. On the other hand, resveratrol inhibits mTORC2 and promotes phosphorylation of PTEN, reducing its catalytic activity, thereby enhancing PI3K-mediated AKT activation, while feedback loops compensate it.

repression. Our results also support the hypothesis that resveratrol may exert its anti-ERa action by impairing proteasome-mediated ER α activation. Interestingly, UPS has been described as necessary for a correct activation of ER α [40] and some proteasome inhibitors have been shown to repress ER α gene expression [41, 42]. Moreover, a recently published work has proposed that mTORC1 inhibition activates the Ubiquitin/Proteasome System (UPS) and autophagy [43], thus sustaining an inverse correlation between mTOR signaling and proteasome activity. Consistently, we have reported the resveratrol-induced over-expression of $\Delta 16$ HER2 eventually results in the activation of mTORC1/p70S6K/ p4EBP1 axis. This observation recapitulates a relevant molecular pathway implicated in endocrine resistance development [44] and may explain why the combination of resveratrol and mTORC1 inhibitors have stood out as more effective anti-tumor therapy than single-agent approaches [45, 46].

Interestingly, despite the claimed anti-aging effect of resveratrol, longevity studies have demonstrated that combination of rapamycin and resveratrol was not able to prolong the overall mice survival as mTOR inhibition does [47]. This aspect further strengthens the connection between resveratrol and mTOR pathway and suggests that our data might be extended to a broader context such as aging-related dysfunctions exhibiting a preferential activation of mTORC1 pathway [48].

In conclusion, this study provides evidence that the effects of resveratrol treatment depend on intrinsic molecular cancer properties, exerting a tumor-promoting effect in luminal B breast cancer subtype by acting as proteasome inhibitor and inducing a multi-target molecular rearrangement (Figure 6).

MATERIALS AND METHODS

Animals

 Δ 16HER2 female mice were housed under controlled temperature (20 °C) and circadian cycle (12 hours light/12 hours dark) in the animal facility of University of Camerino. The animals were fed on chow diet and tap water *ad libitum*.

Cell culture

CAM6 cells, a Δ 16HER2-expressing epithelial tumor cell line derived from a mammary carcinoma spontaneously arisen in a Δ 16HER2 female [17] and BT474 cell line were maintained in DMEM (Lonza) supplemented with 10% FBS (Gibco, Life Technologies) and 1% penicillinstreptomycin (Gibco, Life Technologies). Cells were cultured at 37 °C under humidified atmosphere with 5% CO2.

Resveratrol treatment

8 week-old $\triangle 16$ HER2 female mice were randomly divided into two experimental groups (n=9 each). One group underwent resveratrol treatment and the other was given control vehicle, as previously reported [12]. Briefly, resveratrol (Sigma) was dissolved in methanol to be then diluted in tap water to a final concentration of 1mg/l. Being the daily water intake of about 4 ml/mouse, 4 µg resveratrol/mouse was the daily dose assumed. The control mice were supplemented with 0.02% methanol in tap water (vehicle). Both vehicleand resveratrol-containing water was renewed twice a week. During the treatment (from 8-weeks to 23-weeks of age), mice were weekly monitored for mammary tumor development by palpation and growing masses greater than 2 mm in mean diameter were regarded as tumors. Two perpendicular diameters (a and b) were measured on each tumor using caliper and volumes were calculated by the V = $\pi/6[(a+b)/2]^3$ formula. All animal experiments were carried out in accordance with the U.K. Animals (Scientific Procedures) Act, 1986 and associated guidelines, EU Directive 2010/63/EU for animal experiments, and were approved by the Ethic Committee on Animal Use of the University of Camerino (protocol number 14/2012). At the end of experiment mice were euthanized and tumors and lungs samples were collected for subsequent analyses. For the in vitro experiments resveratrol was dissolved in DMSO (Sigma) and then diluted in complete DMEM to usage concentrations (10-100 μM). 17β-estradiol (Calbiochem) was used as control estrogen treatment (stock solution 40 mM in 100% ethanol and diluted in complete DMEM to 10 nM), as previously described [41]. Cells were treated for 24 hours with resveratrol/17β-estradiol- or vehiclecontaining medium (0.02% DMSO).

Cell viability assay

Resveratrol effect on cell viability was evaluated by seeding $4x10^4$ cells/well (CAM6 cells) or $2.5x10^4$ cells/well (BT474 cells) in 96-well plates in complete DMEM. The day after, fresh medium containing appropriate resveratrol concentrations was added. Cell viability was determined via MTT assay. MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) was purchased from Sigma Aldrich (St. Louis, MO).

Immunohistochemistry (IHC) and confocal microscopy analyses

Tumors and lungs harvested from mice were fixed in 4% paraformaldehyde solution for 24-48 hours at room

temperature and then embedded in paraffin. Paraffinembedded sections were stained with hematoxylin and eosin or immunostained with anti-mouse PCNA monoclonal antibody (Dako) or with anti-cleaved caspase-3 monoclonal antibody (MAB835, R&D Systems, Milan, Italy). After washing, they were overlaid with appropriate secondary antibody. Immunostaining was developed with Vulcan Fast Red (Biocare) alkaline phosphatase method. The number of cleaved caspase-3 positive cells was evaluated on digital images of controls and resveratrol tumors (10 per group, 5 x 400 microscopic fields per tumor). As it regards confocal microscopy analysis, after incubation in blocking buffer for 20 minutes, tissue sections were incubated for 1 hour at 37 °C with anti-NEU polyclonal antibody (diluted 1:50, Santa Cruz). Nuclei staining was performed using DRAQ5 probe (Life technologies) according to the manufacturer instructions. After washing, the coverslips were incubated with Alexa 488conjugated goat anti-rabbit secondary antibody (diluted 1:100, Life technologies) for 1 hour at 37 °C. Slides were viewed using a Zeiss LSM 510 Meta Confocal Microscope. Quantitative measures were obtained via ImageJ software.

Protein extraction and western blot analysis

Tumors and treated cells were homogenized in RIPA buffer (0.1% SDS, 1% NP40, 0.5% CHAPS) supplemented with protease inhibitors aprotinin, sodium orthovanadate and phenylmehylsulfonyl fluoride (Sigma-Aldrich, St. Louis, MO). After 30 minutes' incubation on ice, whole tumor lysates were centrifuged at 14000 rpm, 4 °C, for 20 minutes. The supernatant was collected and proteins were quantified via Bradford assay (Bio-Rad). For western blot analysis equal amounts of protein lysates were separated onto CriterionTM TGXTM precast gels (Bio-Rad) and transferred to a polyvinylidene difluoride (PVDF) membrane (Millipore) using Criterion[™] Blotter (Bio-Rad). After blocking in 5% BSA-TBS-T for 1 hour, membranes were incubated with primary antibodies at 4 °C overnight. Secondary antibody-binding was performed at room temperature for 1 hour. After TBS-T washing, protein bands were incubated with LiteAblot PLUS reagent (Euroclone) and detected via ChemiDoc[™] XRS+ System (Bio-Rad). Densitometry analysis was performed through ImageJ software. Detailed information about the used antibodies is available in Table S1, Supplementary Information.

Co-immunoprecipitation

300 µg of tumor cell lysates were incubated overnight with anti-NEU polyclonal antibody (diluted 1:200, Santa Cruz) at 4 °C. After washing in RIPA buffer at

2500 g, 4 °C for 5 minutes, 200 μ l of protein G Sepharose 4 Fast Flow beads (GE Healthcare) were added to each tube. Incubation was performed for 4 hours at 4 °C under gentle rocking. Following washing procedure, the samples were boiled in Laemli loading buffer for 5 minutes: the collected supernatants underwent western blot procedure.

mRNA extraction, RT-PCR and qRT-PCR

Total RNA was extracted from liquid nitrogen cryopreserved tumors via TRIzol® reagent (Life Technologies) following the manufacturer instructions. RNA was quantified by measuring 260 nm absorbance via NanoDrop 1000 spectrophotometer (Thermo Scientific). RNA purity was considered good with A260/A280 ratio \geq 2.0 and A260/A230 ratio \geq 1.7. RNA (2 µg/tube) was reverse-transcribed using the High-Capacity cDNA Reverse Transcription Kit (Applied Biosystems). Semi-quantitative RT-PCR was performed using Perfect Tag DNA polymerase (5-PRIME) and Eppendorf thermal Cycler. SYBR Premix Ex Taq (Tli RNaseH Plus) reagent (Takara) was used for qRT-PCR analysis. β-actin was taken as housekeeping gene and standard curves for target genes and β -actin were included to evaluate reaction efficiency. Experiments were performed in triplicates. A 2-steps amplification program was carried out on Bio-Rad iCycler Thermal Cycler with iQ5 Multicolor Real-Time PCR Detection System. Primers used: Δ16HER2 forward: 5'-CACCCACTCCCCTCTGAC-3'; Δ16HER2 reverse: 5'-GCTCCACCAGCTCCGTTTCCTG-3'; βactin forward: 5'-CAAGGCCAACCGCGAGAAGAT-3': B-actin reverse: 5'-GTCCCGGCCAGCCAGGTCC AG-3'.

Proteasome activity

The chymotrypsin-like activity of the 20S proteasome was assayed on tumor and cell extracts using the fluorogenic substrate N-Succinyl-Leu-Leu-Val-Tyr-7-Amido-4-Methylcoumarin (sLLVY-NH-Mec, Sigma-Aldrich). Briefly, tissues/cells were homogenized on ice via a Potter-Elvehjem apparatus in a buffer consisting of 50 mM HEPES/KOH pH 7.8, 1 mM Dithiothreitol and 0.25 M Sucrose. The lysates were then cleared by centrifugation at 12.000 rpm for 10 minutes in a refrigerated Eppendorf centrifuge. Twenty and 40 µg of total proteins from each tissue sample were incubated at 37°C in 100 mM HEPES/KOH buffer, pH 7.8, 5 mM MgCl₂ and 10 mM KCl. Cell extracts (10 ug) were preincubated for 30 min at 37°C in the same buffer with the addition of different concentrations of resveratrol or with only the vehicle (DMSO). In both cases the reaction was initiated by addition of the fluorigenic substrate to a final concentration of 0.2 mM. The
breakdown of the peptide was monitored for 30/45 min using a fluorescence microplate reader (FLUOstar OPTIMA, BMG Labtech GmbH, Offenburg, Germany) with an excitation wavelength of 355 nm and an emission wavelength of 460 nm. Proteasome activity in each sample, expressed as fluorimetric units min⁻¹ mg⁻¹, was calculated by submitting data to linear regression analysis ($R^2 > 0.99$).

Statistical analysis

Quantitative data are presented as means \pm SEM from three independent experiments. The significance of differences was evaluated with two-tailed Students ttest, or one-way ANOVA followed by Bonferroni posttest. Statistical analysis was carried out with GraphPad Prism5.

AUTHOR CONTRIBUTIONS

AC, BC, WK performed the laboratory work. BM, CR performed UPS analysis. HA, IM performed IHC. AC, BC, AA, MC designed the experiments. AC, BC, CR, BM, MM, AA, MC analyzed the data. AC, BC, AA, MC conceived the study. AA, MC coordinated the study. AC, MC wrote the manuscript. All authors critically discussed the data, read and approved the final manuscript.

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CONFLICTS OF INTEREST

The authors have no conflict of interests to declare.

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Review



Regulation of Cell Signaling Pathways and miRNAs by Resveratrol in Different Cancers

Ammad Ahmad Farooqi¹, Sumbul Khalid² and Aamir Ahmad^{3,*}

- ¹ Institute of Biomedical and Genetic Engineering (IBGE), Islamabad 44000, Pakistan; ammadfarooqi@rlmclahore.com
- ² Department of Bioinformatics and Biotechnology, International Islamic University, Islamabad 44000, Pakistan; sumbul.khalid@iiu.edu.pk
- ³ Department of Oncologic Sciences, Mitchell Cancer Institute, University of South Alabama, Mobile, AL 36604, USA
- * Correspondence: aahmad@health.southalabama.edu; Tel.: +1-251-445-9874

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Abstract: Genomic and proteomic studies have helped improve our understanding of the underlying mechanism(s) of cancer development and progression. Mutations, overexpressed oncogenes, inactivated/downregulated tumor suppressors, loss of apoptosis, and dysregulated signal transduction cascades are some of the well-studied areas of research. Resveratrol has gained considerable attention in the last two decades because of its pleiotropic anticancer activities. In this review, we have summarized the regulation of WNT, SHH (sonic hedgehog)/GLI (glioma-associated oncogene homolog), TGF β 1 (transforming growth factor beta 1)/SMAD, NOTCH, TRAIL (tumor necrosis factor-related apoptosis-inducing ligand), STAT (signal transducer and activator of transcription), and microRNAs by resveratrol in different cancers. The importance of these signaling pathways in cancer progression, along with their modulation by resveratrol, is discussed. Further, we also evaluate the mechanisms and implications of the downregulation of oncogenic miRNAs and the upregulation of tumor suppressor miRNAs by resveratrol, both of which also define its ability to inhibit tumor growth and metastasis. It is envisioned that designing effective clinical trials will be helpful for the identification of resveratrol responders and non-responders and the elucidation of how this phytochemical can be combined with current therapeutic options to improve their clinical efficacy and reduce off-target effects.

Keywords: resveratrol; cell signaling; miRNAs

1. Introduction

Using high-throughput technologies, it has been shown that the bulk tumor includes a diversified collection of cells that harbor characteristically unique molecular features with variable levels of sensitivity to therapeutic options [1,2]. This heterogeneity results in an uneven distribution of genetically distinct subpopulations of tumor cells across and within disease sites (spatial heterogeneity) [3,4]. In addition, tumors are marked by temporal heterogeneity, wherein cells temporally change their molecular makeup [3,4]. Combining high-throughput genotyping platforms and next-generation sequencing technologies has brought us one step closer in the pursuit for genetic variants, from SNPs (single nucleotide polymorphisms) to large-scale copy number variants. Translational and functional studies have demystified the underlying mechanisms and bio-molecular signatures of difficult-to-treat cancers. Natural product chemistry and the discovery of drugs from plants (phytochemicals) has enjoyed a renaissance in the past decade [5,6]. Based on the insights gleaned from decades of research, it seems clear that off-target effects of modern medicines and rapidly developing resistance against different therapeutics are some of the challenges that must be overcome.

Much attention is currently being given to the identification of natural products that can modulate multiple targets, are significantly effective, and minimize off-target effects [6,7]. In accordance with this approach, there is a rapidly growing list of natural products with considerable medicinal importance and substantial pharmacological properties [8].

Resveratrol, a polyphenolic phytoalexin, is an extensively studied phytochemical with remarkable pharmacological properties and a unique ability to modulate multiple targets in different cancers [9]. It regulates oxidative stress, which is an interesting aspect of its anticancer activity [10,11]. Resveratrol has a molecular weight of 228.247 g/mol and a topological polar surface area of 60.7 A² [12]. Because of the rapidly accumulating wealth of information about resveratrol, many review papers have summarized important biological mechanisms targeted by resveratrol for the treatment of different cancers [13–16]. Most recently published reviews have provided a summary of the role of resveratrol in different cancers; however, in recent years, none of the reviews have provided an in-depth and comprehensive overview of the cell signaling pathways targeted by resveratrol in different cancers [17–19]. We have exclusively focused on various signal transduction cascades and the miRNAs that are modulated by resveratrol in different cancers. In particular, in this review, we have summarized the regulation of TGF β 1/SMAD, WNT, SHH/GLI, NOTCH, TRAIL, STAT pathways, and the oncogenic as well as tumor suppressor miRNAs, by resveratrol.

2. Regulation of the TGF β 1/SMAD Pathway

TGFβ1/SMAD pathway is well known to contribute to cancer development and progression (Figure 1). Signalosome formed by phosphorylated receptor-mediated SMADs triggers the accumulation of active SMAD complexes in the nucleus, which transcriptionally upregulate target genes in conjunction with transcriptional factors, histone modifiers, and chromatin-remodeling machinery [20]. In this section, we will provide an overview of the mode of action of resveratrol to inhibit SMAD-mediated intracellular signaling. Resveratrol effectively inhibits SMAD proteins by either affecting post-translational modifications by different enzymes to target SMAD proteins for degradation or by inhibiting the phosphorylation and activation of SMADs.



Figure 1. TGF/TGFR signaling axis. SMAD proteins play a central role in transducing the signals intracellularly. SIRT7 modulates SMAD4 degradation via β -transducin repeat-containing protein (β -TrCP1). SMAD4, β -TrCP1, and SIRT7 complex formation results in shutdown of the TGF pathway. SMAD: Sma Mothers Against Decapentaplegic; β -TrCP: β -transducin repeat-containing protein; CXCL8: chemokine CXC motif, ligand 8; TGF: transforming growth factor; ANGPTL4: angiopoietin-like 4.

In a study demonstrating regulation of the TGF β 1/SMAD pathway by resveratrol, lung metastases were developed in Balb/c mice by intravenous injection of highly metastatic murine 4T1 cells [21]. Further, intravenous injection of the SIRT7-inhibited development of these metastatic nodules and SIRT7-knockdown induced activation of the TGF- β pathway in 4T1 and MDA-MB-231 cells, while SIRT7 overexpression exerted inhibitory effects on the TGF-β pathway. SIRT7 physically interacted with and de-acetylated SMAD4 [21]. Significantly increased levels of acetylated lysine residues of SMAD4 were noted in SIRT7-silenced cancer cells. The binding affinity of SMAD4 for SMAD2 markedly decreased in cells that ectopically expressed SIRT7. When protein synthesis was inhibited by cycloheximide, ectopically expressed SIRT7 promoted SMAD4 degradation, and SIRT7 inhibition protected SMAD4 from degradation machinery [21]. Furthermore, K428R, which mimicked a hypo-acetylated form of SMAD4, accelerated its degradation, whereas K428Q, which resembled a hyper-acetylated form of SMAD4, inhibited its degradation. SIRT7 deletion by CRISPR/Cas9 inhibited HA-SMAD4 ubiquitination, whereas SIRT7 overexpression increased ubiquitination. SIRT7 modulated SMAD4 degradation by β -transducin repeat-containing protein (β -TrCP1). Protein studies have provided evidence of the interaction of SMAD4, β-TrCP1, and SIRT7 [21] (Figure 1). β-TrCP1 inhibition abolished the increased ubiquitination and accelerated SMAD4 degradation caused by ectopically expressed SIRT7. Resveratrol dose-dependently enhanced deacetylation of HA-SMAD4. It also exerted repressive effects on TGF-β1-induced mesenchymal morphology, downregulated SMAD4, and suppressed cellular migration. TGF- β responsive genes ANGPTL4 and CXCL8, required for breast cancer lung metastases and the development of resistance against drugs, were considerably repressed by resveratrol [21].

Resveratrol has been reported to reduce phosphorylated-SMAD2/3 in colorectal cancer LoVo cells [22]. Resveratrol (150 mg/Kg) reduced metastatic lesions in the lungs and liver of mice orthotopically transplanted with LoVo cells. In alveolar rhabdomyosarcoma PLA-802 cells, resveratrol (40 μ mol/L) downregulated SMAD4 [23]. Upon treatment with resveratrol (20 μ mol/L), no significant changes in expression of TGF- β 1 and SMAD4 were noticed; however, at a dose of 40 μ mol/L, resveratrol significantly decreased the expression of SMAD4 and TGF- β 1 [23]. Resveratrol decreased expression of TGF β -2 in SCCs and skin of p53^{+/-}/SKH-1 mice chronically irradiated with UVB [24]. There was a 2–3-fold increase in the invasive capacity of cells that expressed constitutively active Akt. Overexpression of active Akt induced TGF- β 2 in the absence of resveratrol, which suggested a clear association between TGF β 2 and Akt. Active Akt significantly impaired resveratrol-induced inhibitory effects on TGF- β 2. Resveratrol dose-dependently reduced phospho-SMAD2/3 levels and completely abolished the phosphorylation of SMAD2/3 at a dose of 100 μ M [24].

These findings indicate that resveratrol affects the TGF β 1/SMAD pathway via post-translational modifications, either by degrading SMADs or inhibiting their activity by blocking the phosphorylation of SMADs.

3. Regulation of the WNT Pathway

A WNT ligand is a secreted glycoprotein that binds to Frizzled receptors and results in the formation of a larger cell surface complex with low-density lipoprotein-receptor-related protein (LRP5/6) [25] (Figure 2). In the absence of any signal, β -catenin is post-translationally modified by the APC/AXIN/GSK-3 β -complex leading to its ubiquitination and degradation by proteasomal machinery. When the WNT pathway is active, β -catenin gets sequestered away from degradation machinery and moves into the nucleus to trigger the expression of target genes. There has been a focus on strategies to inhibit the transportation of β -catenin into the nucleus [25,26].

Resveratrol can downregulate WNT2 and upregulate AXIN2 in Colo16 cells [27]. Furthermore, there was an earlier induction of apoptosis in resveratrol-treated β -catenin-silenced Colo16 cells [27]. Resveratrol dose-dependently decreased exogenously overexpressed Myc-tagged TCF4 protein in colorectal cancer cells [28] and increased TCF4 phosphorylation through ERK- and p38-MAPK-modulated pathways. Knockdown of TCF4 reduced TCF/ β -catenin-regulated transcriptional activities and sensitized cancer cells to resveratrol-mediated apoptosis [28].



Figure 2. (**A**) WNT/ β -catenin signaling axis. Resveratrol effectively inhibits the nuclear accumulation of β -catenin. β -catenin works synchronously with various proteins to modulate the transcription of different genes; (**B**) SRSF1 inhibits YAP and represses the β -catenin-mediated upregulation of MALAT1; (**C**) β -catenin works with MALAT1 and increases the expression of MMP7 and C-Myc. APC: adenomatous polyposis coli; CK: casein kinase; GSK-3 β : glycogen synthase kinase 3 beta; LRP: low-density lipoprotein-receptor-related protein; MALAT1: metastasis-associated lung adenocarcinoma transcript 1; MMP&: matrix metalloproteinase-7; SRSF1: serine and arginine rich splicing factor 1; TCF: T-cell factor; YAP: YES-associated protein; 65-KD.

Response to resveratrol was noted to be highly heterogeneous among glioma stem cells. Resveratrol inhibited cell proliferation, increased cell mortality, and strongly reduced the motility of the cells [29]. In GBM2, G166, GBM7, and G179 cell lines, both WNT1 and MYC were upregulated, while in G144 cells these two genes were downregulated by resveratrol. FZD4 and TCF7 changed only in 3 out of 7 GSC lines after resveratrol treatment [29]. Resveratrol significantly reduced cyclin D1 and β -catenin in xenograft breast tumors [30]. β -catenin overexpression markedly reduced resveratrol-mediated cytotoxic effects, which indicated that resveratrol inhibited breast cancer stem-like cells and induced autophagy, at least partially, by suppression of the Wnt/ β -catenin cascade [30]. In HCT116 cells, resveratrol reduced β -catenin [31]. Resveratrol did not appear to influence the total levels of GSK-3 β but did decrease GSK-3 β phosphorylation. A β -catenin/Tcf4 reporter assay provided evidence that resveratrol, concentration-dependently, inhibited reporter activity [31].

β-catenin has been shown to interact with different non-coding RNAs and transcriptionally upregulate their expression, thereby stimulating the expression of a target gene network. Resveratrol increases the cytosolic levels of β-catenin with a concomitant inhibition of its nuclear accumulation (Figure 2), with little effects on the total cellular β-catenin [32]. Resveratrol exerted inhibitory effects on the Wnt/β-catenin pathway through the regulation of MALAT1. The use of lithium chloride inhibited GSK3β from binding to β-catenin and triggered Wnt/β-catenin pathway activation. Resveratrol dose-dependently downregulated long non-coding RNA-MALAT1 [32]. Knockdown of MALAT1 impaired the nuclear accumulation of β-catenin, which resulted in the transcriptional repression of MMP7 and c-Myc, while MALAT1 overexpression promoted the transcriptional upregulation of MMP7 and c-Myc (Figure 2). The data clearly suggest that MALAT1 and β-catenin co-existed in the nucleus, and the targeted inhibition of MALAT1 is necessary to inhibit synchronous activity of MALAT1 and β-catenin for the transcriptional repression of target genes [32]. YES-associated protein (YAP)

upregulated MALAT1 transcriptional and post-transcriptional levels, whereas serine/arginine-rich splicing factor 1 (SRSF1) resisted YAP-mediated effects [33]. SRSF1 exerted inhibitory effects on YAP activity and prevented its co-existence with TCF/ β -catenin on the promoter region of MALAT1 [33] (Figure 2). These two reports together are helpful in putting different pieces of an incomplete jigsaw puzzle together. It seems clear that β -catenin co-operates with different proteins to trigger the expression of MALAT1 and works synchronously with MALAT1 to drive the expression of WNT signaling target genes.

Despite these studies on the regulation of the WNT pathway by resveratrol, there remain a few outstanding questions that need to be adequately addressed to understand mechanistic details. For example, the modulation of LRP5/6 and SFRPs by resveratrol has not been sufficiently studied. Future studies need to comprehensively focus on the detailed mechanism(s) of regulation of WNT signaling by resveratrol so that the information can be utilized for the targeting of WNT signaling by resveratrol in clinical settings.

4. Regulation of the SHH/GLI Pathway

Inappropriate activation of the Sonic hedgehog–GLI signaling cascade has been extensively studied in different cancers [34–36]. BCR-ABL is an oncoprotein that re-wires intracellular signaling cascades in chronic myeloid leukemia and Philadelphia chromosome-positive acute lymphoblastic leukemia [37]. In vitro and preclinical studies have shown that imatinib exerted preferential inhibitory effects on the viability and expression of BCR-ABL in imatinib-sensitive K562 cells, but imatinib was not effective against K562R cells that overexpressed BCR-ABL. Both K562R (imatinib-resistant) and parental K562 cells expressed mRNAs of molecules involved in the SHH pathway, including SHH, Smoothened (SMO), Patched (PTCH), and GLI-1. There was a significant reduction in BCR-ABL in GLI-1-silenced K562R and K562 cells. The use of SHH peptide not only enhanced GLI-1 and SHH but also upregulated BCR-ABL in tested cell lines. Resveratrol effectively inhibited SMO and BCR-ABL and exerted inhibitory effects on the nuclear accumulation of GLI proteins to transcriptionally upregulate the expression of cancer promoting genes [37]. PTCH, SMO, and GLI-1 were also inhibited in resveratrol-treated colorectal cancer HCT116 cells [38]. Resveratrol inhibited the nuclear accumulation of GLI-1 in interleukin-6 (IL-6)-stimulated HL-60 cells [39].

Resveratrol and cyclopamine have been reported to synergistically inhibit metastases and reduce the invasive potential of gastric SGC-7901 cancer cells [40]. Resveratrol was noted to inhibit GLI-1 activity and downregulate Snail and *N*-cadherin in SGC-7901 cells. Previously, it has been reported that Snail repressed the expression of E-cadherin, but resveratrol upregulated E-cadherin and markedly reduced the metastasizing potential of SGC-7901 cells [40]. Based on the reports discussed above, resveratrol seems to significantly affects the SHH-Gli pathway.

It is now well established that CpG islands are heavily hypomethylated in cancer cells [41]. Resveratrol enhances the methylation levels of CpG sites within enhancers of MAML2 and GLI2. Interestingly, active enhancers are enriched with H3K27ac. Data obtained through the chromatin-immunoprecipitation technique provided information about the presence of histone marks at MAML2 in cancer cells but its occupancy reduced considerably in resveratrol-treated cancer cells [41]. Occupancy of activating histone marks (H3K9acetylation) and repressive histone marks (H3K27tri-methylation) was biochemically analyzed. Data suggested a 30% decrease in H3K9ac and a 2-fold increase in H3K27me3 occupancy within the MAML2 enhancer, whereas resveratrol induced an increase in DNA methylation levels. OCT1, a transcription factor, transcriptionally upregulated MAML2; however, resveratrol inhibited the binding of OCT1 to the MAML2 enhancer. Resveratrol with a concentration of 15 μ M promoted the accumulation of DNMT3B in the MAML2 enhancer in MCF10CA1a cells, resulting in epigenetic inactivation [41].

5. Regulation of the NOTCH Pathway: A Double-Edged Sword

The NOTCH pathway is involved in the regulation of different stages of cancer [42,43]. Although some reports document efficient inhibition of different proteins of the NOTCH pathway by resveratrol to inhibit cancer, there are conflicting reports that resveratrol can activate the NOTCH pathway, leading to its anticancer activity. Resveratrol has been noted to induce differentiation-associated genes in anaplastic thyroid carcinoma mainly through Notch1 activation [44]. Resveratrol was a strong inducer of TTF1, which increased 4-fold at 25 μ mol/L and 6-fold at 50 μ mol/L in tested cell lines. Significantly elevated TTF2 was observed at 50 μ mol/L in thyroid cancer cells. Moreover, there was an increase (5-fold) in Pax8 in HTh7 cells at a 50 μ mol/L dose of resveratrol. The upregulation of Pax8, TTF1, and TTF2 was observed in resveratrol-treated NOTCH1-competent 8505C cells. However, no detectable rise has been found in the levels of Pax8 or TTF1 in resveratrol-treated, NOTCH1-silenced ATC cells. Tumor volume decreased considerably (~69%) after five injections of resveratrol in mice xenografted with either HTh7 or 8505C cells [44].

Resveratrol (50 μ M) increased both active p53 and NOTCH-1 in glioblastoma cells [45]. Western blot data suggest that expression of the Notch-1 intracellular domain (NICD) was 3.2-fold and 2.9-fold higher in the A172 and T98G cells, respectively, after resveratrol treatment. Similar patterns were observed and p53 was also found to be upregulated as evidenced by 1.2-fold and 1.1-fold higher expressions in A172 and T98G cells, respectively, after treatment with resveratrol [45]. Taken together, the effect of resveratrol on NOTCH signaling seems to be context-dependent. When NOTCH signaling is oncogenic, it is effectively inhibited by resveratrol; however, when it leans towards a tumor-suppressive action, it is potentiated by resveratrol.

6. Regulation of TRAIL Signaling

The discovery of TRAIL revolutionized the field of molecular oncology because of its ability to differentially target cancer cells while leaving normal cells intact [46]. However, circumstantial evidence has also indicated the development of resistance against TRAIL-based therapeutics. TRAIL resistance emerged as a major setback in the standardization of therapy, and attempts have been made to sensitize resistant cancer cells to TRAIL. Analyses of different cancers have shown an imbalance in stoichiometric ratios of pro- and anti-apoptotic proteins. However, over the past 10 years, there has been a worldwide resurgence of studies emphasizing different strategies for restoring TRAIL-induced apoptosis in resistant cancer cells. Resveratrol has shown potential as a TRAIL sensitizer.

Resveratrol has been found to increase the cell-surface expression of NKG2D ligands and DR4 along with the downregulation of decoy receptor 1 (DcR1) in KG-1a cells [47]. A suppressor of cytokine signaling (SOCS3) was found to considerably impair TRAIL-driven apoptosis in cancer cells [48]. SOCS3 overexpression reduced apoptosis in DU145 cells co-treated with resveratrol and TRAIL. Moreover, SOCS3 inhibition increased apoptosis in TRAIL-treated LNCaP and PC-3 cells [48]. Survivin is a frequently overexpressed protein in TRAIL-resistant cancer cells. Resveratrol dose-dependently downregulated survivin in HepG2 cells. Moreover, 10 ng/mL TRAIL and 50 µmol/L resveratrol worked with effective synergy and increased the apoptotic rate up to 49.6% in HepG2 cells [49]. In xenografted tumors, resveratrol upregulated DR4, DR5, Bax, and p27(/KIP1) and inhibited the expression of cyclin D1 and Bcl-2 [50].

7. Regulation of STAT Signaling

Prostate cancer associated transcript 29 (PCAT29), a tumor suppressor, is frequently overexpressed in prostate cancer and downregulated by interleukin (IL-6) in DU145 and LNCaP cells [51]. Significantly enhanced phopsphorylated-STAT3 has been observed following treatment with IL-6 (10 ng/mL) in DU145 and LNCaP cells [51]. STAT3 knockdown induced an increase in PCAT29 expression in both DU145 and LNCaP cells. Mechanistically, it was shown that STAT3 triggered the upregulation of miR-21, which consequently negatively regulated PCAT29 in PCa cells. Resveratrol repressed STAT

signaling and stimulated expression of PCAT29 via repression of miR-21 [51] (Figure 3). Further, protein inhibitor of activated STAT3 (PIAS3) has been found to be downregulated in medulloblastomas, and resveratrol shown to significantly upregulate PIAS3 in UW228-2, UW228-3, and DAOY cells with the repression of p-STAT3 levels [52].



Figure 3. An overview of resveratrol-mediated targeting of multiple signaling pathways. (**A**) TGF/SMAD signaling pathway regulation by resveratrol; (**B**) WNT/Catenin pathway regulation by resveratrol; (**C**) Resveratrol increases negative regulators of STAT signaling (SHP-2, PIAS, and PTP) and inhibits JAK-mediated STAT phosphorylation. STAT3 transcriptionally upregulates miR-21, and targets the tumor suppressor gene PCAT29.

Resveratrol exerts inhibitory effects on the constitutive activation of STAT3 and STAT5. It inhibits the shuttling of STAT3 and STAT5 into the nucleus and significantly reduces the DNA binding affinity of STAT proteins in 786-O and Caki-1 cells [53]. Resveratrol was also found to markedly reduce the constitutive activation of Janus kinases (JAK1 and JAK2) in 786-O and Caki-1 cells. Protein tyrosine phosphatases (PTP and SHP-2) were considerably upregulated in resveratrol-treated 786-O and Caki-1 cells (Figure 3). Targeted inhibition of either PTP or SHP-2 substantially impaired the resveratrol-mediated decrease in the level of phosphorylated-STAT [53]. Resveratrol has also been shown to prevent the activation of JAK, resulting in the inhibition of the JAK-mediated phosphorylation of STAT1 [54].

8. Regulation of Other Signaling Pathways

8.1. AKT and MAPK

Resistance against different chemotherapeutic drugs is a frequently noted mechanism [55]. Docetaxel increased HER-2 in SK-BR-3 cells and induced Akt (Ser 473) phosphorylation within a time period as short as 30 min. Docetaxel induced extracellular signal-regulated kinase (ERK), c-Jun N-terminal kinase (JNK), and P38 phosphorylation, which was significantly inhibited by resveratrol [55]. It has also been noted that a high glucose-driven increase in the levels of phosphorylated-ERK and phosphorylated-p38 were inhibited by resveratrol in Panc-1 cells [56].

8.2. The ATM/p53 Pathway

ATM (ataxia telangiectasia mutated) is an important sensor of DNA damage and transduces the signals to downstream effectors, particularly p53 [57]. In glioblastoma-initiating cells treated with

a combination of temozolomide and resveratrol, phosphorylated-ATM was found to be moderately upregulated, while p53 and phosphorylated-p53 were found to significantly increase. Resveratrol has also been found to be more effective against HCT-116 p53 wild-type colon carcinoma cells, as compared to HCT-116 p53^{-/-} cells [58]. Resveratrol induced DNA damage, as evidenced by the presence of multiple γ -H2AX foci after treatment with 25 μ M resveratrol. DNA-damage-associated signaling was initiated through the activation of ATM kinase. p53 was found to be phosphorylated on serine 15 by ATM in response to resveratrol [58].

8.3. Multiple Signaling Pathways

Being a pleiotropic agent, resveratrol has been reported to target multiple proteins in ovarian cancer, markedly reducing NOTCH2 and HES1 in OVCAR-3 and CAOV-3 cells [59]. In CAOV-3 cells, resveratrol downregulated WNT2 and reduced the nuclear accumulation of β -catenin [59]. Moreover, the accumulation of STAT3 was evident in the nuclei of naïve OVCAR-3 cells, and resveratrol significantly reduced this nuclear accumulation. Although there is general agreement about the multi-protein targeting of resveratrol, there are still important mechanistic details related to the interwoven network of signal transduction pathways that remain to be elucidated.

9. Regulation of MicroRNAs by Resveratrol

In just over two decades, since the discovery of the first microRNA (miRNA), there has been an exponential rise in the number of reports that provide in-depth analysis of regulation of signaling pathways by miRNAs in different cancers [60]. Categorically, miRNAs are classified into tumor suppressor and oncogenic miRNAs. Different strategies are currently being used to increase the expression of tumor suppressor miRNAs and downregulate oncogenic miRNAs. In this section, we will focus on the regulation of oncogenic and tumor suppressor miRNAs by resveratrol (Figure 4).



Figure 4. Resveratrol profoundly affects the miRNA machinery. It inhibits oncogenic as well as tumor suppressor miRNAs to affect the cellular oncogenic machinery, resulting in reduced expression of oncogenes and increased expression of tumor suppressor genes.

9.1. Regulation of Oncogenic miRNAs

Insulin-like growth factor binding protein-3 (IGFBP3) has been noted to be frequently downregulated in acute lymphocytic leukemia (ALL) cells [61]. Detailed mechanistic insights revealed that miR-1290 and miR-196b quantitatively controlled IGFBP3 in the ALL cell line. More importantly,

resveratrol considerably reduced the expression of miRNA-196b/miRNA-1290 in TALL-104/SUP-B15 cell lines. The research findings were suggestive of a resveratrol-induced upregulation of IGFBP3 (mRNA, protein) in SUP-B15 as well as TALL-104 cells. Resveratrol arrested TALL-104 cells at the G1 phase and arrested SUP-B15 cells at the S phase. Resveratrol strongly induced apoptosis in the SUP-B15 and TALL-104 cells [61].

Activation of natural killer cells is a well-coordinated mechanism, triggered by signals derived from activating receptor ligation [62]. Natural killer group-2 member-D (NKG2D) or killer cell lectin-like receptor, subfamily-K, member-1 (KLRK1) is an extensively studied activating receptor of natural killer (NK) cells. In humans, the NKG2D ligand (NKG2DLs) family has eight glycoproteins present on the cell surface, including the major histocompatibility complex class I chain-related proteins A and B (MICA/B) [62]. Resveratrol was found to dose-dependently enhance MICA and MICB on the surface of breast cancer cells. Resveratrol-mediated increases in MICA and MICB were more pronounced in the MDA-MB-231 and BCap37 cell lines. Transfection of BCap37 cells with miRNA-17 inhibitors resulted in the upregulation of MICA and MICB, while transfection of BCap37 cells with miRNA-17 mimics resulted in the downregulation of MICA and MICB. c-Myc binding sites had previously been identified in transcriptional initiation sites in miR-17-92 clusters, and c-Myc triggered an increase in the expression of this gene cluster [62]. Resveratrol dose-dependently repressed c-Myc (mRNA, protein) in treated breast cancer cells, which consequently resulted in a reduction of miR-17. c-Myc knockdown resulted in a reduction of pri-miR-17-92 and miR-17, whereas c-Myc-overexpression markedly enhanced pri-miR-17-92 and miR-17 [62].

A chromatin immunoprecipitation assay revealed that resveratrol decreases the association of NF-KB with FOXC2 promoter [63]. Specific Akt inhibition resulted in the suppression of phosphorylated-Akt, FOXC2, and mobility of A549 cells. Resveratrol-mediated inhibitory effects on NF-κB activity were impaired in cancer cells with constitutively active Akt [63]. PP2A/C, a catalytic subunit of serine/threonine phosphatase PP2A, inhibited Akt activity by Akt dephosphorylation. Resveratrol, dose- and time-dependently, increased the expression and activity of PP2A/C protein in cancer cells. Resveratrol enhanced the levels of PP2A/C via the inhibition of miR-520h. Intriguingly, the resveratrol-mediated increase in PP2A/C was dramatically abolished after restoration of miR-520h expression [63]. For a deeper understanding of the crosstalk among these proteins, molecular analysis was conducted in cervical cancer cells, and the results suggested that the PP2A/C-driven dephosphorylation of the inhibitor of kappa-B kinase (IKK) resulted in its inactivation [64]. Inactivation of IKK protected IkB from phosphorylation by IKK; consequently, activation of NF-kB was inhibited. Inactivation of NF- κ B resulted in transcriptional repression of its target gene, CXCR4 [64]. These findings provide insight into the mechanisms by which miR-520h quantitatively reduces PP2A/C to facilitate the tumor-promoting activities of NF- κ B via the transcriptional upregulation of its target genes.

9.2. The Regulation of Tumor Suppressor miRNAs

Pyruvate kinase M2 (PKM2) has been found to be overexpressed in different cancers [65]. Resveratrol, dose-dependently, increased the mRNA and protein expression levels of GRP78, CHOP, and caspase-12 in both HeLa and DLD1 cells. A reversal of these changes was observed in PKM2-overexpressing cancer cells. Mechanistically, it was shown that resveratrol repressed PKM2 by increasing the expression of miR-326. Interestingly, resveratrol-mediated repressive effects on PKM2 were impaired in miR-326 inhibitor-transfected cancer cells [65].

Stem cell factor (SCF, KITLG) is frequently overexpressed in colorectal cancer cells [66]. KITLG is quantitatively controlled by miR-34c. Studies have shown that p53 transcriptionally upregulated miR-34c in colorectal cancer tissues and cell lines. Resveratrol was noted to increase p53 in p53-positive HT-29 cells, and miR-34c upregulation was more pronounced in p53-positive HT-29 cells, as compared to p53-negative HCT-116 cells [66]. Overexpression of Isoform A2 of eukaryotic translation elongation factor (eEF1A2) played a contributory role in breast cancer progression [67]. miR-663 and miR-744

have been found to negatively regulate eEF1A2 in breast cancer. Resveratrol induced a 4.5-fold upregulation of miR-663 and a two-fold increase in miR-744. It also reduced EEF1A2 in breast cancer cells. A resveratrol-induced decrease in EEF1A2 levels was not found in MCF7 cells transfected with inhibitors of miR-663 and miR-744 [67]. Resveratrol was noted to reduce MMP2 via upregulation of miR-328 in osteosarcoma cells [68]. The resveratrol-mediated suppressive effects on MMP2 were impaired in HOS cells transfected with miR-328 inhibitors, whereas transient or stable overexpression of miR-328 markedly reduced the invasive potential of HOS cells [68].

10. Resveratrol in Clinical Trials

MPX, powdered muscadine grape skin that contains ellagic acid, resveratrol, and quercetin, was tested for efficacy in biochemically recurrent prostate cancer patients [69]. 6 out of 14 patients dropped out of the ongoing trial because the disease progressed post-treatment for a median of 15 months. Seven patients remained in study. More importantly, the lack of dose-limiting toxicities was encouraging even at a high dose of 4000 mg/day [69].

Randomized double blind placebo control trials have gained appreciation as the "gold standard" of epidemiological studies. Recently, a trial was conducted in which 22 biochemically recurrent prostate cancer patients were enrolled [70]. These patients had a moderate rise rate. Doubling time of prostate specific antigen (PSA) was 4–15 months with no evidence of metastasis. A non-significant rise in the log-slope of PSA was experienced by the treatment group. Pre-treatment doubling time was 10.2 months, whereas post-treatment doubling time was 5.5 months. However, no change in the log-slope of PSA was experienced by the placebo group. Doubling time before treatment was 10.8 months, while the doubling time after treatment was 10.9 months [70].

A Phase I clinical trial was conducted where colon cancer patients were enrolled in a study designed to evaluate the effects of low doses of resveratrol-containing freeze-dried grape powder (GP) and a plant-derived resveratrol formulation on the Wnt signal transduction cascade in the colon [71]. Patients treated with resveratrol/GP did not show any change in the Wnt target gene expression [71]. In another study, SRT501, micronized resveratrol, was given 5.0 g daily for 2 weeks to colorectal cancer patients. SRT501 was also given to patients with liver metastases scheduled to undergo hepatectomy [72]. The mean plasma level of resveratrol after single administrations of SRT501 (up to 2287 ng/g) [72]. The promising pre-clinical data has led to the interest in clinical evaluation of resveratrol. More elaborate trials need to be conducted to further establish the clinical relevance of resveratrol's anticancer properties.

11. Concluding Remarks

Deregulation of spatio-temporally controlled cell signaling pathways contributes to cancer initiation, progression, and its metastatic spread. Therefore, the identification of novel anticancer therapeutics, such as natural products with significant anticancer activity and an ability to target multiple proteins of oncogenic pathways, is required. Resveratrol has been shown to modulate key regulators of oncogenic signaling pathways. It strongly inhibits the TGF/SMAD pathway and reduces phosphorylated SMADs, resulting in the inhibition of cancer cell proliferation and metastasis. Resveratrol has shown experimentally verified activity against WNT signaling and can inhibit the translocation of β -catenin into the nucleus. Resveratrol, context-dependently, regulates the NOTCH pathway in cancer cells, all of which underlines its flexible and potent anticancer activity. Reduced apoptosis is a hallmark of aggressive cancer cells, and resveratrol re-balances pro- and anti-apoptotic proteins to improve the efficacy of TRAIL-based therapeutics. It seems exciting to note that resveratrol may prove to be a clinically effective agent; however, lower bioavailability is a major shortcoming that needs to be overcome. In accordance with this idea, nanotechnological strategies are currently being tested to enhance the bioavailability of resveratrol. Resveratrol has been shown to efficiently upregulate various tumor suppressor miRNAs in different cancers, and its suppressive effects on

oncogenic miRNAs have also been well documented. Keeping in view the multi-targeted approach and its robust anticancer effects involving multiple signaling pathways and molecular targets, resveratrol has enormous potential to be considered as an important and pharmacologically effective agent in the fight against cancer.

Conflicts of Interest: The authors declare no conflict of interest.

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Review Cancer Chemoprevention by Resveratrol: The p53 Tumor Suppressor Protein as a Promising Molecular Target

Danielly C. Ferraz da Costa¹, Eliane Fialho^{2,*} and Jerson L. Silva^{3,*}

- ¹ Instituto de Nutrição, Universidade do Estado do Rio de Janeiro, Rio de Janeiro, 20550-013, Brazil; danielly.costa@uerj.br
- ² Instituto de Nutrição Josué de Castro, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil
 ³ Instituto de Bioquímica Médica Leopoldo de Meis & Instituto Nacional de Ciência e Tecnologia de Biologia Estrutural e Bioimagem, Universidade Federal do Rio de Janeiro, Rio de Janeiro, RJ, 21941-902, Brazil
- Correspondence: fialho@nutricao.ufrj.br or fialho@ufrj.br (E.F.); jerson@bioqmed.ufrj.br or jerson_silva@uol.com.br (J.L.S.); Tel.: +55-21-3938-6799 (E.F.); +55-21-3938-6756 (J.L.S.)

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Abstract: Increasing epidemiological and experimental evidence has demonstrated an inverse relationship between the consumption of plant foods and the incidence of chronic diseases, including cancer. Microcomponents that are naturally present in such foods, especially polyphenols, are responsible for the benefits to human health. Resveratrol is a diet-derived cancer chemopreventive agent with high therapeutic potential, as demonstrated by different authors. The aim of this review is to collect and present recent evidence from the literature regarding resveratrol and its effects on cancer prevention, molecular signaling (especially regarding the involvement of p53 protein), and therapeutic perspectives with an emphasis on clinical trial results to date.

Keywords: resveratrol; cancer; signal transduction; p53; clinical trials

1. Introduction

Cancer is a source of significant and growing mortality worldwide, with an increase to 19.3 million new cancer cases per year projected for 2025. More than half of cancer cases and mortality occur in low- and middle-income countries [1,2]. Current treatments for cancer include surgery, radiotherapy and systemic treatments comprising cytotoxic chemotherapy, hormonal therapy, immunotherapy, and targeted therapies [3].

Epidemiologic and experimental studies have suggested favorable effects of dietary polyphenols through their anti-carcinogenic properties. Resveratrol represents a group of diet-derived cancer chemopreventive agents encompassing, among others, curcumin, tea polyphenols, probiotics, and lycopene, which have attracted great interest in the cancer chemoprevention community because of their ability to minimally engage this process. Thus, these agents have been explored as potential therapeutic agents in humans [4].

The aim of this review is to collect and present recent evidence in the literature regarding resveratrol and its effects on cancer prevention, molecular signaling (especially regarding the involvement of the p53 protein), and therapeutic perspectives, with an emphasis on clinical trial results.

2. Cell Signaling Pathways Regulated by Resveratrol in Cancer

Resveratrol (3,4',5-trihydroxy-trans-stilbene) is a naturally occurring polyphenol that is found at low concentrations in more than 70 plant species, including grapes, cranberries and peanuts, as

well as in a number of herbal remedies [5]. Resveratrol from grapes is efficiently extracted during the wine-making process, and it has been speculated that red wine, in particular, may be the most important dietary source of this microcomponent [6].

In PubMed (http://www.ncbi.nlm.nih.gov/pubmed/), a search for "Resveratrol and Cancer" generated 2325 hits (April 2017). Among its wide range of biological activities, resveratrol has attracted considerable attention due to its role in regulating multiple signal transduction pathways involved in carcinogenesis. Since 1997, when Jang et al. [7] first reported the in vivo antitumor properties of resveratrol, accumulating data have demonstrated its ability to modulate a number of intracellular mediators in cancer initiation, promotion and progression. Therefore, many chemopreventive and chemotherapeutic mechanisms to prevent, arrest, or delay tumor development by this microcomponent have been proposed [5,8–10].

Resveratrol regulates a variety of processes and signaling pathways that involves procarcinogen bioactivation and carcinogen detoxification [11,12]; reduction of oxidative stress [13] and inflammation [14]; apoptosis induction through the activation of both extrinsic and intrinsic pathways [15–20]; and other anticancer effects [21,22]. Resveratrol affects the three phases of carcinogenesis, tumor initiation, promotion and progression, and it also suppresses the final steps of carcinogenesis, e.g., angiogenesis and metastasis [11,23]. Resveratrol also impacts mitochondrial functions (the respiratory chain, oncoproteins, gene expression, among others), including those directly involving the p53 protein tumor suppressor protein [24]. Finally, in various cancer types, resveratrol behaves as a chemosensitizer that lowers the threshold of cell death induction by classical anticancer agents and counteracts tumor cell chemoresistance [25,26].

In vitro and in vivo studies have shown that resveratrol can act as a tumor-initiation suppressor by modulating phase I and phase II cytochrome P450 enzymes (CYPs) [5,12,27–30]. Resveratrol blocks the transcriptional activation of CYPs and inhibits the activity of CYP1A1, CYP1B1 and CYP1A2, which are phase I enzymes responsible for activating xenobiotics, thus halting the transformation of procarcinogen agents into potential carcinogens [12,27,28]. Additionally, resveratrol enhances the expression and/or activity of phase II enzymes, including glutathione peroxidase, glutathione S-transferase, UDP-glucuronyltransferase, NAD(P)H:quinone oxidoreductase, and heme oxygenase, among others [5,29,31], subsequently stimulating carcinogen detoxification processes.

The role of resveratrol in the intracellular redox status has been described in many studies. Like other polyphenols, this microcomponent acts as an important cellular antioxidant, and its effects are dependent on the concentration tested and the cell type used. However, it has been proposed that resveratrol may also act as a pro-oxidant agent, representing one of the antineoplastic mechanisms of action involved in tumor cell death. Likewise, resveratrol has been shown to decrease the mitochondrial membrane potential and increase reactive oxygen species (ROS) generation, thus promoting apoptosis [32,33].

Some effects of resveratrol have been attributed to its estrogenic activity resulting from its structural similarity to diethylstilbestrol, a synthetic estrogen. Resveratrol can bind to estrogen receptors and may function as an agonist or antagonist, leading to opposite responses depending on the concentration, competition and expression of estrogen receptors in the cells. In MCF-7 human breast cancer cells, for example, which express these receptors, resveratrol may act as a superagonist [34].

Resveratrol is recognized as a potent tumor growth inhibitor in diverse experimental models. Previous studies have established its anticancer effects in a variety of cultured tumor cell lines, including colon [35–37], breast [19,38,39], prostate [40,41], pancreatic [42–44], lung [19,45,46], melanoma [47,48], glioma [49,50], and leukemia cells [51,52], among others. It has been suggested that the anti-proliferative properties of this microcomponent are related to its capacity to block DNA synthesis and to interfere with various stages of cell progression by regulating the machinery of proteins involved in cell cycle control. Hsieh and colleagues [53] first reported the ability of resveratrol to control growth and cell cycle transitions in human breast carcinoma cell lines with different metastatic potentials: highly invasive MDA-MB-435 and the minimally invasive MCF-7 cells. Resveratrol exerts

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a greater inhibitory effect on MDA-MB-435 cells, in which a reduction of the fraction of cells in the G1 phase and a corresponding accumulation of cells in S phase was observed. Since then, many other studies have reported that resveratrol at micromolar concentrations arrests the cell cycle of a variety of human cancer cell lines at the G1/S transition, in S phase or in the G2/M phase [5,54,55]. Although several studies have found that the induction of cell cycle arrest by resveratrol is a reversible process and does not trigger apoptosis, many other authors have reported that this process is often followed by apoptotic cell death [56].

Investigations regarding the effects of resveratrol on apoptosis induction in tumor cells have revealed that this compound can stimulate cell death by modulating proteins involved in both the intrinsic and extrinsic apoptotic pathways [56]. Numerous lines of evidence suggest that resveratrol affects the activation of pro-apoptotic and the inhibition of anti-apoptotic molecules. These mechanisms have been described in culture cells and in vivo in tumor models that have been chemically induced in animals and xenographic models in nude mice [55]. Studies suggest that resveratrol-mediated apoptosis includes the activation of death receptors such as Fas and TRAIL; the activation of Bax, Bak, PUMA, Noxa and Bim; and the inhibition of Bcl-2 and Bcl-XL. Some of these responses are mediated by the activation of the p53 tumor suppressor protein by resveratrol, as will be later discussed.

In addition, resveratrol demonstrates important anti-angiogenic effects, thus contributing to the reduction of the metastatic potential of tumor cells. The following mechanisms are involved in this process: the inhibition of extracellular matrix metalloproteinases gene expression, such as MMP-2 and MMP-9, which are involved in tumor invasiveness; and the inhibition of the expression of HIF-1 α and VEGF, factors that are directly related to new blood vessel formation [54,55].

Although some of the anti-carcinogenic effects of resveratrol have already been shown to be triggered by the activation of extracellular receptors [57], there is evidence that its internalization by cells is necessary for the activation of some specific intracellular targets. It has been demonstrated by multiphoton microscopy (two-photon excitation) that resveratrol, but not its glycosylated or sulfated metabolites, is efficiently captured by neuroblastoma cells, allowing this molecule to exert its antitumor effects, unlike metabolites [58]. Additionally, the importance of cell membrane microdomains in the early biochemical events triggered by resveratrol resulting in cancer cell death, as well as in its absorption and distribution, has been previously described. Resveratrol accumulates in lipid rafts and is then taken up by cells through raft-dependent endocytosis. These events allow for the activation of kinase pathways and redistribution of cell death receptors within lipid microdomains, ultimately leading to apoptotic cell death [17].

Although diverse in vitro and cell culture experiments have described the pro-apoptotic potential of resveratrol, a study conducted in a xenograft model has shown that this compound can inhibit tumor growth in vivo when administered orally, but there is no evidence of apoptosis induction. This finding may be due to the low bioavailability of resveratrol in animals. However, the tumor growth inhibition can be explained by other mechanisms that are independent of a pro-apoptotic effect, such as the anti-proliferative and anti-angiogenic activity of resveratrol [59]. The systemic administration of resveratrol inhibits the initiation and growth of tumors in a variety of cancer models in rodents. The efficacy of low daily doses of resveratrol (200 μ g/kg body weight, for example) in animals with induced colon carcinogenesis suggests that even low concentrations of the compound, such as those obtained by the ingestion of red wine, could be therapeutic in some cases. However, the protective effects of resveratrol are observed more frequently when higher and pharmacologically achievable concentrations are used [60]. There are also studies showing that resveratrol, when administered in animals through peritumoral and intratumoral injections, presents a bioavailability in plasma and tumor significantly higher than that found after oral administration, thus improving the responses of tumor cells to this compound [58].

In addition, studies regarding the effects of resveratrol on in vivo models of spontaneous carcinogenesis are limited and contradictory. Resveratrol supplementation in these experimental models has shown positive, neutral as well as negative outcomes, depending on resveratrol route of

administration, dose, tumor model, species, and molecular properties intrinsic to the cancer cell type as already described by others [21,61,62].

Because of these pleiotropic effects, scientists consider resveratrol to have potential as an anticancer drug, and efforts have focused on obtaining a thorough understanding of its mechanisms of action.

3. The p53 Tumor Suppressor Protein as a Chemotherapeutic Target of Resveratrol

p53 is a critical tumor suppressor protein that has an essential role in cancer prevention. Wild-type p53 blocks tumor development through the induction of cell cycle arrest and/or apoptosis. As a transcription factor, p53 regulates the transcription of specific target genes involved in these processes, thus triggering growth arrest, senescence, cell differentiation and/or cell death under different stress conditions, such as DNA damage, oncogene activation, hypoxia, and telomere erosion, among others [63–65].

The p53 pathway is extremely sensitive to small amounts of DNA molecule damage, which is crucial for the early detection of genetic lesions in tumors [66]. In response to this damage, the activity of specific proteins that are responsible for p53 activation is stimulated, such as checkpoint 2 protein (Chk2). Chk2 is a serine/threonine kinase and, when phosphorylated by ATM, may activate p53, thus promoting its stabilization through phosphorylation at the serine 20 residue, which prevents MDM2-mediated p53 degradation [67]. Consequently, p53 stabilization leads to the activation of *cip1*, one of its main target genes. The *cip1* product is the p21 protein, which acts as an inhibitor of cyclin-dependent kinases (CDKs) in G1 phase of the cell cycle. CDKs allow the transition from G1 to S phase and from G2 to M phase, thus promoting the synthesis and replication of DNA and cell division. Inhibition occurs by preventing the phosphorylation of several regulatory proteins, blocking cell cycle progression [68].

p53 also modulates cell death pathways by mechanisms that are dependent or independent of its activity as a transcription factor. p53-mediated apoptosis occurs through the induction of the transcription of its target gene, whereas p53-independent apoptosis occurs mainly by the interaction of p53 with anti-apoptotic or pro-apoptotic proteins. Numerous studies have shown that p53 can induce the expression of proteins involved in both intrinsic and extrinsic apoptotic pathways [69]. Some mitochondrial proteins show increased expression in response to p53, such as NOXA, PUMA and p53AIP1. Additionally, p53 stimulates the transcription of members of the pro-apoptotic Bcl2 gene family, such as Bax and Bak, allowing the release of cytochrome c into the cytoplasm and their binding to protease activating factor apoptotic (Apaf-1), which leads to the oligomerization of Apaf-1 complex/caspase 9 (apoptosome). This complex recruits pro-caspase 9 and activates effector caspases. p53 can also promote apoptosis through the activation of death receptors, including Fas, DR4 and DR5 [70].

The ability of wild-type p53 overexpression to induce apoptosis may be a major reason why cancer cells frequently exhibit disabled p53 or p53-mediated pathways during the oncogenic process. The same genetic changes that cause the loss of apoptosis during tumor development may also result in tumor chemoresistance to anticancer therapies that kill tumor cells by apoptosis. Elucidation of the mechanisms involved in these cellular responses may provide insights into strategies to induce cell death and suggest new targets for improving cancer treatment.

Consistent evidence suggests that resveratrol can induce p53-dependent cell death in a variety of cancer cell lines [19,71–75]. Previous studies have demonstrated that this microcomponent promotes the activation and stabilization of cellular levels of p53 protein in tumor cell cultures by inducing post-translational modifications, such as phosphorylation and acetylation. Such modifications are required for the transcriptional activation of p53-responsive genes [76]. Interestingly, resveratrol and other polyphenolic compounds can also trigger apoptosis independently of the p53 cellular status. Alternative mechanisms, including the role of p73, a p53-related tumor suppressor, have been reported in recent studies [77].

Resveratrol-induced p53 activation and apoptosis pathways have been shown to be mediated by MAP kinases (mitogen-activated protein kinases). She and colleagues [72] demonstrated for the first time that resveratrol could increase endogenous levels of p53, especially in the phosphorylated state, in epidermal JB6 cells, which constitute a well-developed model of cell culture to study tumor progression. Likewise, levels of phosphorylated protein kinases (ERKs, p38 kinase and JNKs) increase in the presence of resveratrol in a time-dependent manner [73]. In MCF-7 human breast cancer cells, a mechanism has been suggested in which resveratrol, when binding to an integrin located in the plasma membrane, triggers the activation of ERKs, which in turn phosphorylate p53 protein [57].

In MCF-7 cells, the mechanisms by which resveratrol induces cell death appear to involve the activation of MAP kinases (MAPK and ERKs 1 and 2), which is associated with the phosphorylation and acetylation of p53 at serine residues [78]. Other authors have demonstrated that in these cells, resveratrol treatment resulted in a dose-dependent inhibition of cell growth and an accumulation of cells in S phase of the cell cycle. In addition, the anti-proliferative effects of resveratrol are associated with inhibition of cyclin D and CDKs and induction of p53 and the inhibitor of CDKs, p21. In these cells, resveratrol-induced apoptosis involves the activation of caspase 9, reduced expression of the anti-apoptotic proteins Bcl-2 and Bcl-xL and increased levels of the pro-apoptotic Bax protein [79].

Another study identified the role of p53-dependent and -independent pathways in resveratrol-induced apoptosis in breast cancer cells and showed that this compound could induce cell death in cells expressing wild-type p53 but not in those expressing a mutant form of the protein [71]. In cancer cells derived from lung (A549), liver (HepG2), thyroid (FTC 236 and FTC 238), and osteosarcoma cells (SJSA1), among others, the anti-proliferative and pro-apoptotic effects of resveratrol have been shown to be mediated by p53 [80–82]. In prostate cancer cells, resveratrol increased the expression of p53-p(ser15) and/or p53-ac(lys382) and total p53 protein without a change in p53 mRNA. This compound also induced p53 translocation to mitochondria and promoted cell cycle alterations, as well as the induction of apoptosis [83–87].

A study by our group highlighted that, despite the p53-independent apoptosis reported for some cancers, a functional wild-type p53 is required to increase the sensitivity of tumor cells to resveratrol. We showed that transient transfection of a wild-type p53 gene caused H1299 lung cancer cells ($p53^{-/-}$) to become more responsive to the pro-apoptotic properties of resveratrol, similar to the findings in p53-positive MCF-7 cells. These findings suggest a possible therapeutic strategy based on the use of resveratrol for the treatment of tumors that are typically unresponsive to conventional therapies due to the loss of normal p53 function [19].

In the last 15 years, our group has also evaluated the stability and aggregation properties of wild-type and mutant p53. We have previously demonstrated the formation of different types of aggregates after the physical induction of p53 core domain (p53C) unfolding [88] and the ability of a small cognate double-stranded DNA to stabilize both p53C and full-length p53, thus rescuing aggregated and misfolded species of the protein [89]. In addition to these in vitro studies, we used co-localization assays to detect p53 aggregates in archived samples of breast cancer tissues expressing the p53 mutant R248Q and other p53 hot-spot mutants [90]. We have also shown that hot-spot mutants have a greater tendency to aggregate than wild-type p53. Using different techniques, we demonstrated the amyloid nature of the aggregates. It has been demonstrated that seeding p53C R248Q mutant oligomers and fibrils triggers the aggregation of wild-type p53, a behavior typical of a prion. We also observed the co-localization of full-length p53 and aggregates in breast cancer cell lines. In MDA-MB 231 cells, R280K p53 mutant expression revealed a massive accumulation of p53 aggregates in the cell nucleus [91]. Co-aggregation of mutant p53 with other proteins has also been described and may lead to a gain-of-function phenotype. Mutant p53 aggregation appears to occur together with its paralogs p63 and p73 [92–94]. Amyloid aggregates of mutant p53 have also been discovered in other types of malignant tumors, such as malignant skin tumors [95] and ovarian cancer [96]. These findings may reveal the biological significance of the prion-like behavior of oncogenic p53 mutants and help with the development of new strategies to disrupt the formation of aggregates [91,97–99].

Resveratrol has been shown to inhibit amyloid aggregation by binding to several amyloidogenic proteins such as transthyretin [100–102], the islet amyloid polypeptide (IAPP) [103], amyloid beta peptide [104] and alpha-synuclein [105]. Our group has studied the interaction of resveratrol with p53 and evaluated its effect on p53 amyloid aggregation [106,107]. The results have shown that part of the anti-tumoral effects of resveratrol might be related to the inhibition of p53 aggregation.

All together, these data demonstrate the involvement of the p53 pathway in the effects triggered by resveratrol in cancer cells, as summarized in Figure 1.



Figure 1. The involvement of the p53 pathway in the effects triggered by resveratrol in cancer cells.

4. Bioavailability of Resveratrol

The low bioavailability and extensive metabolism of resveratrol are a constant source of concern regarding whether the concentrations used for most in vitro studies are even relevant in vivo [108]. One of the biggest challenges for resveratrol in therapy is its poor bioavailability. Due to its rapid phase II metabolism in the liver and intestine [108,109], the bioavailability of ingested and intravenous doses of resveratrol is unable to achieve pharmacologically active concentrations in plasma [110], but the enterohepatic recirculation may contribute to a delayed elimination of the drug from the body and introduce a prolonged effect. By its binding to plasmatic proteins, resveratrol also exhibits a prolonged effect [11].

It is clear that only a small fraction of ingested resveratrol reaches the body as the parent compound. Furthermore, the amount of resveratrol ingested from dietary sources, such as red wine and juices, among others, would very rarely exceed 5 mg, resulting in plasma levels that are either not detectable or are orders of magnitude below the micromolar concentrations employed in vitro. The administration of approximately 25 mg of resveratrol results in plasma concentrations of the free form ranging from 1 to 5 ng/mL [111]; the administration of higher doses (up to 5 g) produced concentrations of free resveratrol up to approximately 500 ng/mL, or just over 2 μ M [112].

The actual plasma level and absorption kinetics are highly dependent on other compounds present in the dietary matrices. Therefore, a higher degree of bioavailability has been observed when resveratrol is obtained through wine and/or ingestion via the diet as a single pure compound [113].

Pignatelli et al. [114] observed a mean increase of 1 μ M resveratrol in the plasma upon ingestion of 300 mL of red wine a day for 15 days. The actual resveratrol level in the wine was not known in these experiments, but assuming a mean level of resveratrol in red wine of 8.2 μ M indicates a relatively high bioavailability [115]. Similarly, a comparison of the metabolic profile of resveratrol as a component of red wine and of grape extract revealed reduced resveratrol absorption and an extended presence in the gut when resveratrol was a component of grape extract [116].

Approximately 20–30% of resveratrol is not recovered in urine or feces [108], causing one to question whether resveratrol is still present in cells throughout the body. It is possible that resveratrol is associated with lipid compartments and released slowly [117].

Some studies have emphasized that other polyphenols present in red wine, such as quercetin, catechin, and gallic acid, could function as potential chemopreventive agents [118–120]. From this perspective, the research group led by Dr. Latruffe has previously shown that a mixture of polyphenolic extracts from grape vine shoots exhibits superior anti-proliferative activity in colon cancer cells to resveratrol alone due to a synergistic interaction between polyphenols [121,122].

The combination of resveratrol with various stilbenes did show synergism (with pterostilbene and polydatin) when analyzing the antioxidant as well as the cytostatic effects [123,124]. The combination of curcumin with resveratrol has been tested in various in vitro models, with the antioxidant capacity, cytostatic effects, and induction of apoptosis being evaluated [125]. Various flavonoids have been tested in combination with resveratrol, including chrysin, quercetin, catechin, genistein, and combinations of several flavonoids. The effects varied depending on the measured activity and combinations of the tested compounds. In general, the same response, but at lower concentrations, was most often observed by using the combined compounds [117]. The role of ethanol is also potentially important in improving the solubility of polyphenols and altering the cell membrane fluidity for cellular uptake, while a high level of ethanol could counteract the beneficial effects of polyphenols [122].

The metabolism of resveratrol by the human microbiota is another confusing factor in relation to the level of resveratrol and metabolites in the body. A changed metabolite profile was observed when using human fecal microbiota [126], which is why metabolism by the gastrointestinal microbiota is also relevant. Aires et al., 2013 [127] have provided significant new insights into the molecular mechanism of resveratrol, and their data support the notion that, despite low bioavailability in vivo, the biological effects of resveratrol could be mediated by its metabolites.

Modifications of resveratrol stability, chemical structure, and metabolism could alter its cellular and molecular targets and could be crucial for improving or decreasing the efficiency of its chemopreventive properties [25]. Interest in the bioproduction and chemical synthesis of stilbenes has also emerged to identify highly active molecules that could be used for medical applications, especially for cell proliferation inhibition [128]. Modification of the hydroxylation and methoxylation patterns of resveratrol had inhibitory effects on the human colorectal tumor SW480 cell line and no effects on non-tumor cells (IEC18 intestinal epithelial cells), demonstrating the selectivity of these molecules for cancer cells [129].

Cisplatin, carboplatin, and oxaliplatin are commonly used chemotherapy drugs that crosslink DNA in rapidly growing cells. In most experiments, an additive effect and sometimes a synergistic effect has been observed on the reduction of the cell viability of various cancer cell lines [130,131]. Similar effects were observed with DNA intercalating drugs such as doxorubicin and docetaxel [132], topoisomerase inhibitors (such as etoposide) [133], and nucleotide analogs (fluorouracil, fludarabine, cladribine, gemcitabine, clofarabine, and decitabine) [134]. Additionally, the combination of resveratrol with DNA-alkylating substances (cyclophosphamide, temozolomide, melphalan, and carmustine) resulted in a potentiation compared with the effect of the drug alone [135]. Reduced or counteracting effects of resveratrol have also been observed when resveratrol is combined with inhibitors of microtubules (vinblastine and paclitaxel), depending on the order of treatment [130]. Similarly, the cytotoxic effect of the proteasome inhibitor MG132 is reduced by resveratrol [51]. In several cases, a synergistic effect has been postulated.

Resveratrol may act in an additive or synergistic manner with other polyphenols and may influence the metabolism or activity of other drugs. The synergism of various polyphenols with resveratrol has been observed experimentally [123,136–138] and underlies the effects of many nutraceutical formulations.

This challenge, the use of natural or synthetic analogs with improved bioavailability or more potency than resveratrol, as well as the combinations of drugs that provide a synergistic effect or improved bioavailability are promising strategies, as in the case of quercetin and other flavonoids [139]. This last method is very attractive as an anticancer drug therapy because the combination of drugs might result in the use of lower doses of individual compounds, leading to better pharmacological action due to additive or synergistic effects, and less collateral effects on the organism [140,141].

Additionally, nanoencapsulated resveratrol has shown enhanced bioavailability relative to the parent compound [142,143]. Encapsulation and the use of alternative routes of uptake have also been explored [144,145].

5. Clinical Trials and Therapeutic Perspectives for the Use of Resveratrol

It is important to note that often there are discrepancies between the doses of resveratrol used in cells and levels obtained in vivo. For example, many studies showing an effect of resveratrol on signaling used concentrations ranging from 10 μ M to 100 μ M [146]. In contrast, a single 25 mg dose of resveratrol, corresponding to high red wine consumption, resulted in marginal levels of plasma resveratrol in human subjects, and a 5 g dose produced a transient peak of only 2.4 μ M [147]. When lower concentrations corresponding to plasma levels are used on cells, the outcomes are variable, and often, no effects are detected [148]. Almeida et al. [111] showed that repeated dosing can increase the plasma half-life of resveratrol by more than two-fold.

The duration of the trials varies from acute exposure [149,150], to a few days [7,151–153] of exposure [154,155], to up to one year [156]. In most trials, the subjects are exposed to resveratrol in time frames of 1–3 months. The relatively short duration of the trials is a challenge because they permit analysis of therapeutic but not preventive potential. Without taking the practical and economical aspects of such studies into consideration, a trial to show a preventive effect of resveratrol should be performed for a minimum of one year. It is obvious that such trials are expensive and not easily funded, but they will be necessary to obtain relevant information regarding the preventive/therapeutic potential of resveratrol [148].

Notably, the resveratrol doses available in supplements and used in many clinical trials are 2–3 orders of magnitude beyond what can be obtained from the diet [157]. It is difficult to estimate normal human consumption of resveratrol because the intake of red wine differs greatly in the population and the content of resveratrol varies (mean, $1.9 \pm 1.7 \text{ mg/L}$), but the dose may reach 4 mg/person/day [115]. A single dose of resveratrol results in plasma levels of 2–18 µµM [149]. Ingestion of 3 g daily in obese individuals for eight weeks caused rapid and extensive conjugation of resveratrol [158].

Resveratrol trials in humans after single [108,147] or multiple daily doses of up to 600 mg/day administered over two or three days [111,159] showed that resveratrol is safe under the tested conditions and that the main metabolites found in the circulation are R3S, R4G, and R3G, with particularly high levels in the case of the sulfo-conjugate [160]. A few phase 1 clinical trials focusing on the pharmacokinetics of resveratrol were published before 2010, but since then, the number of clinical trials exploring the biological effects of resveratrol has increased significantly.

In recent years, resveratrol has been shown to possess a fascinating spectrum of pharmacologic properties that could be useful in human medicine [157,161]. To search for clinical trials with resveratrol to write this review, the clinical trials.gov site was accessed in April 2017, and 129 studies were identified. After excluding non-cancer studies, only 20 trials remained. Oral resveratrol is used as a pure compound or in resveratrol-rich products (grapes, grape juice or a mixture of supplements),

and the doses and durations of the interventions differed, as shown in Table S1. The following are the 20 clinical trials that were identified.

Clinical trial 1: "**Resveratrol for Patients with Colon Cancer**". A trial conducted by Nguyen et al. [162], with biomarker endpoints evaluating the expression of multiple components and target genes of the Wnt pathways, represents the first reported clinical trial of resveratrol in patients with cancer. The first two patients receiving resveratrol will be treated at a dose of 20 mg/day, the third and fourth patients at a dose of 80 mg/day, and the fifth and sixth patients with a dose of 160 mg/day. All patients receiving grape extract will receive 125 mg/day that will have to be mixed with one 8 oz glass of water. There will be no dose adjustments. If a patient has any side effects which are attributed to the resveratrol, it will be discontinued. The conclusion of the study was that grape powder containing low doses of resveratrol in combination with other bioactive components suppressed the expression of Wnt target genes, cyclin D1 and axin in normal colonic mucosa, suggesting that Wnt pathway inhibition might contribute to resveratrol-mediated colon cancer prevention.

Clinical trial 2: "**A Biological Study of Resveratrol's Effects on** Notch-1 Signaling in Subjects with Low Grade Gastrointestinal Tumors" is the work of Emily R. Winslow from the University of Wisconsin, Madison. Resveratrol has been shown to activate Notch-1, the signaling of which prevents tumor cell growth. This trial examines the effects of resveratrol and Notch-1 on neuroendocrine tumor tissue and the tolerance of people with neuroendocrine tumors who take resveratrol for up to three months (5 g per day orally administered in two divided doses of 2.5 g each with minimal dose-limiting toxicities according to the National Cancer Institute (NCI) Common Toxicity Criteria). The levels of tumor markers (e.g., chromogranin, 5-HIAA, gastrin, and others) pretreatment will be compared with the post-treatment levels (collected every three months) as a measure of the tumor response. In addition, serial axial imaging will be used to document tumor response rates according to standard Response Evaluation Criteria in Solid Tumors (RECIST).

Clinical trial 3: "**Resveratrol and Human Hepatocyte Function in Cancer**" is a trial coordinated by Dr. Brian G. Harbrecht from the University of Louisville. Resveratrol has shown a beneficial effect on the cellular function of normal and cancer liver cells in samples of liver tissue collected during elective liver surgery. Outcomes based on three measures will test the hypothesis that resveratrol used as a nutritional supplement (1 g pill daily) for 10 days before surgery will have the following effects: (1) improve metabolic function in liver cells, as assessed by the expression of signaling proteins, such as Akt, p38, MAPK, AMPK and PEPCK; (2) reduce cellular growth and proliferation of cancer cells, based on the expression of genes and proteins such as cyclin and p53 and the apoptosis proteins Bcl-2 and Bcl-xL; and (3) decrease inflammation in the liver, as determined by evaluating different levels of genes and proteins for nitric oxide synthase, cytokines such as interleukin-6, and nuclear factor-kappa B signaling proteins. Unfortunately, this trial was withdrawn prior to enrollment.

Clinical trial 4: "Phase I Biomarker Study of Dietary Grape-Derived Low Dose Resveratrol for Colon Cancer Prevention" from the University of California, Irvine, was conducted by Randall F. Holcombe. The purpose of this study was to determine the minimum amount of resveratrol-rich fresh red grapes needed to exhibit signs of colon cancer prevention. The grape-supplemented diet provided a low dose of resveratrol in conjunction with other potentially active components contained within the grapes. Colon tissue was obtained by limited flexible sigmoidoscopy before and after ingestion of the red grape-containing diet. Different dosages of grapes (1 or 2/3 or 1/3 lb/day fresh red grapes) were utilized. This study showed the effects of dietary grape-derived low-dose resveratrol on biomarkers related to the Wnt pathway and provided critical information regarding the utility of this nutritional approach for the prevention of colon cancer.

Clinical trial 5. The phase 1 trial, "**Resveratrol in Treating Patients with Colorectal Cancer That Can Be Removed by Surgery**", conducted by the research group of Dr. Brenner D., coordinated by the National Cancer Institute, addressed the side effects and the optimal dose of resveratrol for the treatment of patients with colorectal cancer that can be removed by surgery. Resveratrol was offered from eight days before colectomy and potentially halted tumor cell growth by blocking M-1G adducts and levels of cyclooxygenase-2 protein/Ki67.

Clinical trial 6 is a phase 1 trial, "UMCC 2003-064 Resveratrol in Preventing Cancer in Healthy Participants (IRB 2004-535)", led by Dean Brenner from the University of Michigan Cancer Center to study the side effects and optimal dose of resveratrol for the prevention of cancer in healthy participants. The concentration of resveratrol and its metabolites were analyzed in the plasma, urine, and feces. Beginning five days before study drug administration, participants were placed on a controlled diet (avoiding all resveratrol-containing food or drink) for washout. The participants received oral resveratrol once on Day 1 and were followed at two and seven days. To assess safety, pharmacokinetics and the insulin-like growth factor axis after repeated doses of resveratrol, Brown and colleagues [4] from Dr. Dean Brenner research group recruited forty volunteers to ingest resveratrol at dosages of 0.5 g, 1.0 g, 2.5 g or 5.0 g daily for 29 days and only sixteen participants are treated at the maximum tolerable dose. The higher doses (2.5 g and 5.0 g) generated micromolar concentrations of the parent and substantially higher levels of glucuronide and sulfate conjugates in the plasma and caused gastrointestinal symptoms of mild to moderate severity. The observed decrease in circulating IGF-1 and IGFBP-3 may contribute to cancer chemopreventive activity.

Clinical trial 7: "A Clinical Study to Assess the Safety, Pharmacokinetics, and Pharmacodynamics of SRT501 in Subjects with Colorectal Cancer and Hepatic Metastases" is a randomized, double-blind, placebo-controlled, inpatient/outpatient study. Micronized resveratrol (SRT501) was given at a dosage of 5 g daily for 14 days to patients with colorectal cancer with hepatic metastases scheduled to undergo hepatectomy. Micronization allows increased resveratrol absorption, thus increasing its availability, and SRT501 was well tolerated. Mean plasma resveratrol levels following a single dose of SRT501 were 1.9 ± 1.4 ng/mL, exceeding those published for equivalent doses of non-micronized resveratrol by 2- to 3.5-fold [4,147]. Resveratrol was detectable in hepatic tissue following SRT501 administration. Cleaved caspase-3, a marker of apoptosis, was significantly increased by 39% in malignant hepatic tissue following SRT501 treatment compared with tissue from placebo-treated patients [163].

Clinical trial 8: "**Resveratrol in Healthy Adult Participants**" is led by the principal investigator, Dr. Hsiao-Hui (Sherry) Chow, from Arizona Cancer Center, Tucson. Samples of blood and urine from healthy adult participants who are taking resveratrol once daily for four weeks are being studied. This phase 1 trial is studying the side effects of resveratrol and assessing its effects on healthy adult participants. This trial will compare the CYP enzyme activities from baseline to the end of the resveratrol intervention. CYP1A2, 2D6, 2C9, and 3A4 activity will be assessed according to the plasma paraxanthine/caffeine ratio, urinary dextromethorphan/dextrorphan ratio, urinary losartan/losartan metabolite ratio, and area under the plasma buspirone concentration-time curve, respectively. Additionally, GST activity and GST-pi level in blood lymphocytes and serum bilirubin levels will be used to assess phase II enzyme activity. Finally, a safety evaluation using the NCI Common Terminology Criteria for Adverse Events (CTCAE) version 3.0 will be conducted, and any adverse events will be described.

Clinical trial 9: "**Resveratrol in Postmenopausal Women with High Body Mass Index**" is a pilot phase 1 trial examining resveratrol in postmenopausal women with a high body mass index to determine the ability of resveratrol to modulate circulating sex steroid hormones and estrogen metabolites to evaluate its potential for breast cancer prevention. Forty subjects initiated the resveratrol intervention (1 g daily for 12 weeks), and six withdrew early due to adverse events. The resveratrol intervention did not result in significant changes in serum concentrations of estradiol, estrone, or testosterone, but it led to, on average, a 10% increase in the concentrations of sex steroid hormone

binding globulin (SHBG). It also resulted in, on average, a 73% increase in urinary 2-hydroxyestrone (2-OHE1) levels, leading to a favorable change in the urinary 2-OHE1/16 α -OHE1 ratio. One participant had a symptomatic grade 4 elevation of liver enzymes at the end of the study intervention. Two subjects had grade 3 skin rashes. The most common adverse events were diarrhea and increased total cholesterol, which were reported in 30% and 27.5% of the subjects, respectively. The authors concluded that among overweight and obese postmenopausal women, a 1 g dose of resveratrol daily has favorable effects on estrogen metabolism and SHBG [164]. Clinical trial reports indicate that the research group of Dr. Chow intends to evaluate the effects of resveratrol on serum levels of C-peptide, serum C-reactive protein (CRP), and adipocytokine expression and secretion as measured by serum leptin and adiponectin. Urinary 8-isoprostaglandin F2 alpha (8-iso-PGF2 alpha) and 8-hydroxydeoxyguanosine (80HdG) will be assessed to evaluate oxidative stress, and the safety of resveratrol intervention will be measured by the reported adverse events, complete blood count with differential (CBC/diff), comprehensive metabolic panel (CMP), and lipid profile.

Clinical trial 10: "**Resveratrol with or without Piperine to Enhance Plasma Levels of Resveratrol**". There is some evidence that resveratrol in combination with piperine (an alkaloid found in pepper) is more effective for fighting cancer, and therefore, the purpose of this study is to determine whether this combination is more effective than resveratrol alone. Because the investigators do not know the dose of piperine to use in combination with resveratrol, two different doses of piperine will be studied. Twenty-four participants, comprising equal numbers of males and females, will receive, for 30 days, a single dose of resveratrol (2.5 g) without piperine, resveratrol (2.5 g) with piperine at 5 mg, or resveratrol (2.5 g) with piperine at 25 mg. Blood levels of resveratrol and piperine will be measured, and adverse events and side effects will be analyzed. This trial is led by Howard H Bailey from the University of Wisconsin, Madison and has collaborators at the National Institutes of Health (NIH) and the NCI.

Clinical trial 11: "Pilot Study of Resveratrol in Older Adults with Impaired Glucose Tolerance". This proposed pilot study will examine resveratrol treatment (500 mg capsules, three capsules (1500 mg) orally twice a day for six weeks) in older adults with impaired glucose tolerance (IGT) to explore its effects on post-meal blood glucose metabolism.

Clinical trial 12: "Resveratrol and Cardiovascular Health in the Elderly". The objectives of this study are to test the effects of different doses of resveratrol (75 mg or 150 mg, $2 \times /$ day, orally) on heart and blood vessel health. This phase 1/2 trial of resVida (an oral preparation of resveratrol) in 90 overweight/obese people over the age of 50 (30 in each group) will be conducted for 12 months.

Clinical trial 13: "Resveratrol and the Metabolic Syndrome". The investigators propose to validate that resveratrol, administered to subjects with the metabolic syndrome under controlled conditions of weight stability, common diet, and strict compliance with the study drug, will improve the symptoms of the metabolic syndrome, thereby decreasing the chance of developing diabetes or heart disease.

Clinical trial 14: "**Dietary Intervention in Follicular Lymphoma (KLYMF)**" from Oslo University Hospital by Dr. Harald Holte, Jr. The recruitment status of this study is unknown. The completion date has passed, and the status has not been verified for more than two years. This open study projecting to include 45 patients seeks to perform a dietary intervention for 16 weeks and compare the apoptosis rate, proliferation rate and immune cell infiltrate before and after the intervention period. A dietary intervention study in patients with follicular lymphoma (FL) Stage III/IV consists of omega 3 fatty acids (eicosapentaenoic acid (EPA) and docosahexaenoic acid (DHA)) 1000 mg \times 5 daily, selenium (L-Seleno methionine) 100 mcg \times 2 daily, garlic extract (Allicin) 6 garlic pearls daily; and 100% pomegranate juice (ellagic acid), grape juice (resveratrol, quercetin), and green tea (epigallocatechin gallate), in a volume of two cups daily for 16 weeks.

Clinical trial 15: A phase 1 study for metastatic colorectal patients [163] did not report nephrotoxicity. As SRT501 is extensively metabolized, renal failure appeared to be specific to multiple myeloma

patients [165] due to multiple causes, and hence all patients are at risk. "A Clinical Study to Assess the Safety and Activity of SRT501 Alone or in Combination with Bortezomib in Patients with Multiple Myeloma". Twenty-four patients were enrolled in a phase 2 clinical trial of 5 g of SRT501 with and without bortezomib in patients with multiple myeloma who had relapsed or were refractory to at least one prior therapy. Disease stabilization by bortezomib may have prevented renal failure, whereas low efficacy of SRT501 with nausea and vomiting may have resulted in disease progression and dehydration, leading to renal failure. Renal toxicity was observed in five of the twenty-four patients. Renal failure is one of the specific clinical features of multiple myeloma and can be observed in nearly half of patients throughout the disease [166]. This study demonstrated an unacceptable safety profile and minimal efficacy in patients with relapsed/refractory multiple myeloma, highlighting the risks of novel drug development in such populations [167].

Clinical trial 16: "Anti-inflammatory and Antioxidant Effects of Resveratrol on Healthy Adults", is a clinical trial phase 3 that investigated the hypothesis that resveratrol (500 mg) administered orally to healthy adult smokers induces a decrease in inflammatory and oxidative mediators characterizing the low-grade systemic inflammatory state and the oxidant-antioxidant imbalance of tobacco users. Markers of total antioxidant/oxidative stress (C-reactive protein, 4-hydroxynonenal, nitrotyrosine, endothelial nitric oxide synthase (eNOS)-polymorphism, superoxide dismutase (SOD2)-polymorphism, catalase-polymorphism, pentraxin 3, interleukin-6, tumor necrosis factor- α) will be analyzed at baseline and every 30 days for three months. This trial will be conducted by Dr. Simona Bo from the University of Turin, Italy.

Clinical trial 17: "Study of Supplement's Antioxidant Properties That Contains Natural Extracts". The possibility has been raised that the complex mixture of phytochemicals in foods may contribute to their protective effects. In this view, it is possible that multiple compounds act through complimentary or synergistic mechanisms to provide a greater biologic effect than can be achieved by any individual component/nutrient. To investigate this hypothesis, a double-blind, randomized, and placebo-controlled clinical trial was conducted by Dr. Elizabeth Fragopoulou, from Harokopio University to investigate the effects of a multi-micronutrient supplement against oxidative stress (isoprostane, DNA/RNA damage, protein carbonyl levels, oxLDL, TBARS, resistance to serum oxidation, antioxidant enzymes) in apparently healthy adults for four or eight weeks. The supplement contained the following per 80 mL (a daily dose): *Aloe barbadensis* miller gel (USA/Mexico 36%); grape juice, *Polygonum cuspidatum* extract (containing 10% resveratrol); green tea extract; 1.1 mg of vitamin B1 (100% RDA); 2.5 μ g of vitamin B12 (100% RDA); 12 mg of vitamin E (α -TE) (100% RDA); coenzyme Q10; 200 μ g of folic acid (100% RDA); ascorbic acid; 27.5 μ g of selenium (100% RDA); and 4.2 mg of iron (100% RDA).

Clinical trial 18: "Effects of Micronized Trans-resveratrol Treatment on Polycystic Ovary **Syndrome (PCOS) Patients**". The purpose of this study, conducted by Dr. Beata Banaszewska from Poznan University of Medical Sciences, Poland with the University of California as a collaborator, is to determine whether three months of therapy with micronized trans-resveratrol (500 mg) can improve clinical (excessive hair, menstrual cycle), endocrine (androgens) and metabolic (lipids, markers of systemic inflammation) profiles in women with PCOS.

Clinical trial 19: Resveratrol is able to potentiate simvastatin-induced inhibition of cell proliferation in a concentration-dependent manner and inhibit the mevalonate pathway, suggesting a novel mechanism of action of resveratrol and underscoring the potential translational/clinical relevance of the interaction of this microcomponent with simvastatin [150]. The phase 4 clinical trial "Effects of Simvastatin and Micronized Trans-resveratrol Treatment on Polycystic Ovary Syndrome (PCOS) Patients" is being conducted by Beata Banaszewska, Poznan University of Medical Sciences, Poland. This study is designed to evaluate the endocrine and metabolic effects of simvastatin (20 mg daily) and micronized trans-resveratrol (500 mg daily) on PCOS. Evaluations are performed at baseline and repeated after

three and six months of treatment, and the main outcome is a change in serum total testosterone and fasting insulin levels.

Clinical trial 20: "Evaluation of Oral Lipid Ingestion in Relation to Ovarian Androgen Secretion in Polycystic Ovary Syndrome (PCOS) (ELI-ROAS)". The purpose of this phase 1 trial is to determine the relationship between lipid-induced inflammation and ovarian androgen secretion in women with PCOS, and to examine the effect of the drug salsalate (2 g twice daily) and Polygonum cuspidatum extract (PCE) (200 mg containing 20% of resveratrol twice daily) for 12 weeks on lipid-induced inflammation, ovarian androgen secretion, body composition and ovulation in a subset of normal weight women with PCOS. The principal investigator, Dr. Frank González, Director of the Division of Reproductive Endocrinology and Infertility, from Indiana University, hypothesizes that in women with PCOS, HCG administration will stimulate an exaggerated ovarian androgen response, dairy cream ingestion will stimulate white blood cells to generate an inflammatory response and that there is a relationship between HCG-stimulated ovarian androgen secretion and the inflammatory response to dairy cream ingestion regardless of body fat status. Thirty (30) women with PCOS (10 normal weight with normal abdominal adiposity, 10 normal weight with increased abdominal adiposity and 10 obese) and 30 ovulatory control women (10 normal weight with normal abdominal adiposity, 10 normal weight with increased abdominal adiposity and 10 obese) will participate over a three-year period. The investigator also hypothesizes that both salsalate and PCE administration for 12 weeks will attenuate the ovarian androgen response to HCG administration and the inflammatory response to dairy cream ingestion, reduce abdominal adiposity, increase insulin sensitivity and induce ovulation in normal weight women with PCOS. In a subset of 16 women with PCOS, eight will receive salsalate (four normal weight with normal abdominal adiposity and four normal weight with increased abdominal adiposity) and eight will receive PCE (four normal weight with normal abdominal adiposity and four normal weight with increased abdominal adiposity) over a three-year period. This pilot project will help determine the feasibility of conducting a larger double-blind, randomized trial in women with PCOS to further test the latter hypothesis.

A summary of clinical evidence for the preventive effects of resveratrol in human health, especially in cancer, is presented in Figure 2.



Figure 2. In vitro, in vivo and clinical evidence for the preventive effects of resveratrol in human health.

Considering the twenty studies shown above, only ten (50% of total) were completed. Most of them are phase 1 clinical trials with the aim to look at doses and side effects. Eight of the clinical studies are associated to different types of cancer, showing that until now resveratrol is associated to preventive effects. We further suggest that the quality of clinical trials in future should be improved through an increased number of participants, appropriate study designs, new formulations and/or routes of administration, and biomarkers relevant to healthy participants. Unfortunately, at this moment, the preventive and therapeutic effects of resveratrol in humans are still only supported by in vitro and in vivo model organism studies.

6. Adverse Effects

Based on animal studies, resveratrol is generally well tolerated, and very few short-term or acute exposure experiments in humans have been performed. When eight healthy subjects were exposed to 2 g of resveratrol twice daily for eight days, six of eight subjects had mild episodic diarrhea/loose stool, typically at the beginning of the eight-day treatment period, and one of the subjects developed a temporary rash and headache [168]. In a double-blinded, randomized, placebo-controlled study, up to 975 mg/day were given to healthy volunteers, among which two adult subjects (male and female) in each group were subjected to 25 mg, 50 mg, 100 or 150 mg six times/day for a total of two days. Adverse effects were mild in severity and similar among all groups. Repeated administration of resveratrol was well tolerated but produced relatively low plasma concentrations of resveratrol, despite the high doses and short dosing interval used [111]. Exposure of up to 270 mg resveratrol to nineteen volunteers for one week did not cause any discomfort [150].

According to Elliott et al. [169], healthy volunteers tolerated resveratrol well in a seven-day exposure study, but experimental details were not provided, making evaluation of the results challenging. The same article describes very briefly a study that included daily exposure to 2.5 g or 5 g resveratrol for 28 days. The authors reported that adverse events were generally mild in nature and reversible, but no experimental details were provided, precluding a closer evaluation [169]. Twenty colon cancer patients who received 0.5 g or 1.0 g resveratrol daily for eight days before surgical resection showed good tolerance [154].

7. Recommendations

The first international conference on resveratrol and health, Resveratrol 2010, was held in September 2010 in Denmark, with the purpose of assessing the current state of knowledge in the field and making recommendations for human use and future studies of resveratrol. A clear theme of the conference, which was attended by all of the authors, was that multiple mechanisms are likely to contribute to the beneficial effects of resveratrol, making it difficult to agree on a specific dose, biomarker, or outcome that can define the molecule [157,170].

The second international conference on resveratrol and health, Resveratrol 2012, occurred at the University of Leicester in England and concluded that the published evidence from human trials is not sufficiently strong to justify the recommendation of chronic resveratrol consumption by humans for any given indication. New animal data and recent short-term clinical trials are promising and indicate the need for further long-term human clinical trials, and the use of resveratrol is not an alternative to maintaining a healthy lifestyle.

During the third International Conference on Resveratrol and Health, Resveratrol 2014 (Hawaii), longer exposure times to resveratrol in new trials were recommended. To date, no real clinical trials exploring resveratrol in relation to cancer have been published [171]. At the fourth International Conference on Resveratrol and Health, Resveratrol 2016 (Taiwan), the highlights were focused on the interesting effects of resveratrol on hemorrhagic and septic shock models, its promising neuroprotective abilities and positive influence in psoriasis, and its role in bacterial shift.

8. Conclusions

This review describes recent evidence regarding resveratrol as a chemopreventive agent and a conceptual framework for a new approach to cancer prevention and therapeutics, which is in high demand. A broad-spectrum approach involves synergistic combinations of multiple low-toxicity agents as an association of microcomponents (e.g., resveratrol plus another bioactive compound) or with chemotherapeutic drugs that can collectively impact many pathways that are known to be important for carcinogenic processes, in addition to angiogenesis and metastases. The potential targets of the effect of resveratrol were presented, and p53 as an important protein involved in carcinogenesis could represent a new focus for exploration in translational studies.

Supplementary Materials: The following are available online: Table S1. Synthesis of clinical trials with resveratrol and cancer presented in the site of www.clinicaltrials.gov (accessed in April 2017).

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Review

Differential Methylation and Acetylation as the Epigenetic Basis of Resveratrol's Anticancer Activity

Mohd Farhan ¹, Mohammad Fahad Ullah ², Mohd Faisal ³, Ammad Ahmad Farooqi ⁴, Uteuliyev Yerzhan Sabitaliyevich ⁵, Bernhard Biersack ⁶ and Aamir Ahmad ^{7,*}

- ¹ College of Basic Sciences, King Faisal University, Hofuf 400-Al Ahsa-31982, Saudi Arabia; mfarhan@kfu.edu.sa
- ² Department of Medical Laboratory Technology, Faculty of Applied Medical Sciences, University of Tabuk, P.O. Box 741, Tabuk 71491, Saudi Arabia; m.ullah@ut.edu.sa
- ³ Department of Psychiatry, University Hospital Limerick, Limerick V94 T9PX, Ireland; mohd.faisal@hse.ie
- ⁴ Institute of Biomedical and Genetic Engineering (IBGE), Islamabad 44000, Pakistan; ammadfarooqi@rlmclahore.com
- ⁵ Department of Postgraduate Education and Research, Kazakhstan Medical University KSPH, Almaty 050004, Kazakhstan; e.uteuliyev@ksph.kz
- ⁶ Organic Chemistry Laboratory, Department of Chemistry, University of Bayreuth, Universitaetsstrasse 30, 95447 Bayreuth, Germany; bernhard.biersack@yahoo.com
- ⁷ Department of Oncologic Sciences, Mitchell Cancer Institute, University of South Alabama, Mobile, AL 36604, USA
- * Correspondence: aahmad@health.southalabama.edu

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Abstract: Numerous studies support the potent anticancer activity of resveratrol and its regulation of key oncogenic signaling pathways. Additionally, the activation of sirtuin 1, a deacetylase, by resveratrol has been known for many years, making resveratrol perhaps one of the earliest nutraceuticals with associated epigenetic activity. Such epigenetic regulation by resveratrol, and the mechanism thereof, has attracted much attention in the past decade. Focusing on methylation and acetylation, the two classical epigenetic regulations, we showcase the potential of resveratrol as an effective anticancer agent by virtue of its ability to induce differential epigenetic changes. We discuss the de-repression of tumor suppressors such as BRCA-1, nuclear factor erythroid 2-related factor 2 (NRF2) and Ras Associated Domain family-1 α (RASSF-1 α) by methylation, PAX1 by acetylation and the phosphatase and tensin homologue (PTEN) by both methylation and acetylation, in addition to the epigenetic regulation of oncogenic NF- κ B and STAT3 signaling by resveratrol. Further, we evaluate the literature supporting the potentiation of HDAC inhibitors and the inhibition of DNMTs by resveratrol in different human cancers. This discussion underlines a robust epigenetic activity of resveratrol that warrants further evaluation, particularly in clinical settings.

Keywords: resveratrol; epigenetic; methylation; acetylation

1. Introduction

Resveratrol (3,5,4'-trihydroxy-*trans*-stilbene) (Figure 1) is a naturally occurring polyphenol found in peanuts and the skin of grapes and berries. It is a phytoalexin produced in response to injury, ultraviolet radiation or a pathogen attack. The initial interest in resveratrol was because of its antioxidant properties [1], which led to the recognition of its chemopreventive ability [2]. Resveratrol was also found to generate reactive oxygen species, leading to effective anticancer activity through a prooxidant mechanism [3,4] which also happens to be a hallmark of several other polyphenols [5–7]. It is now believed that resveratrol exhibits both antioxidant and prooxidant

properties [8–10], which depend largely on the tumor microenvironment and the presence of transition metal ions, particularly copper ions. Besides its anticancer properties, resveratrol has also been investigated to explain the 'French paradox' [11], a phenomenon of the relatively low incidence of coronary heart diseases in the French population despite a diet rich in saturated fats, perhaps due to the consumption of red wine with high resveratrol content.



Figure 1. Chemical structure of resveratrol.

The realization of the potent anticancer properties of resveratrol was followed by numerous investigations into the various signaling pathways that it affects, leading to the observed effects [12–17]. In recent years, the focus of cancer research has shifted to stem cells, epithelial-to-mesenchymal transition (EMT) and epigenetic regulation, even in the context of lead compounds such as resveratrol that have a natural origin. Accordingly, a number of studies have documented the ability of resveratrol to affect stem cell populations [18,19] and EMT [20,21]. This article focuses on epigenetic regulation by resveratrol, which is increasingly being proposed as contributing to its anticancer properties.

2. Epigenetic Regulation by Resveratrol

Even though 'epigenetics' was originally intended to define heritable changes in phenotypes that were independent of changes in the DNA sequence, the meaning of this word has now considerably broadened to describe the alterations in human chromatin that influence DNA-templated processes [22,23]. Epigenetic changes do not result in any changes in the DNA sequence, but can still have lasting effects on gene expression. Epigenetic changes involve at least four known modifications of DNA and sixteen classes of histone modifications [22–24].

A number of studies have recognized the effects of nutraceuticals, including polyphenol resveratrol, on the epigenetic machinery in humans [25–35]. Resveratrol can modulate epigenetic patterns by altering the levels of S-adenosylmethionine and S-adenosylhomocysteine or by directing the enzymes that catalyze DNA methylation and histone modifications [27]. It also activates the deacetylase sirtuin and regulates oncogenic and tumor suppressor micro-RNAs [36]. Methylation and acetylation are two classical epigenetic modifications, and these will be the subject of our discussion in this article as we showcase the epigenetic basis of the anticancer action of resveratrol.

3. Methylation

The DNA methylation of gene promoters has a profound effect on their eventual expression and function. Differential DNA methylation can lead to a disease condition in healthy phenotypes. This is particularly true for cancer wherein the differential DNA methylation of the promoters of oncogenes and tumor suppressor genes helps maintain a delicate balance. The increased (hyper) methylation of promoter CpG islands causes gene silencing, while the decreased (hypo) methylation of promoter CpG islands leads to the expression of the gene.

3.1. Breast Cancer

Breast cancer is a widely studied cancer when it comes to epigenetic regulation, particularly differential methylation, by resveratrol. Studies have been conducted to elucidate the genome-wide methylation patterns after resveratrol treatment, and there have also been efforts to understand the

epigenetic basis of the de-repression of tumor suppressors by resveratrol. The subsection to follow will focus on this activity of resveratrol.

3.1.1. Genome-Wide Analyses

A study on the genome-wide methylation-modifying effects of resveratrol, which involved exposing MCF10CA1h and MCF10CA1a cells to resveratrol for 9 days followed by Illumina 450K array analysis, revealed a profound effect of resveratrol on genome-wide DNA methylation with approximately 75% differentially methylated genes being hypermethylated [37]. This study evaluated the epigenetic activity of not only resveratrol but also pterostilbene, an analog of resveratrol. While treatment with resveratrol was done at a dose of 15 μ M, pterostilbene treatment was at a 7 μ M dose. The compounds targeted genes that are over-expressed in tumors because of DNA hypomethylation. Since increased DNA methylation results in the silencing of genes, it makes sense that the resveratrol-induced hypermethylated genes have predominantly oncogenic functions [37], such as the Notch signaling pathway. However, in another study that also looked at genome-wide DNA methylation after resveratrol treatment (in this case, 24 h and 48 h treatment), only about 12.5% of CpG loci were found to be differentially methylated by resveratrol [38]. This study used MDA-MB-231 breast cancer cells and the concentration of resveratrol was 100 µM. Additionally, this study predominantly found DNA hypomethylation by resveratrol. It is possible that the differences in genome-wide DNA methylation (75% vs. 12.5%) in these two studies might be reflective of the different experimental setups, in particular, the time-durations of the resveratrol treatment as well as the doses used, with longer treatment leading to substantially more methylation.

3.1.2. Effects on Tumor Suppressors

Tumor suppressor genes are typically inactivated at the onset of tumorigenesis and, therefore, their reactivation by anticancer therapy is a mechanism through which tumor progression can be controlled. Several studies have documented the epigenetic reactivation of the tumor suppressor genes by resveratrol in breast cancer (Figure 2), as discussed below.



Figure 2. Activation of tumor suppressor genes by resveratrol through promoter DNA hypomethylation. The CpG islands in the DNA promoter regions of the tumor suppressor genes are hypermethylated resulting in their silencing. De-methylation of these CpG islands by resveratrol results in the activation of transcription and the eventual expression of tumor suppressor genes such as the phosphatase and tensin homologue (PTEN), BRCA-1 and nuclear factor erythroid 2-related factor 2 (NRF2).

Phosphatase and tensin homologue (PTEN) is a well-characterized tumor suppressor in breast cancer [39]. In one of the earlier studies describing an effect of resveratrol on promoter DNA methylation, it was reported that resveratrol was highly efficient in reducing PTEN promoter DNA methylation in MCF7 breast cancer cells [40]. Since reduced DNA methylation leads to gene expression, this action of resveratrol induced the expression of PTEN which could explain its anticancer effects. Further, it was reported that the epigenetic effects were complex as not only PTEN was induced but

the cell cycle regulator p21 was up-regulated as well, in addition to the down-regulation of DNMT (DNA methyltransferase). This is interesting because DNA methyltransferases increase methylation. Thus, it appears that resveratrol is able to reduce DNA methylation possibly through two different ways—by reducing methylation and by inducing de-methylation.

BRCA-1 (breast cancer type 1) is another tumor suppressor gene. Its expression is known to be regulated by epigenetic mechanisms. In a study that demonstrated the effects of resveratrol on BRCA-1 methylation [41], it was shown that exposure of breast cancer cells MCF7 to tumor promoter TCDD (2,3,7,8 tetrachlorodibenzo-p-dioxin) resulted in the hypermethylation of BRCA-1 promoter CpG island concomitant with an increased association of trimethylated histone H3K9 and DNMTs, namely DNMT1, DNMT3a and DNMT3b, with BRCA-1 promoter. Resveratrol, at physiologically relevant doses, was able to repress these TCDD effects. In a follow-up study, the research group evaluated the effects of TCDD alone, and in combination with resveratrol, on pregnant Sprague–Dawley rats [42]. It was found that, similar to in vitro observations in MCF7 cells, gestational exposure to TCDD led to the reduced DNA CpG island methylation of BRCA-1 promoter in the mammary tissues of the offspring, which was preceded by the occupation of BRCA-1 promoter by DNMT-1. Also, confirming a possible therapeutic role, resveratrol was found to partially attenuate TCDD effects [42].

Nuclear factor erythroid 2-related factor 2 (NRF2) is also a tumor suppressor that is epigenetically regulated by resveratrol. In a study that looked at the effects of resveratrol on E2 (17 β -estradiol)-induced carcinogenesis [43], resveratrol alone up-regulated NRF2 in mammary tissues of rats, and attenuated the repressive effects of E2 on NRF2. E2 suppressed NRF2 through DNA methylation, an activity that was inhibited by resveratrol, thus providing further evidence in support of its regulation of promoter DNA methylation in breast cancer.

3.1.3. DNMTs as Mediators of Resveratrol Effects in Breast Cancer

There is much evidence supporting an inhibitory effect of resveratrol against DNMTs [40,41,44–46]. However, most of the evidence comes from in vitro studies. To validate these findings, a pilot study was conducted that enrolled 39 women with increased breast cancer risk [47]. The subjects were divided into three groups—placebo and those receiving 5 or 50 mg resveratrol. Resveratrol was administered twice daily for twelve weeks and the focus was on the DNA methylation of four cancer-related genes—p16, Ras Associated Domain family-1 α (RASSF-1 α), Adenomatous Polyposis Coli (APC) and Cyclin D2 (CCND2). An inverse relationship between serum resveratrol levels and RASSF-1 α methylation was observed, i.e., when resveratrol levels increased, the methylation of RASSF-1 α decreased, thus leading to the expression of this tumor suppressor gene. In another study by this group [48], an in vivo effect of resveratrol on DNMT expression was examined in normal vs. tumor tissues. The model evaluated was ACI rats, an inbred line derived from the August and Copenhagen strains. An interesting observation was that resveratrol affected DNMT3b, but not DNMT1. Two different doses of resveratrol were tested and while DNMT3b differed in normal vs. tumor tissues of rats treated with low resveratrol, a high resveratrol dose resulted in decreased DNMT3b in tumor tissues with increased DNMT3b in the normal tissues [48]. This observation is a little different from the one performed in vitro in immortalized breast cancer epithelial cells, MCF10A [49], where resveratrol, at a non-cytotoxic dose, only induced subtle changes in the DNA methylation of eight pre-determined genes. However, the involvement of DNMT3b in resveratrol activity was also identified in a genome-wide DNA methylation study in breast cancer cells [37].

Further confirming the importance of targeting DNMTs in breast cancer patients, the elevated expression of DNMT transcripts was reported in a study that evaluated breast cancer tissues from 40 breast cancer patients and compared those with tissues from 10 paired normal breast tissues [50]. This study further confirmed the down-regulation of DNMT transcripts in vitro in breast cancer cells.

3.2. Glioma

Glioblastoma multiforme was the other malignancy where evidence of the effect of resveratrol on methylation was initially presented. It was shown that resveratrol could sensitize resistant glioblastoma T98G cells to temozolomide, inhibiting temozolomide IC-50 with increased apoptosis [51]. Interestingly, temozolomide-resistant cells have increased MGMT (O(6)-methylguanine-DNA-methyltransferase) activity and the protein expression of MGMT is an important determinant of temozolomide-resistance [51]. These results are suggestive of yet another DNA methylation-suppressing activity of resveratrol. In a recent report, inhibition of Wnt signaling has been identified as the mechanism by which resveratrol induces cell death in T98G cells [52]. Epigenetic regulation has been identified as one of the bases of perturbed Wnt signaling [53] and it is plausible that Wnt signaling might be another piece in the puzzle.

3.3. Lung Cancer

Lung cancer, the majority of which is non-small cell lung cancer (NSCLC), is the leading cause of cancer-related deaths in the United States, as well as worldwide. A number of studies have described the inhibitory effects of resveratrol against various lung cancer models [54–56], albeit, a majority of the studies have focused on NSCLC with little information on the other lung cancer types. In recent years, efforts have been made towards the personalized management of lung cancer [57], with a focus on epigenetics in such personalized therapy [58]. Further, it has recently been demonstrated that resveratrol can epigenetically regulate the expression of zinc finger protein36 (ZFP36) through differential DNA methylation [59]. Specifically, resveratrol reduced the methylation of ZFP36, resulting in its up-regulation in A549 NSCLC cells. A role of ZFP36 in human malignancies is increasingly being realized, making it an attractive target for therapy [60]. Thus, its epigenetic targeting by resveratrol further underlines the anticancer potential of resveratrol, particularly in lung cancer.

4. Acetylation

Even before the realization of the methylation potential of resveratrol, it has been known to modulate acetylation within the cellular microenvironment. A quarter century back, resveratrol was reported to be an activator of sirtuin-1 (SIRT1), the NAD-dependent deacetylase, marking its influence on acetylation, and thereby epigenetic regulation [61]. While the activity of resveratrol against Class III HDACs sirtuins is well characterized, it has been suggested that perhaps resveratrol possesses a pan-HDAC inhibitory property and can inhibit HDACs representing class I, class II as well as class IV [62]. Recently, resveratrol has been identified as an inhibitor of bromodomains [63] and the bromodomain and extraterminal (BET) family [64]. Bromodomains affect epigenetic machinery by recognizing lysine acetylation on histones, thereby functioning as epigenetic regulation by resveratrol which is not yet fully explored. The next few subsections discuss the reported effects of resveratrol on the acetylation of different genes in various human cancers.

4.1. Breast Cancer

Acetylation and its impact on breast cancer progression is well appreciated. It is because of this knowledge that HDAC inhibitors still remain an attractive therapeutic strategy against breast cancers [65–67]. It is not only the HDAC inhibitors but also the inhibitors of HATs (histone acetyltransferases) that are being evaluated [68], which provides a good example of how dynamic the process of acetylation and deacetylation is, and how an imbalance can lead to tumor onset and progression. In a study [69] that is indicative of an intricate connection between methylation and acetylation, the two classical epigenetic modifications, it was reported that lysine acetylation within the signal transducer and activator of transcription 3 (STAT3) can impact the interaction of DNMT1 with STAT3 and is accompanied by the demethylation and, thereby, the re-expression of tumor suppressor genes. This study used resveratrol as an acetylation inhibitor and the observations in triple negative breast cancer (TNBC) were further confirmed in melanoma. TNBCs are characterized by the absence of the estrogen receptor (ER) and progesterone receptor (PR), as well as human epidermal growth factor receptor 2 (HER2), and it has been reported that the absence of the *ER* α gene in tumor cells is often a result of methylation [70]. With the observation that STAT3 is acetylated and, therefore, highly expressed in TNBCs, it was evaluated whether inhibiting STAT3 acetylation could reactivate $ER\alpha$ [69]. The TNBC cell line MDA-MB-468 was used as the model and it was observed that treatment with resveratrol significantly reduced STAT3 acetylation as well as $ER\alpha$ gene promoter DNA methylation (Figure 3). This resulted in the increased expression of $ER\alpha$ and the sensitization of otherwise resistant cells to the ER-targeted therapy, tamoxifen. Further, growth of in vivo tumors in mice was not significantly reduced by tamoxifen alone, as expected, but by the combinational treatment comprising resveratrol and tamoxifen, thus validating the in vitro findings [69]. As further evidence of the effect of resveratrol on acetylation [71]. Thus, there seems to be evidence suggesting a modulatory effect of resveratrol on protein as well as histone acetylation.



Figure 3. Epigenetic regulation in triple negative breast cancers (TNBCs). TNBCs are characterized by activated STAT3 signaling, involving acetylated STAT3. ER α signaling in TNBCs is silenced through promoter DNA hypermethylation which might be related to STAT3 acetylation but the mechanisms remain unclear (and are therefore shown with a dotted line). Resveratrol is an effective inhibitor of STAT3 acetylation as well as ER α promoter DNA methylation. Restoration of ER-signaling makes TNBC cells sensitive to the ER-targeting therapy, tamoxifen.

4.2. Cervical Cancer

In cervical cancer models, paired box gene1 (PAX1) is a tumor suppressor whose expression is repressed during tumorigenesis by DNA hypermethylation. In a study that evaluated the effect of nutraceuticals, including resveratrol, on the inhibition of cervical cancer through the reactivation of PAX1, it was reported that resveratrol was capable of reactivating PAX1 expression in Caski cells [72]. However, surprisingly, the reactivation of PAX1 was not found to be due to the effect of resveratrol on the DNA methylation of PAX1 promoter. Rather, it possibly involved the acetylation modulating ability of resveratrol through its regulation of HDAC activity. Similar to an effect of resveratrol on histone H3 acetylation in breast cancer cells above, resveratrol has been reported to induce H3 acetylation in HeLa cervical cancer cells as well [71]. Such an effect of resveratrol on H3 acetylation assumes significance given the proposed role of histone H3 acetylation as a prognostic marker for cervical cancer patients [73].

4.3. Colon Cancer

NF- κ B signaling is known to be important to the progression of colon cancer [74], especially in resistance to cisplatin [75]. An increase in the protein acetylation of the NF- κ B p65 subunit leads to the activation of the NF- κ B pathway and its nuclear accumulation. Therefore, the inhibition of the acetylation of p65 can potentially be an effective strategy to check the growth of colon cancer as well as to overcome resistance to cisplatin. In an in vitro study performed in HK2 cells, resveratrol was found to decrease the protein acetylation of the p65 subunit, thus reversing the cell viability-inducing activity of cisplatin [76]. Such down-regulation of NF- κ B protein acetylation by resveratrol in colorectal cells was confirmed in another study [77] and this resulted in reduced tumor invasion and metastasis because of the down regulation of NF- κ B-regulated factors, such as MMP-9 and CXCR4.

4.4. Leukemia and Lymphoma

In leukemia, resveratrol can potentiate the activity of HDAC inhibitors [78], while in a Hodgkin lymphoma represented by L-428 cells, resveratrol can effectively induce apoptosis as well as cell cycle arrest [79]. As the mechanism, it was observed that resveratrol induced the tumor suppressor p53 through an increase in the p53 K373-acetylation (Table 1). Additionally, resveratrol treatment was found to induce the lysine acetylation of FOXO3a [79]. In leukemia U937 cells, resveratrol potentiates reactive oxygen species production by retinoic acid, particularly the production of superoxide anions, primarily through the up-regulation of the gp91-phox gene that is part of the membrane-bound cytochrome b₅₅₈ [80]. As a mechanism, it was elucidated that resveratrol promoted acetylation within the promoter region of the gp91-phox gene, particularly the Lys-9 residues and Lys-14 residues of histone H3 within the chromatin surrounding the gene promoter.

Table 1.	Epigenetic effe	ects of resverat	ol on tumo	r suppressors:	mechanisms	of t	heir re	e-activation
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Tumor Suppressor	Cancer Type	Effect of Resveratrol	Reference
BRCA-1	Breast	Reduced promotor DNA methylation in vitro Reduced promotor DNA methylation in vivo	[36] [37]
NRF2	Breast	Reduced promotor DNA methylation	[38]
p53	Lymphoma Prostate	Induced acetylation	[73] [75]
PAX1	Cervical	Regulation of histone acetylation	[66]
PTEN	Breast Prostate	Reduced promoter DNA methylation Acetylation and activation	[35] [77]
RASSF-1α	Breast	Reduced DNA methylation	[42]

4.5. Prostate Cancer

In prostate cancer, metastasis-associated protein 1 (MTA1) is oncogenic with its expression correlating with tumor progression. It is itself involved in the transcriptional repression of target genes through the post-translational modifications of histones as well as non-histones by virtue of it being a part of the nucleosome remodeling deacetylation corepressor complex, the 'NuRD complex'. Resveratrol was shown to down-regulate MTA1, leading to acetylation and the activation of the tumor suppressor p53 through the destabilization of the corepressor complex [81]. The NuRD complex plays a role in maintaining chromatin conformation, which it achieves through the deacetylation of histone proteins [82]. HDAC1 and HDA2 are components of the NuRD complex, with the MTA1-HDAC1 subunit responsible for the deacetylation of histones by NuRD. With a direct regulation of MTA1, and the observation that HDAC1 was decreased in resveratrol-treated MTA1 immunoprecipitates, it is evident that resveratrol has a profound effect on histone acetylation. Further, the effects of resveratrol were similar to those of the HDAC inhibitor SAHA, thus underlying the acetylation-affecting epigenetic activity of resveratrol. The results were further confirmed in vivo in a follow-up study [83], and it was shown that the MTA1-mediated tumor progression was, in part, due to PTEN inactivation and that resveratrol could acetylate and reactivate PTEN [84] (Table 1).

Signaling through the androgen receptor (AR) is important in prostate cancer, even in the advanced castrate-resistant prostate cancers. In a study that specifically looked at the regulation of AR signaling by resveratrol, it was observed that treatment with 10 μ M resveratrol for just 3 h inhibited the acetylation of AR and affected the binding of AR to the enhancer region of prostate-specific antigen (PSA) [85]. At a slightly longer treatment of 24 h, resveratrol inhibited the nuclear accumulation of AR as well. Given the important role that AR plays in prostate cancer, such epigenetic regulation of its activity and the effect on down-stream signaling by resveratrol is an encouraging finding that gives hope for its possible use as a therapy against prostate cancer.

5. Conclusions and Perspectives

While various cellular signaling pathways and genes (oncogenes as well as tumor suppressor genes) are still being evaluated as therapeutic targets of anticancer agents such as resveratrol, in recent years, attention has also turned to epigenetic regulation. In fact, epigenetic regulation of classical signaling pathways is increasingly being realized. For example, two of the very well characterized signaling pathways, NF-KB and STAT3, are epigenetically regulated by resveratrol [69,76,77,86]. This represents a fundamental evolution in our understanding with regards to the intricate regulation of oncogenic pathways. Our discussion on the topic, as presented in this article, detailed many studies that provided evidence supporting the epigenetic activity of resveratrol. However, resveratrol does not regulate gene expression only through epigenetic mechanisms. For example, in a study in acute lymphoblastic leukemia [87] that looked at the possible effect of resveratrol on the methylation of MDR1 (multidrug resistance gene 1), no evidence of the differential DNA methylation of MDR1 promoter by resveratrol was found. While resveratrol had a visible suppressive effect on MDR1, there did not seem to be any epigenetic perspective. This is a perfect reminder that not all regulation of gene expression and function by resveratrol has an epigenetic basis. Additionally, regulation through microRNAs (miRNAs) is within the realm of epigenetic regulation, but we decided to cover just the classical epigenetic mechanisms with regards to methylation and acetylation so as to keep the discussion more focused. Finally, the bioavailability of resveratrol still remains a concern, but that should not deter us from fully elucidating its mechanism of action and its potential as a viable anticancer lead. Several groups are working hard on improving the bioavailability through novel approaches and once they achieve success, resveratrol should be ready for further evaluations in clinical settings as an anticancer agent with multifaceted epigenetic activity.

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Mucosal and Cutaneous Human Papillomavirus Infections and Cancer Biology

Tarik Gheit*

Infections and Cancer Biology Group, International Agency for Research on Cancer (IARC), Lyon, France

Papillomaviridae is a family of small non-enveloped icosahedral viruses with double-stranded circular DNA. More than 200 different human papillomaviruses (HPVs) have been listed so far. Based on epidemiological data, a subgroup of alphapapillomaviruses (alpha HPVs) was referred to as high-risk (HR) HPV types. HR HPVs are the etiological agents of anogenital cancer and a subset of head and neck cancers. The cutaneous HPV types, mainly from beta and gamma genera, are widely present on the surface of the skin in the general population. However, there is growing evidence of an etiological role of betapapillomaviruses (beta HPVs) in non-melanoma skin cancer (NMSC), together with ultraviolet (UV) radiation. Studies performed on mucosal HR HPV types, such as 16 and 18, showed that both oncoproteins E6 and E7 play a key role in cervical cancer by altering pathways involved in the host immune response to establish a persistent infection and by promoting cellular transformation. Continuous expression of E6 and E7 of mucosal HR HPV types is essential to initiate and to maintain the cellular transformation process, whereas expression of E6 and E7 of cutaneous HPV types is not required for the maintenance of the skin cancer phenotype. Beta HPV types appear to play a role in the initiation of skin carcinogenesis, by exacerbating the accumulation of UV radiation-induced DNA breaks and somatic mutations (the hit-and-run mechanism), and they would therefore act as facilitators rather than direct actors in NMSC. In this review, the natural history of HPV infection and the transforming properties of various HPV genera will be described, with a particular focus on describing the state of knowledge about the role of cutaneous HPV types in NMSC.

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> *Correspondence: Tarik Gheit gheitt@iarc.fr

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INTRODUCTION

Papillomaviridae is a family of small non-enveloped icosahedral viruses with double-stranded circular DNA, which range in length from 5,748 bp for *Sparus aurata* papillomavirus 1 (SaPV1) to 8,607 bp for canine papillomavirus type 1 (CPV1). Papillomaviruses (PVs) infect basal keratinocytes of the mucosal and cutaneous epithelia of both animals (reptiles, birds, marsupials, and others) and humans (1). In 2016, the first characterization of a PV in fish (SaPV1) rendered this family of viruses much older than expected, with an emergence 450 million years ago (2). PVs are considered to be host-restricted; however, in rare cases cross-species transmission may also occur (3, 4).

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Based on the nucleotide sequences of the major capsid protein L1, the PV study group within the International Committee on Taxonomy of Viruses (http://ictv.global/report/papillomaviridae) has classified the PVs into 53 genera, among which only 5 genera include PVs that infect humans (HPVs). To be classified as a novel PV type, the nucleotide sequence of L1 must share <90% similarity with other PVs (5). During the past decade, there has been an exponential increase in the identification of new betapapillomaviruses (beta HPVs) and gammapapillomaviruses (gamma HPVs) that have been discovered with the advent of new technologies such as next-generation sequencing. More than 200 different HPV types have been listed by the International HPV Reference Center (www.hpvcenter.se) (6), and this number continues to expand (7).

HPV types are organized into five major genera: alpha, beta, gamma, mu, and nu (5). The genus gamma includes the majority of the known HPVs, with 99 types, followed by the genera alpha (n = 65) and beta (n = 54). The genera mu and nu include only 3 and 1 types, respectively (www.hpvcenter.se, on 2019-01-30). A recent study reported the identification of the complete genome of 83 previously unknown HPV types, among which 69 were classified as gamma (8).

Based on epidemiological and biological data, a subgroup of 12 mucosal HPV types classified in the genus Alphapapillomavirus (alpha HPV), i.e., HPV16, 18, 31, 33, 35, 39, 45, 51, 52, 56, 58, and 59, referred to as high-risk (HR) HPV types, has been classified as carcinogenic (IARC Group 1), and eight other HPV types, i.e., HPV26, 53, 66, 67, 68, 70, 73, and 82, have been classified as probably or possibly carcinogenic (IARC Groups 2A and 2B) (9, 10). The HR HPV types are the etiological agents of several cancers, such as those of the cervix, vagina, vulva, anus, penis, and a subset of head and neck cancers (HNCs), particularly oropharyngeal cancer (11). In 2012, 15.4% of cancers worldwide were attributed to carcinogenic infections (12). Together, the HPV-related cancers represent 630,000 new cancer cases per year, which account for \sim 30% of all cancers induced by infectious agents (10). Epidemiological and biological studies showed that HPV16 is the most oncogenic of the HR HPVs. The genus alpha also includes low-risk (LR) HPV types that cause benign lesions. HPV6 and 11, the most studied LR HPV types, induce benign genital warts or condylomata acuminata (13). These HPV types are also found in recurrent respiratory papillomatosis (14), in children. The genus alpha also includes a few cutaneous HPV types (HPV2, 3, 7, 10, 27, 28, and 57), which cause common and plantar warts (15–18).

The genera beta, gamma, mu, and nu contain HPVs that infect cutaneous epithelia. The genus alpha also contains some HPV types, such as HPV2, 3, and 10, that colonize the human skin. The mu and nu genera include only a few HPV types, whereas the genus beta includes more than 54 HPV types, which are subdivided into five species (β 1–5), and the genus gamma includes 98 types subdivided into 27 species (6). In the immunocompetent population, these so-called cutaneous HPV types induce asymptomatic chronic infections. However, members of the genera gamma, mu, and nu can induce benign skin lesions, e.g., cutaneous papillomas or warts (5). In addition, there is growing evidence of an etiological role of beta HPVs in non-melanoma skin cancer (NMSC), most likely in association with ultraviolet (UV) radiation [reviewed in (19–21)].

In this review, we describe the natural history of mucosal and cutaneous HPV infections, and discuss the transforming properties of a subset of them that have been shown or are suspected to play a causative role in various human cancers. In particular, we focus on describing the state of knowledge about the role of cutaneous HPV types in NMSC, because many existing reviews already cover all the aspects of mucosal HPV type infection and its role in transformation.

GENOMIC ORGANIZATION OF HPV AND VIRAL GENE PRODUCTS

The HPV genome is organized into three major regions: (i) a long control region (LCR), also called the upstream regulatory region (URR), located between the L1 and E6 open reading frames (ORFs), which contains the early promoter and regulatory element involved in viral DNA replication and transcription; (ii) the early region, which encodes the E1, E2, E4, E5, E6, and E7 proteins involved in viral gene expression, replication, and survival; and (iii) the late region, which encodes the structural proteins (L1 and L2). This organization is shared among all alpha HPVs (Figure 1). However, only four ORFs (those of E1, E2, L1, and L2) are necessary to fulfill the requirements to ensure the viral replication and shedding of the virus, and are present in all known PVs (22). Certain HPV genera and types lack an ORF. For example, the E5 ORF is lacking from HPV types that belong to the genera beta, gamma, and mu, and both the E5 and E6 ORFs are lacking from three gamma HPV types (HPV101, 103, and 108) (23, 24). LR HPV types (i.e. HPV6 and 11) encode for two E5-like proteins E5 γ and E5 δ (25). Beta and gamma HPV types have the particularity of harboring a shorter LCR compared with members of other genera (Figure 1).

All PVs also have the potential to express an E8^{\wedge}E2C transcript (or equivalent), encoding for a protein that includes the E8 domain fused to the hinge and DNA-binding domains of E2 (26). This protein acts as a transcriptional repressor, and represses E1/E2-dependent replication of the viral origin (27–29).

NATURAL HISTORY OF MUCOSAL HPV INFECTIONS

Mucosal HPV infections occur during the first sexual exposures in early adulthood (30), although non-sexual infection may also be possible (31). Although a majority of sexually active women will acquire a genital HPV infection, most (>90%) cervical HPV infections are resolved by the host immune system within 1– 2 years (32, 33) and give rise only to asymptomatic infections. However, a minority of HPV infections become persistent. The risk of developing epithelial cell abnormalities and cancer is then increased (32). Persistent infection may be explained by several factors. Alcohol consumption and the HR HPV load synergistically increased the risk of persistent HR HPV infection in women (34). Cigarette smoking alone also plays an important role in the acquisition of persistent HPV infections in women,



by decreasing the probability of clearing oncogenic infections (35). Smoking is also a risk factor for a persistent oral HPV infection (36). Host genetic risk factors may also predispose an individual to persistent HPV infection and developing cervical cancer, as supported by the high rate of heritability of cervical cancer (37–39). Defective immune response due to genetic variations (e.g., inflammasome genetics) has been associated with virus persistence and progression to cervical cancer (39–41). Human leukocyte antigen (HLA) genes also play a key role in the persistence of HPV infections and progression to cervical cancer, depending on their ability to bind to HPV antigens (39, 42).

Many natural HPV intra-type variants that differ from the prototypes have been identified, and some of them have been associated with the persistence and clinical outcome of cervical HPV infections (43–46). Several studies showed that EUR-350 T and EUR-350 G, which are HPV16 E6 variants, could influence viral persistence (47, 48). Recently, Mirabello et al. (49) evaluated a large collection of 5,570 HPV16-infected case-control samples using HPV whole-genome sequencing, and showed that E7 variation from the prototype sequence greatly decreases the risk of invasive cancer. That study also highlighted the presence of rarely detected variants of HPV16 that are consistent with the antiviral activity of the human APOBEC3 cytidine deaminase family. Moreover, APOBEC3A is stabilized in human keratinocytes by HR HPV E7, but not by E7 of LR HPV types (50).

The HR mucosal HPV genome integrates into host chromosomes in anogenital and oropharyngeal cancers, and it is considered an important driver of carcinogenesis.

There is not yet consensus on whether this is an early or a late event in carcinogenesis (51, 52). The integration occurs frequently within the E1 or E2 proteins, leading to dysregulation of expression of the oncoproteins E6 and E7 due to loss of the E2 repression function (53). The stability of E6 and E7 mRNAs is increased when HPV16 DNA is integrated into the human genome (54).

The frequency of viral integration increases with the severity of the cervical precancerous lesions. Integration of HPV into the host genome is reported in a majority of cervical cancers (83%) (55), and HPV18 has been found integrated into almost all cervical cancers (56, 57). HPV16 can be present as episomal or integrated forms, or both (58).

The DNA integration event could contribute to the HPVdriven malignant transformation of cervical cells, by affecting the expression of key host genes near the integration site (59). In addition, the existence of long-distance regulation among the integrated HPV fragment, the MYC gene, and the 8q24.22 region has been reported (60).

Although it was commonly accepted that integration occurred randomly into the host genome, several studies have shown that non-random HPV integration occurs. Integration of HPV16 sequences appears to take place preferentially in common fragile sites in human chromosomes (61, 62), in transcriptionally active regions (63), or near microRNAs (64).

Carcinogenesis can also be enhanced by epigenetic events. In cervical cancer, HPV16 E2 binding sites (E2 BS1 and E2 BS2), which play a role in transcriptional repression of E6 and E7 oncoproteins, are heavily methylated. The binding of E2 protein on these sites is then prevented, which leads to the upregulation of E6 and E7 oncoproteins (65). Host or viral epigenetic changes may be enhanced by the integration of HPV. A recent study showed that L1 gene methylation increases significantly according to the grade of the cervical lesion, and a high methylation rate of this gene correlates with the physical status of HPV integration (66, 67).

Data on HPV integration in HNC are still sparse and contradictory. Parfenov et al. (68) reported that 25 out of 35 HNCs showed integration of HPV into the human genome. Other studies reported HPV integration rates of 39% in oral squamous cell carcinoma (SCC) (69) and 43% in HNC (70), which is lower compared with HPV-positive cervical cancer. Episomal, integrated, and mixed forms of HPV are found in HPV-positive HNC. Moreover, a recent study, based on analysis of the Cancer Genome Atlas sequencing data, reported for the first time the presence of viral-human hybrid episomes in HPV-positive HNC (71).

NATURAL HISTORY OF CUTANEOUS HPV INFECTIONS AND CLINICAL IMPLICATIONS

Cutaneous HPV types are ubiquitous and are widespread in the general population. Up to 90% of healthy individuals tested positive for beta HPV types (72-74). The infection occurs in young children through skin-to-skin contact (75, 76). The cutaneous HPVs have been proposed to infect hair follicle stem cells of healthy individuals, where they constitute a reservoir of persistent infection (77, 78). DNA from cutaneous HPVs is frequently detected in hair bulbs, independently of the anatomical region where the hairs were plucked (79). Schmitt et al. (80) showed that keratinocyte stem cells (KSCs) in rabbit hair follicles co-localize with the primary target cells of cottontail rabbit papillomavirus (CRPV). They showed presence of CRPV early transcripts in clonogenic cells of the hair follicles soon after infection, suggesting that hair follicle stem cells are the initial target cells for CRPV (80), which was shown to induce cutaneous warts and carcinomas (81).

Epidemiological studies in humans showed that the cutaneous HPV population present in hair follicles mirrors the HPV prevalence in the skin of the same individual, which makes eyebrow hair an excellent sampling method to characterize the individual cutaneous HPV population (79, 82). Studies on intra-familial transmission showed that similar spectra of beta HPV types are present within members of the same family. Babies and their parents share some of the beta HPV types (83), which can persist for many years on healthy skin (84, 85). Transmission of beta and gamma HPVs has been demonstrated in couples (86).

Exposure to cutaneous HPV is common. Serological studies measuring antibodies against the type-specific L1 major capsid protein of HPV showed that 52% of the Dutch population and 67% of the Italian population were exposed to beta HPV infections (74). A recent seroprevalence study, based on ten beta HPV types, showed that 39% of healthy men were seropositive for at least one beta HPV type (87). Seroconversion for beta and gamma HPV types appears to be slow and to increase with age (88). Low viral loads in immunocompetent individuals (89) and continuous renewal of the infected keratinocytes may explain why only half of the infected individuals develop antibodies against cutaneous HPV types (90, 91).

Cutaneous HPVs are highly prevalent in the rare hereditary disease epidermodysplasia vertuciformis (EV), which tends to progress to cutaneous SCC (cSCC), frequently located at sunexposed anatomical sites (92). HPV5 and 8, two members of species β 1, were isolated from cSCC in patients with EV (93). These two types were classified as possibly carcinogenic to humans (IARC Group 2B) (10).

In organ transplant recipients, a 65–250-fold increased risk of developing SCC compared with the general population was reported (94, 95). In addition, in HIV-positive individuals, several studies reported at least a 2-fold increased risk of cSCC compared with HIV-uninfected people (96, 97). The correlation between the immunodeficiency state and an increased risk of developing NMSC suggested a possible role of infectious agents (98), such as cutaneous HPV.

This observation is corroborated by growing evidence showing an association between cutaneous infection and the risk of developing NMSC in immunocompetent individuals under certain conditions (e.g., UV radiation exposure) [reviewed in (21, 99)], in particular in cSCC (100–102).

Epidemiological and biological data suggested that beta HPV types, and species $\beta 1$ and $\beta 2$ in particular, may be linked to cSCC development in immunocompetent individuals (99, 100) [reviewed in (21)].

Interestingly, the cutaneous HPV viral load was higher in actinic keratosis, which is considered to be the precursor lesion of cSCC, compared with cSCC (<1 copy per cell), suggesting a possible role of cutaneous HPV types in the initiation of skin carcinogenesis but not in the maintenance of the cancer phenotype, by exacerbating the accumulation of UV radiation-induced DNA breaks and somatic mutations (the hit-and-run mechanism) (103, 104). The absence of HPV mRNA (105) and the lack of evidence for the integration event in skin tumors support this scenario.

The Mastomys natalensis papillomavirus (MnPV)-infected rodent model Mastomys coucha was previously described and used to evaluate the role of PVs in NMSC. In these mice, which can be naturally infected by MnPV, skin lesions such as papillomas or keratoacanthomas can be induced (106). Using this model, Hasche et al. (107) clearly demonstrated cooperation between UVB radiation exposure and MnPV infection in the first step of NMSC initiation. MnPV-positive animals chronically exposed to UVB radiation developed lesions significantly more frequently than MnPV-negative animals (107). Moreover, the authors showed higher MnPV viral loads in well-differentiated and keratinizing SCCs (KSCCs) compared with normal skin. Of note, these KSCC lesions share histological similarities to human SCC pre-malignant lesions, such as actinic keratosis, that normally show higher cutaneous HPV DNA loads than SCC, as discussed above. In addition, non-keratinizing SCCs (nKSCCs) occurring in mice UV-irradiated at higher doses showed low levels of (or no) viral DNA and often harbored p53 mutations, again mirroring the evolution of SCC in humans. The loss of viral DNA and viral gene expression in nKSCC lesions is most likely due to their undifferentiated state, which no longer sustains the infection. However, despite the lack of viral DNA, animals with nKSCCs developed antibody response to MnPV capsids, which clearly highlights past exposure to the virus, similar to the situation observed in SCC cases (108). Therefore, the Mastomys model shows parallels with a natural infection by cutaneous HPV and provides a good model to study the association between cutaneous HPV infection, UV radiation and SCC. Most importantly, this model provides further evidence for a hit-and-run mechanism.

Many independent studies reported the presence of beta HPV types at different anatomical regions other than the skin, such as the oral mucosal epithelium, genital sites, and the anal canal (109–112), or investigated the role of cutaneous HPV in various malignancies (e.g., male external lesions, breast cancers, salivary gland tumors, esophageal cancer) other than skin cancer, without showing any association (113–116). However, a recent study reported an increased risk of HNC in individuals who tested positive for HPV5 of species β 1, as well as other HPV types of species γ 11 and γ 12 (117). The same trend was reported in another study, in which β 1 HPV5 and β 2 HPV122 were significantly associated with HNC (118).

Whereas, beta HPVs are known to infect cutaneous tissues, epidemiological data showed that β 3 HPV types are also present in the mucosal epithelium, suggesting a dual tropism (111, 119). Moreover, this species shares biological similarities with mucosal HR HPV types such as HPV16 in *in vitro* and *in vivo* experimental models (120, 121). A study showed that β 3 HPV49 transgenic mice, after 4-nitroquinoline 1-oxide treatment, were prone to develop upper digestive tract tumors (121).

Epidemiological and biological data on the role of gamma HPV types are sparse, and do not support an etiological role in NMSC. However, this genus includes an increasing number of members that may deserve more investigation. Using deep sequencing, a member of species $\gamma 27$ (HPV197) has been isolated exclusively from skin cancers. However, additional studies are required to demonstrate an etiological link between this type and skin cancer (122, 123).

ENTRY AND LIFE CYCLE OF HPV

The viral particle reaches the basal layer of the epithelium via micro-wounds or micro-fissures, or via hair follicles (80, 124, 125), to infect basal keratinocytes or stem epithelial cells. In the cervix, HR HPV may directly reach the single layer of cuboidal epithelial cells from the squamocolumnar junction located between the endocervix and the ectocervix (126); this anatomical region is therefore more sensitive to infection. In the oral cavity, HPV infection is believed to occur in tonsillar crypts, where a comparable cellular structure exists (127).

The infectious entry of the virus into the cell is intimately linked to proliferating cells of the regenerating basal epithelium. Broniarczyk et al. (128) showed that the viral particle can remain infectious after several weeks on the surface of senescent cells, which are resistant to HPV infection; however, reactivation of the cell cycle by p53 siRNA led to the entry of the virus (128).

To initiate the infection, the virus binds to the heparan sulfate chains of proteoglycans (HSPGs) located on the cell membrane or on the extracellular matrix (ECM) through the major capsid protein L1, leading to cyclophilin (CyP) B-mediated conformational changes of the capsid structure, which expose the minor capsid protein L2 on the surface of the viral particle (**Figure 2**). The cleavage of L1 in the extracellular space by a serine protease, kallikrein-8, appears to be crucial for the efficient

externalization of L2 (129). On the ECM, the virus can also bind to a transient binding receptor, laminin-322 (formerly called laminin-5) (130).

Next, the N-terminus of the minor capsid protein L2 is cleaved with a CyP-independent mechanism at a conserved furin cleavage consensus site to expose the L2 amino acids 17–36 (the RG1 neutralizing epitope), which appears to be important for the interaction of the capsid with an unidentified secondary receptor (131, 132). The binding of HPV to the secondary receptor allows subsequent internalization.

Using HPV16 pseudovirion (PsV) particles covalently labeled with some fluorophores Schelhaas et al. (133) showed that HPV16 PsVs moved along the outside cell membrane in correspondence to the actin protrusions and were transported inside the cells by actin retrograde flow. Upon inhibition of the actin flow by blebbistatin, the virus particles could not be actively transported along actin-rich protrusions, which resulted in reduced efficiency but not in complete abolishment of the infection (133). In a more recent work, using different compound inhibitors and siRNAs, Schelhaas et al. (134) showed that the entry of HPV16 into HeLA and HaCaT cells was actin-dependent and clathrin-, AP2-, caveolin-, flotillin-, and dynamin-2-independent (134). Although the exact mechanism of membrane protrusion/vesicle formation during virus endocytosis remains unclear, Schelhaas's study clearly showed that actin polymerization and depolymerization are crucial for HPV16 endocytosis, in particular for scission of endocytic vesicles (134). Once inside the cell, the virus needs to reach the replication machinery within the nucleus (Figure 2). The virus is delivered to an early endosome or macropinosomelike endosome that matures into a late endosome [reviewed in (135)]. Inside the late endosomes, the capsid of the viral particle is disassembled in a low-pH environment, leading to the dissociation of the major capsid protein L1 from the minor capsid L2, mediated by host-cell CyPs (136). However, a recent study showed that residual conformationally intact L1 protein remains in complex with the viral genome (137). The L2-viral DNA complex traffics to the trans-Golgi network, mediated by the retromer complex (138). Retromer is a heteropentameric complex composed of dimer of sorting nexins (SNX1, SNX2, SNX5, and SNX6) and a vacuolar protein sorting (Vps) trimer containing Vps26, Vps29, and Vps35, which play a central role in the retrieval of several different cargo proteins from the endosome to the trans-Golgi network. The trafficking also involves retriever, a multi-protein complex analogous to retromer (139), and involves the cellular adaptor protein SNX17. This complex is associated with endosomes and is essential for the recycling of multiple cargoes. A proteomic approach has shown that SNX17 interacts with HPV16 L2 (140). The observation that the SNX17 binding site is conserved among different PV genera suggests that it has an important role in regulating the PV life cycle and replication. The SNX17/L2 interaction is indeed required for HPV16 infection and appears to play key roles at different stages of the infection, being important for effective capsid disassembly and L1 dissociation. The interaction of L2 with SNX17 also contributes to the maintenance of viral capsids in the late endosomal compartment, by protecting them



from lysosomal degradation and allowing L2–DNA complexes to egress from the endosomes (141). A related protein, SNX27, is part of the retromer complex and also interacts with L2, but through its PDZ domain. SNX27 appears to be important for virion trafficking and to cooperate with SNX17 in this event (142).

L2 is required for efficient trafficking of the viral genome to the nucleus (138) and remains associated with the viral DNA when the transport vesicles deliver the L2–viral DNA complex inside the nucleus [reviewed in (143)], most likely together with residual L1.

Delivery of the L2-viral DNA complex into the nucleus requires cell cycle progression into early mitosis (144). Nuclear envelope disruption is also required for nuclear import of the L2-viral DNA complex (145) (**Figure 2**).

Inside the nucleus, L2 mediates the viral genome delivery to the nuclear domain (ND10) (146, 147), also known as promyelocytic leukemia (PML) bodies, where early viral transcription and replication will take place, as for many DNA viruses. ND10 structures are host restriction factors that limit viral infection as part of the intrinsic defense against viral infection (148). Stepp et al. (149) showed that Sp100 nuclear antigen, one of the components of ND10, represses transcription, replication, and establishment of incoming HPV DNA in the early stages of infection. Upon initial infection, the minor capsid protein L2 leads to the alteration of the composition of ND10 protein, leading to the release or degradation of Sp100 (150). The Daxx protein, another component of ND10, is also recruited (150). It was previously reported that this protein modulates the early gene expression and the transient replication of HPV genomes in U2OS cells (151).

The replication cycle of HPV is linked to the differentiation of the infected epithelium, and starts with a first step, called "establishment replication," which consists of maintaining a constant number of episomal copies (50-100 per cell) (Figure 3) [reviewed in (152)]. Viral DNA replication relies on the host DNA replication machinery and is supported by the early viral proteins E1 and E2 (153). Upon nuclear entry, viral DNA replication is initiated by the binding of E2 on specific sites located on the LCR, which is required for the recruitment and binding of E1 helicase to the viral origin of replication (154). The cellular proteins TopBP1 and Brd4 are involved in the initiation of the HPV16 E1/E2-mediated DNA replication (155). Limited viral genome amplification may be obtained by the interaction of NCOR/SMRT repressor complexes with E8^AE2C proteins, which inhibits viral replication (156, 157). After this initial step, which aimed to generate a low copy number of genomes, the maintenance phase is initiated (Figure 3) [reviewed in (152)]. This phase consists of creating the conditions to maintain a constant number of viral genomes in the nuclei of undifferentiated basal cells as an extrachromosomal genome to create a persistent infection. The viral genomes need to be correctly segregated during cell division through attachment/tethering of the virus genome to the hostcell chromosome. The transactivation domain at the N-terminal part of E2, with the bromodomain protein Brd4, interacts with the host mitotic chromosomes. Concomitantly, the E2 DNAbinding/dimerization domain binds to E2 binding sites in the LCR of the viral genome (158-162). Brd4 interacts with the E2 transactivation domain of most PVs (163). ChIR1, an ATPdependent DNA helicase, seems to play a key role by regulating the chromatin association of HPV16 E2, and in maintaining the episomal form of HPV16 (164-166). The structural maintenance of chromosomes (SMC) proteins SMC5 and SMC6 may also play a role in viral genome maintenance by interacting with E2 (167). In addition to E1 and E2, the oncoproteins E6 and/or E7 are required for stable episomal maintenance of HPV (168, 169).

Upon cell differentiation in stratified epithelium, vegetative or productive viral replication is initiated, with the subsequent production of progeny virions (170, 171), [reviewed in (152)] (Figure 3). Uninfected cells leave the basal layer for terminal differentiation, are withdrawn from the cell cycle, and stop the replication of the DNA. Because the amplification of the viral genome requires cellular conditions that enable cell proliferation and thus DNA replication, the virus has developed strategies to prevent cell-cycle arrest and apoptosis signals. Here, the oncoproteins E6 and E7 expressed at relatively low levels in differentiated cells play a key role by inactivating tumor suppressor proteins (e.g., p53, retinoblastoma protein [pRb]) and activating signal transduction, to ensure that the infected cells remain active and progress to the S phase. The activation in differentiated epithelial cells of the late promoter (P670 for HPV16, P811 for HPV18, and P742 for HPV31), located in the E7 region, leads to the production of the high levels of E1 and E2 viral proteins required to ensure viral DNA replication. E4 and E5 contribute to efficient productive replication (172, 173). The capsid proteins L1 and L2 are expressed from the late promoter, and are involved in the encapsidation of newly replicated genomes, resulting in virion release in the superficial layers during desquamation (174) (Figure 3). E4 also plays a role at this step of the viral life cycle, by interacting with the keratin network (175). A more complete description of the function of each of the viral proteins is provided in Table 1.

Epigenetic regulation of HPV transcription plays an important role in the virus life cycle. HPV regulatory epigenetic mechanisms have recently been partly elucidated by Pentland et al. (176). The key players in this regulation are the chromatinorganizing CCCTC-binding factor (CTCF) and Yin Yang 1 (YY1), binding, respectively, to the E2 ORF and the viral LCR. CTCF and YY1 are involved in the formation of a loop allowing E2 and LCR interaction and leading to the formation of epigenetically repressed chromatin in the HPV18 genome. This event leads to attenuated expression of oncoproteins in undifferentiated cells. CTCF genome, carrying a mutation in the CTCF binding site, shows higher H3K4me3 and reduced H3K27me3 marks in the viral enhancer and in the downstream

early promoter. This is coherent with reduced recruitment of polycomb repressor complex 2 (PCR2), enrichment of RNA pol II binding, and a consequent increase in the transcriptional activity of the viral early promoter. Pentland et al. (176) also showed that both CTCF and YY1 are necessary to repress viral transcription. During cell differentiation, a drop in YY1 expression levels leads to loss of chromatin loop formation and to increased expression of the oncoproteins consecutive to epigenetic depression of the viral genome (176).

TRANSFORMING ACTIVITIES OF PVS

Studies performed on mucosal HR HPV types, such as HPV16 and 18, showed that both oncoproteins E6 and E7 play a key role in cervical cancer by altering pathways involved in the host immune response to establish a persistent infection and promote cellular transformation. The E6 (150 amino acids) and E7 (100 amino acids) oncoproteins play a central role in carcinogenesis by interacting with a large number of cellular proteins involved in key cellular events, such as the cell cycle and apoptosis control. In addition to E6 and E7, HR HPV types encode a small hydrophobic oncoprotein of <90 amino acids, E5, which also appears to play a role in HPV-induced carcinogenesis. Continuous expression of the E6 and E7 oncoproteins is essential to initiate and to maintain the cellular transformation process. Indeed, the use of different strategies to inhibit the function of E6 and E7 in HPV-positive cancer cells resulted in cell growth arrest by apoptosis or senescence (177, 178). The main targets of the E6 and E7 oncoproteins are p53 and pRb, respectively; p53 regulates DNA damage response and apoptosis, and pRb tightly controls the cell cycle. Although E6 and E7 of mucosal HR HPV types were extensively studied, functional data on E6 and E7 of beta HPV types are sparse. Moreover, the absence of cutaneous E6 and E7 transcripts in skin tumors suggests an alternative mechanism for promoting cancer development (hit-and-run mechanism). The beta and gamma HPVs lack the E5 ORF.

Transforming Activities of E6

The E6 oncoprotein of HPV16 is a small protein of \sim 150 amino acids, made up of two zinc-like fingers joined by an interdomain linker (179). E6 of HR HPV types has the ability to bind to the LXXLL peptide motif of cellular proteins. Among them, the E6associated protein (E6AP) is an E3 ubiquitin ligase that targets proteins for ubiquitination and degradation by the proteasome (180). The best-characterized E6/E6AP interaction is with the p53 tumor suppressor (181). In normal cells, p53 plays a key role to safeguard the integrity of the cellular genome, avoiding the proliferation of cells with damaged DNA. Therefore, upon DNA damage insults, p53 will either induce cell-cycle arrest at the G1 phase to allow DNA repair or, if the DNA damage is too extensive, activate apoptotic pathways. E6/E6AP interaction leads to conformational changes of E6 that allow the association with the p53 pro-apoptotic tumor suppressor (182), leading to its ubiquitin-mediated proteasome degradation and, as a consequence, to accumulation of DNA damage and to genomic instability (183).



Although E6 of the β 3 HPV49 type also showed the ability to degrade p53 by an E6AP-dependent mechanism, E6s of HPV species β 2 do not share this property and have evolved alternative mechanisms to counteract p53 functions [reviewed in (19)]. For example, E6 of HPV23 interferes with the ability of the homeodomain-interacting protein kinase 2 (HIPK2) to phosphorylate p53 on serine 46 to activate its apoptotic function upon UVB irradiation (184).

In addition to inducing its degradation, E6 of the mucosal HR HPV types can inactivate p53 and abolish its transactivation *in vivo* (185), by targeting its transcriptional coactivator CBP/p300. This event leads to the displacement of p53 from CBP (186) and to the inhibition of p300-dependent p53 acetylation (187).

As for HR HPV types, the E6 oncoproteins of β 1 HPV types (HPV5, 8) also have the ability to interact with p300 with high efficiency (188). HPV5 and 8 E6s inhibit the association of AKT with the p300 C-terminus that is needed to ensure p300 stability, thus leading to its proteasomal degradation (188). The degradation of p300 results in decreased protein levels of ATR, a

PI3 kinase family member, which plays a key role in UV radiation damage signaling. This event in turn reduces ATR's ability to protect cells against UVB radiation-induced damage (189). The reduced ATR level results in decreased phosphorylation and subsequent attenuated accumulation of p53 in cells in response to UVB radiation exposure. In addition, in HPV5, 8, and 38 E6-expressing cells, arrest in the G1 phase of the cell cycle is prevented, which hampers DNA repair. Both events lead to increased persistence of thymine dimers and UVB radiationinduced double-strand breaks in these cells (189). More recently, Hufbauer et al. (190) showed a lack of phosphorylation of ATM, ATR, and Chk1 in HPV8 E6 expressing-monolayer and organotypic cultures leading to the impairment of DNA damage sensing and repair. Consistent with impaired activation of the ATM/ATR pathway, immunohistochemical analysis revealed the presence of thymine dimers in UVB radiationtreated E6-expressing cells (190), further confirming a role of beta HPV E6 proteins in facilitating UV radiation-induced DNA damage.

Gene products	Alpha HPV features	Beta HPV features					
LCR	 Also called upstream regulatory region (URR), contains the ear involved in viral DNA replication and transcription 	n regulatory region (URR), contains the early promoter and regulatory element replication and transcription					
E6	 Required for the maintenance of the cancer phenotype Required for stable episomal maintenance 	 Not required for the maintenance of the cancer phenotype Inhibition of UV radiation-induced damage repair Hampers the differentiation of HPV8-expressing keratinocytes by targeting the PDZ domain-containing protein syntenin 2 Interacts with Notch pathway and promote the transformation process of the infected keratinocytes 					
	Deregulation of cell cycle						
	 Inhibition of apoptosis 						
	Cell polarity, migration and at	tachment					
	The PDZ domain-binding mc	tif of E6 proteins regulates HPV life cycle					
	 Upregulation of the hTERT promoter activity 						
E7	Required for the maintenance of the cancer phenotype	Not required for the maintenance of the cancer phenotype					
	Required for stable episomal maintenance	 E7 from HPV38 shows the ability to counteract p53-mediated apoptosis by inducing accumulation of the p73 isoform, ΔNp73 					
	Deregulation of cell cycle						
	 Inhibition of apoptosis 						
E5	 Not required for the maintenance of the oncogenic phenotype Increases the immortalization effects of HPV16 E6 and E7 Promotes tumor cell motility and cancer metastasis Promotes cell-cycle progression Inhibition of apoptosis 						
E8^E2	Acts as a transcriptional repressor, and represses E1/E2-dependent replication of the viral origin						
E1	Viral DNA replication						
E2	Ensure the segregation of the viral genome during cell division						
E4	Contributes to efficient productive replication in differentiating cells						
L1	Major capsid protein						
L2	Minor capsid protein						
	• L2 is required for an efficient	trafficking of the viral genome to the nucleus					
	L2 mediates the viral genome	e delivery to the nuclear domain (ND10)					

TABLE 1 | Main features and functions of the early and late gene products from alpha and beta HPV types.

E6 of HPV8 may also play a role in skin carcinogenesis by down-regulating CCAAT/enhancer-binding protein α (C/EBP α), a transcription factor with a role in cell differentiation. MicroRNA-203 (miR-203), previously shown to be an important regulator of epidermal proliferation and differentiation, is induced by C/EBP α . In HPV8 E6 expressing keratinocytes, downregulation of C/EBP α via E6-mediated p300 degradation led to loss of miR-203 expression and induction of the Δ NP63 α protein, altering the proliferation abilities of the infected epithelial cells (191).

Similar to E6s of HPV species $\beta 1$, E6 of HPV38 (species $\beta 2$) was able to prevent p300-mediated acetylation of p53, an event that resulted in its inhibition and thus led to the immortalization of primary keratinocytes (192), indicating that the ability of E6 proteins of HR cutaneous HPVs to induce changes in p53 acetylation status is crucial for the transforming ability of these viruses (192).

E6 has additional cellular targets that play an important role in apoptosis (e.g., Bak, survivin, TNF R1, FADD, procaspase 8) (193–197).

The anti-apoptotic protein Bak, a member of the Bcl-2 family of proteins, plays an important role in regulating the apoptotic process by forming pores with Bax to permeabilize the outer mitochondrial membrane. Bak has been shown to be targeted for degradation by different HPVs from the alpha and beta genera, an event that contributes to preventing UV radiation-induced apoptosis. The ability of the E6 proteins of beta HPVs (e.g., HPV5, 8, or 38) to target Bak for degradation, is important for promoting the survival of DNA-damaged cells and therefore for the progression of NMSC. Bak interacts with the ubiquitin ligase E6AP; however, E6 proteins of HPV5 or 8 that do not interact with E6AP (198) can still induce Bak degradation. Moreover, HPV5 E6 mediates Bak proteolysis when expressed in E6AP-null mouse embryo fibroblast (MEFs) (199), indicating that HPV5 degrades Bak via an E6AP-independent mechanism. Holloway et al. (200) have shown that HERC1 ubiquitin ligase is required for HPV5 E6-mediated Bak degradation (200). In response to UV irradiation, Bak is dephosphorylated on K113 and interacts with HERC1. The association of HERC1 and Bak is dependent upon E6 expression. In fact, HERC1 is recruited by HPV5

E6 to degrade Bak upon UV radiation-induced damage. The degradation of Bak by E6 prevents the release of proapoptotic factors including apoptosis-inducing factor (AIF) from the mitochondria into the nucleus, an event that prevents cells from undergoing UV radiation-induced apoptosis (201).

Those experiments highlight the ability of beta HPVs to enhance UV radiation-induced DNA damage, supporting a role of beta HPVs at the early stage of skin carcinogenesis.

Beta HPVs display additional features for increasing the oncogenic potential of UV radiation exposure by attenuating DNA damage repair. For instance, the binding and destabilizing of p300 by beta HPV5 and 8 E6s also lead to lower levels of BRCA1 and BRCA2, critical to the homology-dependent repair of double-strand breaks (202). Viarisio et al. (104, 121) reported a strong reduction of IL-18 production in HPV38 transgenic mice exposed to UV radiation (104, 121). IL-18 reduces UV radiation-induced DNA damage by the induction of DNA repair (203), suggesting that by inducing a reduction of IL-18 secretion in the mouse skin, HPV38 early proteins may repress the UV radiation-induced inflammasome response, favoring DNA damage accumulation and therefore promoting the carcinogenic process (104).

All HR HPV E6 proteins contain C-terminal PDZ domainbinding motifs (PBMs) that enable interaction with several cellular PDZ domain-containing proteins involved in the regulation of different processes, such as cell polarity, migration, and attachment (204). The interaction of HR HPV E6 with the PDZ proteins leads to their proteasome-mediated degradation (205). The PBM is absent from E6s of LR HPV types, suggesting a key role for this domain in HR HPV-induced carcinogenesis.

A phosphor-acceptor site for protein kinase A (PKA) is located within the PBM. Phosphorylation at this site negatively regulates the PDZ domain-binding activity. The PKA recognition sequence is highly conserved among E6 of HR HPV types and is not present in LR HPV E6 oncoproteins, further suggesting that the PDZ domain-binding activity is crucial in HR HPV-mediated transformation (206, 207). In addition, phosphorylation at this site is required for HPV18 E6 to interact with 14-3-3 ξ , contributing to the stabilization of the oncoprotein (208).

Different PDZ domain-containing proteins have been identified as targets of E6 of HR HPV types: DLG1, a human homolog of Drosophila discs large 1, and hScrib, a homolog of the Drosophila scribble protein (209-211), which play an important role in the polarity of the epithelial cells and have been identified as tumor suppressors (212); the molecular scaffolds membrane-associated guanylate kinase homology proteins, such as MAGI-1 (213), which is involved in the modulation of epithelial cell adhesion and tight junction integrity, acts as a tumor suppressor through the stabilization of PTEN (214, 215); and another HPV16 PDZ domain-containing protein, CAL, which is involved in the regulation of intracellular vesicular trafficking (216). The multi-PDZ domain protein MUPP1, which negatively regulates cellular proliferation, is targeted for degradation by HPV18 E6 and possibly by other HR HPV E6 oncoproteins, thus contributing to the transforming activities of E6 oncoproteins (217). The PDZ domain-containing proteins PSD95, TIP-2/GIPC, and NHERF1, which are involved in different signaling pathways, are also targeted by E6 (218–220).

In addition to playing a role in many cellular processes, the PBM of E6 proteins also regulates the HPV life cycle; mutations of this motif were shown to lead to lower levels of episomal HPV genome and cell growth (221). HPV8 E6, which lacks the PBM, can target the PDZ domain-containing protein syntenin 2, by reducing its expression level in a MAML1-independent manner, by an epigenetic mechanism. This event plays a key role in hampering differentiation of HPV8-expressing keratinocytes (222) and provides a further example of how skin and mucosal HPV types evolved different mechanisms to alter normal cell homeostasis and induce cellular transformation.

Using a proteomic approach, Thomas et al. (223) compared the ability of E6 PBMs of HPV types with different oncogenic potentials to interact with PDZ substrates (223). This comprehensive analysis showed that the number of PDZ substrates varies according to the HPV type. Most of the PDZ substrates were recognized by HR types (i.e., HPV16 and 18), whereas HPV66, which is a possible HR HPV type, recognizes only a limited number of substrates. Of note, whereas PDZ substrates such as DLG1 are common targets of the E6 proteins irrespective of their oncogenic potential, the ability of E6 PBMs to interact with hScrib, a component of the Scribble polarity complex, is correlated with the transforming ability of the studied HPV types (223).

Telomerase activity also plays an important role during cervical carcinogenesis, because it increases with the grade of the cervical lesions (224). The ability to activate the promoter of hTERT (human telomerase reverse transcriptase), the catalytic subunit of the telomerase, by different HPVs was assessed using a luciferase-based assay. The results of that study showed that several HR HPV types significantly upregulated hTERT promoter activity (225). The induction of hTERT requires the E6/E6AP complex to interact with the heterodimer c-Myc/Max (226–229). Moreover, E6 recruits histone acetyltransferase (HAT) at the hTERT promoter, which facilitates the access of transcriptional activators to key regulatory sites through the opening of the chromatin (230).

NFX1-91, a constitutive hTERT repressor, is targeted by E6/E6AP for ubiquitin-dependent degradation (230). The induction of hTERT expression by E6/E6AP is also dependent on the activation of NFX1-123, which constitutes a level of posttranscriptional regulation (231). Together, these events lead to extending the life span of primary human keratinocytes, and to their immortalization. Proteomics studies comparing the cellular protein-binding partners of the E6s of HPV types of different genera have shown that whereas all the studied alpha HPV E6s have a high affinity for E6AP and HERC2 (232), beta and gamma HPV E6s specifically interact with the cellular transcriptional co-activator MAML1 (233). The latter interaction is required to inhibit Notch1, a key player in skin differentiation and in the activation of transcription of the cell-cycle inhibitor p21. Interaction of beta HPV E6 with the Notch pathway appears to be important to promote the transformation process of the infected keratinocytes (234, 235). The different affinities of E6s of different genera for specific cellular targets could be a consequence of their tropism and co-evolution with different type of tissues (236).

Transforming Activities of E7

The E7 oncoprotein is made up of \sim 100 amino acids and has a C-terminal zinc-binding domain. HPV E7 presents three conserved regions, homologous to adenovirus E1A: CR1, CR2 in the N-terminal part, and CR3 in the C-terminal part. Moreover, HPV E7 comprises two nuclear localization sequences (NLSs) and one nuclear export sequence (NES), which enable E7 to be located in both the nuclear and cytoplasmic compartments, where E7 has different functions (237).

The CR1 domain has an UBR4/p600 binding site; the 600kDa pRb-associated factor p600 is required for membrane morphogenesis, anchorage-independent growth, and cellular transformation (238, 239). Moreover, the interaction between BPV-1 E7 and p600 inhibits apoptosis, contributing to viralinduced transformation (240). UBR4/p600 ubiquitin ligase also appears to be involved in E7-mediated proteasomal degradation of the potential tumor suppressor PTPN14 (241), identified as a target of HR HPV E7 in cervical tumors (241, 242). The ability of HPV16 E7 to bind to p600 correlates with its capacity to transform cells (238). Similarly to E6, E7 binds to CBP/p300 and to its associated factor (pCAF) by interacting with the CBP TAZ2 domain (also known as CH3). The E7 binding site responsible for its interaction with the CBP TAZ2 domain overlaps with the LXCXE motif, which is crucial for E7 to bind to pRb. Formation of the ternary complex of E7/pRb and pCAF leads to the acetylation of pRb, an event that appears to play an important role in HPV-mediated transformation, probably by stabilizing the E7/pRb interaction (243, 244).

The CR2 domain comprises serine residues at positions 31 and 32 that are susceptible to phosphorylation by casein kinase II (CKII). Phosphorylation at these sites contributes to modulating some of the E7 functions. For example, CKII phosphorylation of E7 increases the binding affinity of HPV16 E7 for the TATA box-binding protein (TBP) (245), and it is required for efficient transformation by E7 (246). Interestingly, an additional phosphorylation site at serine position 29 exists in a natural E7 variant (N29S) and leads to increased levels of phosphorylation by CKII, which increases the interaction of E7 with TBP and pRb, and its transforming activity in primary rodent cells (247).

CR2 also comprises a conserved LXCXE motif located at residues 22-26 in HPV16 E7. This motif is essential for the interaction with pRb and related pocket proteins (p107 and p130) (248). An intact LXCXE motif is needed to induce cellular DNA synthesis and mediates cell transformation of immortalized NIH3T3 cells. Residues in the CR3 domain of E7 also seem to be required for its interaction with pRb (249). pRb and related pocket proteins (p107 and p130) play a key role in the regulation of the cell cycle by binding to and inhibiting E2F transcription factors (E2Fs), which regulates the expression of genes required for DNA synthesis and cell division. HR HPV E7 oncoproteins are able to target pRb and other members of the retinoblastoma family for proteasome-mediated degradation. This event requires the recruitment of the cullin-2 ubiquitin ligase complex, which binds to the CR1 region (250). Upon pRb interaction with HPV E7, E2F is released, with subsequent transcriptional induction of G1–S cell-cycle genes, such as cyclin A and cyclin E. The latter products are required for the activation of the cyclindependent kinase (CDK) complexes, which force the entry of HPV-infected cells into the S phase (251). This event leads to unscheduled growth and accumulation of genomic instability. LR HPV E7s bind to but are not efficient in targeting pRb for degradation (252). The ability of E7 to interact with pRb is not sufficient for HPV-induced transformation, which, as mentioned above, requires the interaction of E7 with additional cellular proteins (253).

The functionally and structurally pRb-related proteins, p107 and p130, are also targeted by the HPV E7 via the LXCXE motif, and both have the ability to bind to and inactivate E2Fs. These proteins are important negative regulators of the cell cycle, and they are believed to also act as tumor suppressors. However, unlike pRb, their role as tumor suppressors is still controversial, because related genetic alterations are not frequent in human cancers. Both HR and LR HPV E7s target p130 for proteasomal degradation, most likely by different mechanisms, thus highlighting an important role of this pocket protein in the HPV life cycle (254).

Analysis of HPV E7-interacting proteins showed that HPV16 E7 interacts with E2F6, which has the particularity of lacking the binding domain for pRb and acts as a transcriptional repressor. The association of HPV16 E7 with E2F6 abrogates its repressive activity on target genes, which results in increased DNA replication of HPV16-infected cells (255).

Using an organotypic culture of skin, Akgül et al. (256) showed that beta HPV8 E7-transduced keratinocytes displayed an invasive phenotype, in addition to losing their polarity (256). HPV8 E7-transduced keratinocytes also showed enhanced production of extracellular proteinases (MMP-1, MMP-8, and MT1-MMP) that play a role in the degradation of components of the basement membrane and the ECM during cell invasion. In another study, the same group used a transgenic mouse model expressing the E7 oncoprotein of HPV8 in the epidermis to investigate the molecular basis for HPV-induced invasion of skin keratinocytes. HPV8 E7 expression in mouse skin led to a reduction of E-cadherin and a subsequent upregulation of N-cadherin, an event that causes epithelial-mesenchymal transition. E7-positive keratinocytes also showed increased fibronectin expression and secretion. In addition, HPV8 E7expressing cell surface showed enhanced levels of the integrin α 3 chain, which plays a crucial role at the pre-invasive stage (257). E7 of beta-HPVs may play an important role in promoting an invasive phenotype in keratinocytes and may provide additional evidence to support a role of cutaneous HPVs in skin carcinogenesis.

HPV8 also has the ability to maintain cells in a "stemness-like" phenotype. Using *in vitro* colony formation and tumor sphere assays, Hufbauer et al. (258) showed that beta HPVs are able to increase the number of stem cell-like cells, as determined by measuring the number of HPV8 E2-, E6-, and E7-expressing cells harboring high levels of epithelial stemness cell surface markers, such as CD44 and epithelial cell adhesion molecule (EpCAM). EpCAM induction was also observed in organotypic skin cultures of HPV5, 8, and 16 E7-expressing cells, as well as in skin lesions of patients with EV (258). E7 expression

also led to a reduction of the epithelial differentiation marker calgranulin B. Together, these results highlight a possible role of beta HPVs in skin carcinogenesis by increasing the number of stem cell-like cells present during early carcinogenesis and delaying cell differentiation.

Lanfredini et al. (259) evaluated KSC populations located in different regions of the hair follicle (259). In that study, using HPV8 transgenic (HPV8tg) mice that express the entire HPV8 early region, the authors identified KSCs from the upper part of the junctional zone as the site from which the expansion to the interfollicular epidermis takes place during the initial step of skin carcinogenesis. This population of stem cells express leucinerich repeats and immunoglobulin-like domains protein 1 (Lrig-1) and are characterized by nuclear staining for the stemness marker p63. Skin accumulation of the p63 isoform, $\Delta Np63$, which is induced by the expression of HPV8 early proteins, promotes the proliferation and expansion of Lrig1-positive KSCs. In healthy skin, the $\Delta NP63\alpha$ transcript is directly targeted by miR-203, an event that plays a major role in the regulation of epidermal proliferation and differentiation, leading to "stemness" loss (260, 261). Of note, the skin lesions of patients with EV show strong p63 immunostaining associated with very low levels of miR-203.

In addition to features cited above, E7 can also deregulate the cell cycle by binding and abrogating the inhibitory effect of CDK inhibitors like p21^{Cip1} and p27^{Kip1}. This interaction abolishes their inhibitory effect on the cell cycle and highlights a different mechanism by which E7 favors cell proliferation (262–264).

E6 and E7 of HPV38 and 49, which can efficiently immortalize human primary keratinocytes, do not have the ability to target pRb for degradation when expressed in these cells (120). However, similarly to E7 of LR mucosal types HPV38 and 49 E7s can efficiently bind to pRb. In contrast, beta HPV8 E7 binds to pRb to a lesser extent compared with HPV16 E7, but it is still able to repress pRb levels when expressed in keratinocytes (265, 266).

Studies from our laboratory have shown that different beta HPV types (e.g., HPV38) are able to trigger pRb hyperphosphorylation, an event that leads to release of E2F and to the transcriptional activation of E2F target genes [reviewed in (19)]. In addition, E7 of HPV38 shows the ability to counteract p53-mediated apoptosis by inducing accumulation of the p73 isoform, Δ Np73, by two different mechanisms: (i) by inducing the recruitment of a post-translationally modified form of p53 to the promoter of Δ Np73, which activates its transcription (267), and (ii) by mediating Δ Np73 protein stabilization with an IkB kinase beta (IKK β)-mediated mechanism (268). The latter studies highlight that cutaneous HPVs have evolved different mechanisms than HR mucosal HPVs, to target key cellular proteins (pRb and p53) and promote cellular transformation.

Transforming Activities of E5

Although the transforming activities of E6 and E7 oncoproteins are well characterized, the role of the E5 oncoprotein is still poorly understood (269). E5 is a hydrophobic membraneassociated protein that localizes to the endoplasmic reticulum, Golgi apparatus, and plasma membrane (270, 271). E5 forms a hexameric viroporin complex, which modulates ion homeostasis (269). E5 viroporin is required for the hyperactivation of mitotic signaling, and it plays a key role during the life cycle of HR HPV types. Recombinant HPV16 E5 membrane channel activity is sensitive to compounds such as adamantine and rimantadine. Inhibition of E5 viroporin activity in primary human keratinocytes harboring HPV18 genome leads to decreased ERK-MAPK phosphorylation and cyclin B1 levels, and to an increase in the expression of differentiation marker (272). E5 viroporin activity is therefore critical for maintaining mitogenic signaling and delaying expression of differentiation marker during the productive stages of the HPV18 life cycle; therefore, targeting viroporin could pave the way for an effective antiviral strategy.

The expression of E5 increased the immortalization effects of HPV16 E6 and E7 (273). E5 is involved in the transformation of primary human keratinocytes by potentiating epidermal growth factor receptor (EGFR) signaling (274). In 16E5 transgenic mice, EGFR is required for epithelial hyperplasia (275). The activation of EGFR leads to induction of the expression of cyclooxygenase-2 (COX-2), which plays an important role in cervical carcinogenesis, through nuclear factor-kappa B (NF- κ B) and AP-1 (276). Via stimulation of EGFR, HPV16 E5 induces Met, a growth factor receptor involved in tumor cell motility and cancer metastasis; moreover, Met signaling is required for proper differentiation-dependent viral gene expression (277).

HPV16 E5 protein enhances, in cooperation with EGFR signaling, the down-regulation of tumor suppressor p27^{Kip1} levels, which promotes cell-cycle progression (278). The level of another CDK inhibitor, p21, is reduced in cells that over-express E5 (279). Both events lead to an increase in cell proliferation and in the percentage of cells in the S phase.

HPV16 E5 also contributes to carcinogenesis by inhibiting apoptosis by multiple molecular strategies. The effect of HPV16 E5 on apoptosis was assessed using raft cultures in which E5 prevented FasL- or TRAIL-mediated apoptosis (280). A recent study reported that HPV16 E5 specifically down-regulates miR-196a in cervical cancer cells. The same study showed that miR-196a expression affects cell proliferation, cell growth, and apoptosis, thus confirming the role of HPV16 E5 in cervical cancer development (281). Another anti-apoptotic strategy consists of decreasing pro-apoptotic Bak and Bax levels, and increasing the expression of the anti-apoptotic Bcl-2. HPV16 E5 inhibits apoptosis of cervical cancer cells by stimulating the ubiquitin-proteasome-mediated degradation of Bax protein (282). It has also been reported that HPV16 E5 protects E5expressing foreskin keratinocytes from UVB radiation-induced apoptosis (283).

All these data indicate that expression of E5 contributes to HPV-driven cellular transformation. However, unlike E6 and E7, E5 is not required for the maintenance of the oncogenic phenotype, because the E5 ORF is frequently disrupted during HPV integration, thus rather highlighting a role of E5 at the initial step of carcinogenesis (284).

HPV types from different genera (beta, gamma, and mu) lack the E5 ORF, suggesting that the corresponding functions are performed by other viral proteins.

E5 forms a complex with EVER1 and EVER2, proteins encoded by the TMC6 and TMC8 genes, respectively, (92). Most of the patients with EV who are susceptible to persistent beta HPV infections carry mutations in these genes. The EVER proteins interact with the zinc transporter ZnT-1 in order to regulate intracellular zinc homeostasis. Zinc sequestration by the ZnT-1/EVER complex may inhibit the replication of EV-associated HPV types. In contrast, mutations in EVER proteins lead to the disruption of the ZnT-1/EVER complex, and an increase in the level of zinc in the cytoplasm, resulting in increased replication of EV-associated HPV types (285), [reviewed in (286)]. A recent study reported that patients with EV can also display the typical EV phenotype, bearing nonsynonymous calcium- and integrin-binding protein 1 (CIB1) mutations and lacking TMC6 and TMC8 mutations (287). CIB1 does not seem to interact with ZnT-1, but this protein forms a complex with EVER1 and EVER2. The CIB1-EVER1-EVER2 complex appears to act as a restriction factor for infection by cutaneous HPVs that do not express E5. In patients with EV, impairment of CIB1, EVER1, or EVER2 allows replication of these HPV types and development of EV lesions on the skin (287).

CONCLUSIVE REMARKS, CHALLENGES, AND OPEN QUESTIONS

In the past decades, epidemiological and biological studies have clearly demonstrated the role of mucosal HR HPV types in human carcinogenesis. While co-evolving with the human host, HPVs have developed strategies to evade the immune system and create the optimal conditions to persist in the host for many years. During HPV chronic infection, the E6 and E7 oncoproteins interact with different cellular proteins to prevent apoptosis, counteract the cellular senescence program, and promote unscheduled cell growth. These activities of HR HPV E6 and E7 are part of a viral strategy to complete the viral life cycle and generate progeny. The expression of the oncoproteins is kept under the tight control of E2. Loss of E2 repressive functions, by viral integration or by other mechanisms, which are discussed in this review, leads to constitutive high expression of E6 and E7, a key event in HPV-mediated transformation (Figure 3). Although the mechanisms leading to cervical cancer have been well-characterized, there is still a gap in the understanding of the pathogenesis of other HPVrelated malignancies, e.g., oropharyngeal cancer. The proportion of HPV-driven oropharyngeal cancers has been increasing over the past decades in many parts of the world, mainly in Europe and North America (288-290). The natural history of HPV infection in the oral cavity and oropharynx is poorly studied and needs further investigation.

Of note, recent studies identified HPV16 E6 antibody as a good diagnostic and prognostic marker of oropharyngeal cancer. HPV16 E6 seropositivity was detected more than 10 years before the diagnosis (291, 292).

Moreover, although the available prophylactic vaccines have demonstrated their effectiveness in the context of prevention

of anogenital cancers (293), very limited epidemiological data are available on the efficacy of the HPV vaccine on oral HPV infection (294). This deserves further investigation.

Prophylactic vaccines show a good efficiency in covering targeted HPVs, but they are inefficient in existing infections. Therefore, therapeutic vaccines are needed to fill this gap. Several studies have reported the development of promising therapeutic vaccines. Their use in the near future could be expected; however, their cost could be high. This limitation could be overcome by the use of inexpensive technologies (i.e., plant-made therapeutics) (295–299).

One of the most recurrent questions regarding the prophylactic vaccine is whether HPV vaccination will result in the occupation of a newly vacant ecological niche by non-targeted HPV types. This hypothesis has been referred as "type replacement." To date, the available data do not support this hypothesis. However, as reported in recent studies, a few types (i.e., HPV51 and 52) may need to be monitored after vaccination (300, 301).

The bacterial microbiome composition may also play a role in the outcome of mucosal HPV infection. A chronic mycoplasma infection was shown to promote cervical dysplasia induced by HPV (302). Therefore, identifying the bacterial microbiome could allow the identification of patients at high risk for developing cervical cancer.

Our knowledge of the biology of beta and gamma HPV types is still uncomplete. For example, the expression patterns of cutaneous HPV types and associated splicing patterns are largely unknown, except for HPV5 and 8 (https://pave.niaid. nih.gov/). There are also important gaps in the understanding of the life cycle of cutaneous HPV types, which also deserve further research.

In February, 2009, an IARC Monograph Working Group met at IARC to assess the carcinogenicity of biological agents including beta and gamma HPV types. HPV5 and 8 were classified as possibly carcinogenic to humans in patients with EV (IARC Group 2B), whereas the other cutaneous HPV types were each determined to be "not classifiable as to its carcinogenicity to humans" (IARC Group 3), on the basis of insufficient epidemiological and biological data available at that time (10). In fact, although several epidemiological and biological studies support a role of β 1 and β 2 HPV types in NMSC, the lack of cutaneous HPV E6 and E7 expression in SCC has raised the question of whether the viral proteins are required in the carcinogenesis process.

Since that 2009 meeting, strong epidemiological and experimental data in favor of a role of cutaneous HPV types as cofactors in skin carcinogenesis have been published, as described in this review. Indeed, recent findings from our group and others have shown that unlike the expression of oncoproteins of HR HPV types, cutaneous HPV E6 and E7 expression appears to be required only at the initial step of skin carcinogenesis by exacerbating the deleterious effects of UV radiation (104). Over the past decade, studies using experimental animals (HPV38 transgenic mice and the MnPV-infected rodent model *Mastomys coucha*) have provided strong *in vivo* evidence for a synergism between UV radiation and cutaneous HPV types

in the development of cSCC (104, 107). Most importantly, both models provided further evidence for a hit-and-run mechanism. However, additional studies are still necessary to validate this hypothesis in humans.

In addition to these experimental data, a recent prospective study of two organ transplant recipient cohorts showed that having five or more different beta HPV types in eyebrow hair, and a high beta HPV viral load, was associated with cSCC carcinogenesis, providing strong evidence for a role of beta HPVs in this cancer, whereas no evidence was found for basal cell carcinoma (303). The development of vaccination strategies that target cutaneous HPV infections would be of great benefit to these patients (304, 305).

Another open question regards the tropism of certain HPVs. As previously specified in this review, a dual tropism of HPV species β 3 has been proposed. Moreover, this species displays biological similarities with mucosal HR HPV types (111, 120). Our recent data highlighted that E6 and E7 of HPV49 share some features with HR mucosal types, and efficiently transform epithelial cells in *in vitro* and *in vivo* models (120, 121). In addition, in line with these biological data, epidemiological studies have shown β 3 HPVs and other cutaneous types in the oral cavity mucosa. Beta and gamma HPV types have also been isolated from the nasopharynx and the nasal mucosa (119, 306). Moreover, a recent study based on a prospective design reported that beta or gamma HPV types were associated with the incidence of HNC (117). Those findings warrant further studies to better

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understand the role of those so-called "cutaneous HPV types" in mucosotropic cancers (111, 119).

A large number of gamma HPV types have been isolated; however, their biological activities are poorly studied and deserve more investigation. Finally, some of the known but not yet biologically characterized beta or gamma HPV types may display transforming activity and also deserve attention. In addition to these not-yet-studied types, one may also consider the large number of novel HPVs found in recent years, as well as the rapid evolution of viral detection and screening techniques and large data set analysis pipelines.

For all these reasons, we believe that in the coming years the field of HPV research will continue to be a source of surprises and excitement for the scientific community.

AUTHOR CONTRIBUTIONS

The author confirms being the sole contributor of this work and has approved it for publication. TG wrote the manuscript and designed the figures.

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(-)-Epigallocatechin-3-gallate inhibits human papillomavirus (HPV)-16 oncoprotein-induced angiogenesis in non-small cell lung cancer cells by targeting HIF-1 α

He L, Zhang E, Shi J, Li X, Zhou K, Zhang Q, Le AD, Tang X.

Institute of Biochemistry and Molecular Biology, Guangdong Medical College, 2 Wenming Donglu, Xiashan, Zhanjiang, 524023, Guangdong, People's Republic of China.

Abstract

PURPOSE: To investigate the effects of (-)-epigallocatechin-3-gallate (EGCG) on human papillomavirus (HPV)-16 oncoprotein-induced angiogenesis in non-small cell lung **cancer** (NSCLC) cells and the underlying mechanisms.

METHODS: NSCLC cells (A549 and NCI-H460) transfected with EGFP plasmids containing HPV-16 E6 or E7 oncogene were treated with different concentrations of EGCG for 16 h. The effects of EGCG on angiogenesis in vitro and in vivo were observed. The expression of HIF-1 α , p-Akt, and p-ERK1/2 proteins in NSCLC cells was analyzed by Western blot. The levels of HIF-1 α mRNA in NSCLC cells were detected by real-time RT-PCR. The concentration of VEGF and **IL-8** in the conditioned media was determined by ELISA. HIF-1 α , VEGF, and CD31 expression in A549 xenografted tumors of nude mice was analyzed by immunohistochemistry.

RESULTS: HPV-16 E6 and E7 oncoproteins HIF-1 α -dependently promoted angiogenesis in vitro and in vivo, which was inhibited by EGCG. Mechanistically, EGCG inhibited HPV-16 oncoprotein-induced HIF-1 α protein expression but had no effect on HIF-1 α mRNA expression in NSCLC cells. Additionally, 50 and 100 µmol/L of EGCG significantly reduced the secretion of VEGF and **IL-8** proteins induced by HPV-16 E7 oncoprotein in NSCLC A549 cells. Meanwhile, HPV-16 E6 and E7 oncoproteins HIF-1 α -dependently enhanced Akt activation in A549 cells, which was suppressed by EGCG. Furthermore, EGCG inhibited HPV-16 oncoprotein-induced HIF-1 α and HIF-1 α -dependent VEGF and CD31 expression in A549 xenografted tumors.

CONCLUSIONS: EGCG inhibited HPV-16 oncoprotein-induced angiogenesis conferred by NSCLC through the **inhibition** of HIF-1 α protein expression and HIF-1 α -dependent expression of VEGF, **IL-8**, and CD31 as well as activation of Akt, suggesting that HIF-1 α may be a potential target of EGCG against HPV-related NSCLC angiogenesis.

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Meta-Analysis Shows Importance of HPV Vaccines

By Leah Lawrence

July 2, 2019

Cervical Cancer, Gynecologic Cancers, News

Significant reductions in several strains of human papillomavirus (HPV) and HPVassociated diseases have occurred in the up to 8 years of follow-up since implementation of the girls-only HPV vaccination, according to results of a metaanalysis<u>published</u> in *Lancet Oncology.*

The review and meta-analysis included data from 65 articles from 14 high-income countries (most of which had girls/women-only programs), encompassing follow-up data from more than 60 million individuals over 8 years.

During that time, the prevalence of HPV 16 and 18 decreased by 83% among girls age 13 to 19 years old, and by 66% among women age 20 to 24 years. In addition, cross protection occurred, with the prevalence of HPV 31, 33, and 45 decreasing by 54% among girls age 13 to 19 years.

There was also evidence of herd protection from the vaccine. Specifically, anogenital warts decreased by 67% among girls age 15 to 19 and by 54% among women age 20 to 24, but also by 31% among women age 25 to 29, 48% among boys age 15 to 19, and 32% in men age 20 to 24.

"Our results provide strong evidence of HPV vaccination working to prevent cervical cancer in real-world settings, as both the cause (high-risk HPV infection) and proximal disease endpoint (CIN2+) are significantly declining," wrote <u>Mélanie</u> <u>Drolet, PhD</u>, of Laval University in Quebec, and colleagues from the HPV Vaccination Impact Study Group. "In terms of global policy implications, these results reinforce the recently revised position of WHO recommending HPV vaccination of multiple age cohorts of girls, and provide promising early signs that the WHO call for action on cervical cancer elimination might be possible if sufficient population-level vaccination coverage can be reached."

After a period of 5 to 9 years of vaccination, the rate of CIN2+ decreased by more than half (51%) among screened girls age 15 to 19 years and by about one-third (31%) among women age 20 to 24.

In an <u>editorial</u> that accompanied the article, <u>Silvia de Sanjosé, PhD</u>, of PATH in Seattle, and <u>Sinead Delany-Moretlwe, MBBCh, PhD</u>, of Wits Reproductive Health and HIV Institute in South Africa, pointed out that one limitation of the study is its lack of inclusion of data from low- and middle-income countries, "where the burden of disease accounts for over 80% of deaths attributable to HPV-related cancer."

However, collection of these data in low- and middle-income countries would be challenging due to a lack of surveillance system to link vaccinations with outcome data. In addition, vaccine cost and inadequate supply may slow the process of vaccine introduction to these countries.

"For the next 5 years, vaccine supplies are projected to be constrained and unable to accommodate demand because of fewer requirements to introduce HPV vaccines in countries supported by Gavi, the Vaccine Alliance, increased interest in multiple age-cohort vaccination, and introduction of a gender-neutral approach," they wrote. "The scale-up of HPV vaccine introduction in low- and middle-income countries will be particularly affected by these constraints."

Data from studies like this meta-analysis can help implementers to concentrate on high-priority targets.

"The data presented by Drolet and colleagues emphasize the importance of redoubling our efforts to tackle the fiscal, supply, and programmatic barriers that currently limit HPV vaccine programs; with these efforts, HPV vaccination could become a hallmark investment of cancer prevention in the 21st century," they concluded.

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ORIGINAL ARTICLE



TriCurin, a synergistic formulation of curcumin, resveratrol, and epicatechin gallate, repolarizes tumor-associated macrophages and triggers an immune response to cause suppression of HPV+ tumors

Sumit Mukherjee^{1,2,3} · Rahman Hussaini³ · Richard White³ · Doaa Atwi³ · Angela Fried^{1,3} · Samay Sampat⁴ · Longzhu Piao^{5,6} · Quintin Pan^{5,6} · Probal Banerjee^{2,3}

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Abstract

Our earlier studies reported a unique potentiated combination (TriCurin) of curcumin (C) with two other polyphenols. The TriCurin-associated C displays an IC50 in the low micromolar range for cultured HPV+TC-1 cells. In contrast, because of rapid degradation in vivo, the TriCurin-associated C reaches only low nano-molar concentrations in the plasma, which are sub-lethal to tumor cells. Yet, injected TriCurin causes a dramatic suppression of tumors in TC-1 cell-implanted mice (TC-1 mice) and xenografts of Head and Neck Squamous Cell Carcinoma (HNSCC) cells in *nude/nude* mice. Here, we use the TC-1 mice to test our hypothesis that a major part of the anti-tumor activity of TriCurin is evoked by innate and adaptive immune responses. TriCurin injection repolarized arginase1^{high} (ARG1^{high}), IL10^{high}, inducible nitric oxide synthase^{low} (iNOS^{low}), IL12^{low} M2-type tumor-associated macrophages (TAM) into ARG1^{low}, IL10^{low}, iNOS^{high}, and IL12^{high} M1-type TAM in HPV+ tumors. The M1 TAM displayed sharply suppressed STAT3 and induced STAT1 and NF-kB(p65). STAT1 and NF-kB(p65) function synergistically to induce *iNOS* and *IL12* transcription. Neutralizing IL12 signaling with an IL12 antibody abrogated TriCurin-induced intra-tumor entry of activated natural killer (NK) cells and Cytotoxic T lymphocytes (CTL), thereby confirming that IL12 triggers recruitment of NK cells and CTL. These activated NK cells and CTL join the M1 TAM to elicit apoptosis of the E6+ tumor cells. Corroboratively, neutralizing IL12 signaling partially reversed this TriCurin-mediated apoptosis. Thus, injected TriCurin elicits an M2 \rightarrow M1 switch in TAM, accompanied by IL12-dependent intra-tumor recruitment of NK cells and CTL and elimination of cancer cells.

Keywords Curcumin · TriCurin · Papillomavirus · Tumor-associated macrophages · NK cells · CTL

Rahman Hussaini and Richard White contributed equally	Abbreviations ARG1 Arginase-1 C Curcumin
Electronic supplementary material The online version of this article (https://doi.org/10.1007/s00262-018-2130-3) contains supplementary material, which is available to authorized users.	— CD8 Cluster of differentiation 8 protein CD8α Cluster of differentiation 8 alpha
Probal Banerjee probal.banerjee@csi.cuny.edu	⁴ College of Arts and Science, New York University, New York, NY 10003, USA
¹ CUNY Doctoral Program in Biochemistry, CUNY Graduat Center, New York, NY 10016, USA	⁵ Department of Otolaryngology-Head and Neck Surgery, The Ohio State University Medical Center, Columbus, OH 43210 USA
² Department of Chemistry, Building 6S, The City University of New York at The College of Staten Island, 2800 Victory	⁶ Arthur G. James Cancer Hospital and Richard J. Solove

Arthur G. James Cancer Hospital and Richard J. Solove Research Institute, The Ohio State University Comprehensive Cancer Center, Columbus, OH 43210, USA

CTL	Cytotoxic T lymphocytes
CUNY	City University of New York
E	Epicatechin gallate
E6 16/18	Early 6 protein 16/18
E7	Early 7 protein
HaRas	Harvey ras protein
HC1	Hydrochloric acid
HNSCC	Head and neck squamous cell
	carcinoma
HPV	Human papillomavirus
IACUC	Institutional Animal Care and Use
	Committee
Iba1	Ionized calcium-binding adapter mol-
	ecule 1
IF	Integrated fluorescence
IFNγ	Interferon gamma
IgG	Immunoglobin G
IL10	Interleukin-10
IL12	Interleukin-12
iNOS	Inducible nitric oxide synthase
LEEP	Loop electrosurgical excision
	procedure
LR	Lower right
NCr	Athymic nude mice
NKp46	Natural killer cell p-46-related protein
NOS2	Nitric oxide synthase 2
PFA	Paraformaldehyde
P-NF-kB	Phospho-NF-kB
P-p65	Phospho-p65
P-ser	Phosphor-serine
P-STAT1/3	Phospho-STAT1/3
P-Tyr	Phospho-tyrosine
R	Resveratrol
S.E.	Standard error
SEM	Standard error of the mean
SSC	Saline-sodium citrate
TAM	Tumor-associated macrophage
TriCur+IL12Ab	'IL12 antibody infusion followed by
	TriCurin treatment' group
UL	Upper left
UMSCC47	University of Michigan-squamous cell
	carcinoma-47
UR	Upper right
w/v	Weight/volume
	-

Introduction

The human papillomavirus (HPV) is the major risk factor for cervical cancer that claims numerous lives globally and is a major threat to women especially in the developing countries where screening and vaccinations are not affordable or realistic due to the lack of infrastructure. The incidence of cervical cancer is rather low in the developed countries because of extensive screening programs [1–3]. Though the availability of two vaccines, Cervarix[®] and Gardasil[®], offers preventive measures against the usual tumorigenic HPV16/18+ cervical lesions, effective therapy for postinfection lesions is currently unavailable [4]. High-risk HPV16+ infection has also emerged as an etiologic factor for the development of head and neck squamous cell carcinoma (HNSCC), with new cases escalating worldwide. The standard of care for HNSCC consists of surgery, radiation therapy, chemotherapy, or a combination of treatments, which have significant side effects and/or are associated with high morbidity [2, 5, 6]. This emphasizes the need for safe therapeutic approaches to treat HPV+ cervical cancer and HNSCC.

In earlier studies, we developed a formulation, termed TriCurin, containing curcumin (C) with two other foodderived natural polyphenols, resveratrol (R) and epicatechin gallate (E) at a unique and synergistic molar ratio. TriCurin is non-toxic to normal cells and selectively eliminates cancer cells in vitro and also in HaRas+, HPV16 E6+ and E7+TC-1 cell-evoked mouse tumors and xenografts of HNSCC tumors in athymic nude/nude mice (NCr) [7, 8]. Poor bioavailability of C seriously limits its anti-tumor efficacy and the increased potency of TriCurin against cancer cells has been attributed to the stabilization of C in the presence of R and E and increased uptake of C from TriCurin into tumor cells [8]. Thus, such improved delivery of C has enabled us to use TriCurin to efficiently eliminate a wide array of tumor cells [7–15]. Although enhanced delivery increases the plasma concentration of C, it never reaches beyond the low nanomolar range, which is not high enough to cause direct elimination of cancer cells, which requires micromolar curcumin (Sumit Mukherjee et al., unpublished). We have postulated that the nano-molar level of C in the plasma is sufficient to activate the innate and adaptive immune system against tumor [12, 13, 16-21].

We demonstrate here for the first time that TriCurin treatment of tumor-bearing mice leads to an overall repolarization of the milieu of HPV+ tumor-associated macrophages from an M2 state to M1 phenotype. In addition, we also demonstrate that TriCurin-evoked repolarization of TAM is associated with intra-tumor recruitment of activated NK cells and CTL which are known to have tumoricidal activity [16, 17, 19, 20]. These changes in the tumor microenvironment play a major role in TriCurin-evoked elimination of HPV+ tumors [1, 7, 8, 12, 14].

Promising clinical trials using chimeric antigen receptor (CAR) T-cell treatment and regulators of T-cell activation (checkpoint inhibitors) have recently yielded immunotherapy drugs for cancer. Our therapeutic strategy using Tri-Curin also depends on the activation of the immune system against tumor, but unlike other approaches, it involves a highly potent agent (TriCurin), which does not elicit the side effects commonly experienced in other therapies [22, 23]. Thus, TriCurin is a promising immunotherapeutic agent for various types of cancer.

Materials and methods

Animals

Please see the 'Animal Source' subsection under 'Compliance With Ethical Standards'.

Preparation of TriCurin

1.28 mM + TriCurin solution in PBS was prepared according to our earlier reports [7, 8].

Cell culture

HPV+ mouse TC-1 cells and UMSCC47 human cells were procured, authenticated, and cultured as reported earlier. HPV16+ UMSCC47 HNSCC cells were obtained from Dr. Thomas Carey (University of Michigan) [7, 8].

Implantation of cancer cells in mice

To generate the TC-1 mouse model, experiments were performed according to our previous report [8]. The tumors were allowed to grow to a diameter of 0.5 cm before intratumor infusion of TriCurin.

To generate the pre-clinical UMSCC47-derived HNSCC (UMSCC47) xenograft tumors in athymic *nudelnude* mice (NCr), experiments were performed according to our earlier report. The tumors were allowed to be palpable before intra-tumor infusion of TriCurin [7].

Treatment of pre-clinical HPV+ tumor-bearing mice with TriCurin

When the TC-1 tumors assumed the approximate length of 0.5 cm, eight mice were randomly divided into two groups: "Vehicle" (PBS plus 5% DMSO) (n=6), "Tri-Curin" (n=6), and "TriCurin + IL12Ab" (n=3). Each tumor was marked into four quadrants and 2.5 µl of the 1.28 mM + TriCurin solution (or Vehicle) was infused into each of the four quadrants every 24 h for 5 days (final estimated intra-tumor concentration for each injection: 64 µM+). On the sixth day from the first treatment (the day of first treatment was marked as day 1) (TriCurin or Vehicle or TriCurin + IL12Ab), the mice were sacrificed, tumors extricated, and the final tumor volumes were measured by displacement of water. The Tumors were divided into two halves: one-half for preparing single-cell suspensions for post-immunostaining flow cytometry and the other half for immunohistochemistry and confocal microscopy.

Athymic mice (*nulnu*) bearing human UMSCC47 cellderived HNSCC xenograft tumors were treated with 1.28 mM + TriCurin (or Vehicle) and tumors were subsequently processed according to our earlier report [7].

Neutralization of IL12 signaling on NK cells and CTL by intra-peritoneal infusion of IL12Ab

On day 0 (24 h before the first TriCurin treatment) and day 3, each TC-1 implanted mouse in the TriCurin + IL12Ab group received intra-peritoneal injection of IL12-neutralizing Anti-IL12 (p40/p70) antibody (BD, 554,475) (60 µg, each dose) [24]. Mice in the other two groups (Vehicle and TriCurin) received rat serum (60 µg, per mouse, per dose) and subsequent drugs (Vehicle or TriCurin) as stated in the previous section.

Preparation of single-cell suspensions from TC-1 tumors and immunostaining for flow cytometry

One-half of the extricated TC-1 tumor was placed in RPMI-1640 medium containing 100 U/ml penicillin and 100 μ g/ ml streptomycin. Next, the tumors were rinsed with PBS and subsequently minced into 1–2-mm pieces and immersed in serum-free RPMI-1640 medium containing 0.05 mg/ml collagenase I (Fisher #NC0847850), 0.05 mg/ml collagenase IV (Fisher #ICN19511080), 0.025 mg/ml hyaluronidase IV (Fisher #NC9725814), 0.25 mg/ml DNase I, 100 U/ml penicillin, and 100 μ g/ml streptomycin. The resultant cocktail was incubated at 37 °C for 15 min with periodic agitation in a mechanical shaker. The tumor digest was strained through a 70- μ m nylon filter to remove undigested tissue fragments. The resultant single tumor cells were pelleted, washed with PBS, and fixed in 4% PFA [25].

For flow cytometry, 2 million fixed cells from each animal were immunostained as described earlier [12]. After each antibody treatment, the cells were pelleted and resuspended in wash buffers. Antibodies against Iba1 (C20) (1:50), iNOS (1:100), Arginase1 (1:100), NKp46 (1:100), active-caspase 3 (Asp175) (1:100), and E6 (1:75) were used for staining. Cells treated with the secondary antibody alone were used to set the threshold. The double-stained fluorescent events from ARG1+/Iba1+ and iNOS+/Iba1+ cells appeared as sub-populations in the upper right (UR) quadrant within the coordinates 520 nm (green for ARG1 or iNOS) (FL1-A) and 580 nm (red for Iba1) (FL2-A). Single-stained fluorescent events from the scatter plots and from Nkp46+ (580 nm, red) and E6+ (520 nm, green) cells appeared as sub-populations in the upper left (UL) and the lower right (LR) quadrants, respectively. Integrated fluorescence intensity was measured for comparison between groups by multiplying the number of positive events (single-stained or double-stained cells) by the mean fluorescence intensity per event (cell).

Immunohistochemistry

Randomly chosen sections were subjected to pre-immunostaining antigen-retrieval using formamide: 2×SSC as reported earlier [7, 8, 12] only for IL12 and IL10 by treating with 0.1% (w/v) pepsin (Fisher, AC417071000) dissolved in 0.01 N HCl for 20 min at room temperature, followed by two PBS washes. For immunostaining, the sections were blocked overnight at 4 °C in 0.1% Triton X-100, 3% goat serum and 10% rabbit serum in 100 mM PBS, and then treated overnight with primary antibodies: anti-Iba1 (goat IgG) (C20) (sc28530) (1:50), iNOS (rabbit IgG) (NOS2 sc-651) (1:100), anti-Arginase1 (rabbit IgG) (sc-20150) (1:100), anti-STAT3 (rabbit IgG) (sc-7179) (1:100), anti-P-Tyr⁷⁰⁵-STAT3 (goat IgG) (sc-7993) (1:100), anti-STAT1 (rabbit IgG) (sc-592) (1:100), anti-P-Tyr⁷⁰¹-STAT1 (mouse IgG) (sc-8394) (1:100), anti-p65 (NF-kB) (mouse IgG) (sc-8008), anti-P-Ser²⁷⁶-p65 (NF-kB) (rabbit IgG) (sc-101749) (1:100), IL12p40 (rabbit IgG) (sc-7926) (1:100), IL10 (goat IgG) (sc-1783) (1:100), anti-NKp46 (rabbit IgG) (sc-292796) (1:100), anti-CD8-a (D-9) (mouse IgG) (sc-7970) (1:100), anti-E6 antibody (mouse IgG)(sc-460) (1:75) (Santa Cruz Biotechnology), and anti-active-caspase 3 (Asp175) (Rabbit IgG) (CST#9661, Cell Signaling Technology) (1:200). All antibodies were diluted in 2% goat serum plus 2% rabbit serum and 0.1% Triton X-100 in PBS (GRT-PBS). After washing three times with PBS, the respective secondary antibodies (Alexa Fluor 568 rabbit anti-goat, Alexa Fluor 488 goat antirabbit, Alexa Fluor 568 goat anti-rabbit, Alexa Fluor 633 rabbit anti-goat, Alexa Fluor 633 goat anti-mouse, Alexa Fluor 488 rabbit anti-goat, Alexa Fluor 568 goat anti-mouse, Alexa Fluor 633 goat anti-rabbit, and Alexa Fluor goat 488 anti-mouse) (Invitrogen) (1:1000 dilutions in GRT-PBS) were added to wells treated with the respective primary antibodies as well as those not treated with primary antibodies (2° Ab controls). Following overnight incubation at 4 °C and three washes with PBS, the sections were treated with HOECHST33342 (10 µg/ml) for 30 min at room temperature, followed by three washes with PBS and mounting on microscope slides with Gold anti-fade mounting fluid. Confocal Imaging was conducted using a Leica SP2 microscope from multiple randomly chosen fields.

ImageJ was used to quantify the fluorescence intensity for iNOS, ARG1, p65 (NF-kB), P-Ser²⁷⁶-p65, STAT-1, P-Tyr⁷⁰¹-STAT1, NKp46, E6, anti-active-caspase 3 (Asp175), and HOECHST33342. The fluorescence intensity for each marker was normalized to HOECHST33342 intensity (blue). Since STAT3, STAT1, and p65 NF-kB displayed both induction as well as phosphorylation-mediated deactivation/

activation, the HOECHST-normalized staining intensities were expressed both as P-STAT3/STAT3, P-STAT1/STAT1, and P-p65 NF-kB/p65 NF-kB, as well as P-STAT3/HOE-CHST, P-STAT1/HOECHST, and P-p65 NF-kB/HOECHST.

Statistical analysis

We used two-tailed *t* tests with unequal variance while comparing between two groups and one-way ANOVA with Tukey for post-hoc analysis to compare among three groups ($p \le 0.05$ was considered as significant).

Results

Five days of TriCurin treatment is adequate to cause repolarization of tumor-associated macrophages from M2 to M1 phenotype in TC-1 tumor. Immunostaining of the tumors from the Vehicle and TriCurin groups revealed that the 'tumor-core' harbors mostly E6+ tumor cells, while the 'tumor-periphery' harbors mostly Iba1+TAM (Supplementary Fig. 1) [8, 12]. TriCurin-evoked repolarization of ARG1high M2 TAM into iNOShigh M1 TAM was studied using flow cytometry analysis of immunostained cells dissociated from Vehicle-treated and TriCurin-treated TC-1 tumors [8, 12]. The integrated fluorescence (IF) from ARG1+/Iba1+ (M2 TAM) (Fig. 1a, b) and iNOS/Iba1+(M1 TAM) (Fig. 1e, f) double-stained events occurring in the upper right (UR) quadrant (red ellipse) was used to quantitatively compare between the two groups. Whereas the Iba1+ cells in the tumor were ARG1^{high}/iNOS^{low} (Fig. 1a, e) in the Vehicle-treated mice, in the TriCurin-treated tumors, the Iba1+cells were ARG1^{low}/iNOS^{high} (Fig. 1b, f). We observed a 55.5% decrease in ARG1 IF (Fig. 1c, d) and a 305% increase in iNOS IF (Fig. 1e, h). The intra-tumor iNOS high M1 TAM liberate NO, which is expected to be cytotoxic toward the surrounding tumor cells [12, 13, 26].

The Iba1 IF of these double-stained events (ARG1+ or iNOS+) was also sharply dissimilar between the two groups. TriCurin treatment elicited an 80% decrease in Iba1 IF in the ARG1+ cells in the tumor (relative to Vehicle-treated) (Fig. 1i), but the Iba1 IF in the iNOS+ cells in the TriCurin-treated tumors was 989% higher than in the Vehicle-treated tumors (Fig. 1j). In contrast, the total Iba1 IF (total number of Iba1+ cells in the iNOS+/Iba1+ and ARG1+/Iba1+ populations) did not significantly differ between the TriCurin and Vehicle-treated groups (Fig. 1k). This supported the possibility that TriCurin treatment causes suppression of M2 TAM and simultaneous activation/recruitment of a discrete population of M1 TAM [12].

TriCurin treatment causes suppression of P-STAT3 in the tumor-associated macrophages. C has been known to inhibit the ARG1-inducing transcription factor STAT3, which is a



Fig. 1 Five days of TriCurin treatment causes repolarization of tumor-associated macrophages (TAM) from M2 to M1-type in TC-1 tumor. Cells from TC-1-implanted mice with 5 days of TriCurin or Vehicle (PBS) treatment (daily, see "Materials and methods") were dispersed, fixed, permeabilized, and immunostained using iNOS, ARG1, and Iba1 (marks activated macrophages) antibodies, and the stained cells analyzed by flow cytometry. **a–c** Integrated fluorescence intensity (IF) (fluorescence per event x total number of events in a segregated population) obtained from double-stained events (red ellipse, upper right (UR) quadrant) for ARG1 (green) and Iba1 (red) was considered and the IF profiles of ARG1+cells were obtained for both the groups. **e–g** Similarly, IF for iNOS+cells were obtained from both groups (Vehicle: red, TriCurin: black) val-

marker for the immunosuppressive M2-type TAM [13, 20, 27]. To understand if STAT3 was a major player in the Tri-Curin-mediated repolarization of Iba1+TAM (Supplementary Fig. 1) from M2 to M1-type, we performed immunohistochemistry of tumor sections from Vehicle and TriCurin groups for STAT3 and activated STAT3 (P-Y⁷⁰⁵-STAT3, or P-STAT3). The M2 TAM in the Vehicle-treated TC-1 tumor harbored elevated levels of P-STAT3. In contrast, the M1 TAM in the TriCurin-treated tumors exhibited 80% suppression of P-STAT3 (Fig. 2a, b). A comparison with the corresponding total STAT3 levels revealed that the overall suppression of P-STAT3 was due to a combination of suppressed STAT3 expression (56% decrease) (Fig. 2a, c) and

ues obtained from double-stained events [red ellipse, UR quadrant for iNOS (green) and Iba1 (red)]. **d**, **h** Graphs showing a 56% decrease in ARG1 IF (p=0.022) and a 305% increase in iNOS IF (p=0.042) (with respect to Vehicle-treated) using Vehicle-treated and TriCurin-treated mice (mean±S.E.) (n=4 for each group). **i**, **j** Similarly, Iba1 IF quantified from **a**, **b**, **e**, and **f** shows a concomitant decrease in Iba1 integrated fluorescence in the ARG1+cells (80%) (p=9.14×10⁻³) and an increase in Iba1 integrated fluorescence (989%) in iNOS+cells (p=0.035) with respect to the Vehicle-treated for each group (mean±SEM) (n=4 for each group). **k** No significant difference in Iba1 IF between double-positive cells from the Vehicletreated and the TriCurin-treated groups

inhibited STAT3 phosphorylation (51% decrease) (Fig. 2a, d).

TriCurin treatment causes an induction in P-STAT1 and P-NF-KB (P-p65) in the TAM. STAT3 activation causes IL10-mediated suppression of the transcription factor STAT1 in the TAM [28]. Based on our previous results (Fig. 2), inhibition of STAT3 by TriCurin is expected to result in the activation of STAT1 [12], a transcription factor that triggers iNOS and IL12 synthesis in the TAM [29]. To investigate the activation status of STAT1 in both groups (Vehicle and TriCurin), we immunostained the TAM using antibodies against STAT1 and activated STAT1 (P-Tyr⁷⁰¹-STAT1). The Iba1+ cells in the Vehicle-treated mice showed



Fig. 2 Five days of TriCurin treatment causes a dramatic suppression of P-STAT3 in the tumor-associated macrophages (TAM). TC-1 tumor sections parallel to those used in Supplementary Fig. 1 were used to assess the levels of STAT3 and P-Tyr⁷⁰⁵-STAT3 (activated) in the Iba1+ macrophages. **a**, upper and middle rows, and **b** the Vehicle-treated mice displayed a high level of activated STAT3 (P-Y⁷⁰⁵-STAT3) in the TAM, which was suppressed by 80% ($p=1.0 \times 10^{-3}$) in the TriCurin-treated group. This overall suppression of P-STAT3 was due to a combination of **c** suppression of STAT3 expression

(STAT3 fluorescence normalized to HOECHST fluorescence) and **d** STAT3 activation (P-STAT3 normalized to STAT3). Four randomly chosen sections per mouse were used for imaging and the data (mean \pm SEM) obtained from Vehicle-treated (*n*=4) and TriCurintreated (*n*=4) groups. HOECHST=HOECHST33342. (Scale bar: 47.62 µm). **a**, lower row, absence of non-specific staining in sections treated with three 2° antibodies consecutive to one another (see "Materials and methods")

basal levels of activated STAT1, whereas the M1 TAM in the TriCurin-treated tumors exhibited a 532% increase in P-STAT1 (Fig. 3a, b). A comparison with the corresponding total STAT1 levels revealed that the overall increase in P-STAT1 was due to a combination of induced STAT1 expression (219% increase) (Fig. 3a, c) and increased STAT1 phosphorylation (activation) (97% increase) (Fig. 3a, d).

Activated NF-kB (p65) has been known to be overexpressed in M1 TAM [30]. In addition, earlier work in macrophages shows that co-activated NF-kB (p65) and STAT1 cooperate by binding to enhancer elements on the *iNOS* gene [12, 31, 32]. To effect such alterations in the tumorassociated macrophages, TriCurin treatment should cause simultaneous activation these two transcription factors. As expected, immunostaining of the TAM using antibodies against NF-kB (p65) and activated NF-kB p65 (P-Ser²⁷⁶⁻ p65) revealed a 2071% increase in P-p65 (P-NF-kB) in the TAM (Fig. 4a, b). A comparison with the corresponding total NF-kB (p65) levels revealed that the overall increase in P-p65 was due to a combination of induced NF-kB (p65)



Fig. 3 TriCurin treatment causes an induction in P-STAT1 in the TAM. TC-1 tumor sections parallel to those used in Supplementary Fig. 1 were stained to determine the levels of STAT1 and P-Tyr⁷⁰¹-STAT1 (activated) in the tumors from Vehicle-treated and TriCurin-treated mice. **a** Upper and middle rows, and **b** the Vehicle-treated mice displayed basal levels of activated STAT1 (P-Tyr⁷⁰¹-STAT1) in the Iba1+TAM, which was increased by 532% (p=3.04×10⁻⁴) in the TC-1 tumor sections from the TriCurin-treated group. This over-

all increase in P-STAT1 was due to a combination of (c) induction of STAT1 expression (STAT1 normalized to HOECHST) and d STAT1 activation (P-STAT1 normalized to STAT1). Four randomly chosen sections per mouse were used for imaging and the data (mean \pm SEM) were compared between Vehicle-treated and TriCurin-treated groups (n=4 per group). (Scale bar: 47.62 µm). (a, lower row) Absence of non-specific staining from the 2° antibodies (see "Materials and methods")

expression (226% increase) (Figs. 4a, 2c) and increased NF-kB (p65) phosphorylation (activation) (536% increase) (Figs. 4a, 2d).

Five days of TriCurin treatment is adquate to cause repolarization of IL12^{low}, IL10^{high} tumor-associated M2 macrophages to IL12^{high}, IL10^{low} M1-type in TC-1 tumor. Suppression of P-STAT3 is known to cause reduced IL10 (M2 TAM marker) expression along with increased IL12 (M1 TAM marker) expression [33]. Based on this understanding, we wanted to verify if the observed

TriCurin-mediated M2 \rightarrow M1 polarization (Fig. 1) was associated with a switch in the Iba1+ TAM to IL12^{high} and IL10^{low} (M1) phenotype. As expected, tumors from the Vehicle-treated group had high IL10 and very low IL12 in the Iba1(+) TAM, whereas the TAM in tumor sections from the TriCurin-treated mice showed a 70% decrease in IL10 and a 244% increase in IL12 expression (Supplementary Fig. 2). This further demonstrated the TriCurinevoked M2 \rightarrow M1 switch using a second set of markers for M2 and M1, IL10, and IL12, respectively.



Fig. 4 TriCurin treatment causes an induction in P-NF-KB (P-p65) in the TAM. TC-1 tumor sections parallel to those used in Supplementary Fig. 1 were stained to determine the levels of NF-kB (p65) and activated NF-kB p65 (P-Ser²⁷⁶-p65) in the tumors from Vehicle-treated and TriCurin-treated mice. **a** Upper and middle rows and **b** the Vehicle-treated mice displayed basal levels of activated NF-kB p65 (P-Ser²⁷⁶-p65) in the iba1+TAM, which was increased by 2071% in the TriCurin-treated TC-1 tumor sections ($p=4.20 \times 10^{-3}$). This

overall increase of P-NF-kB (P-p65) was a result of **c** induction of NF-kB (p65) expression (NF-kB (p65) normalized to HOECHST) and **d** NF-kB (p65) activation (P-NF-kB (P-p65) normalized to NF-kB (p65)). Four randomly chosen sections per mouse were used for imaging and the data (mean \pm SEM) compared between Vehicle-treated and TriCurin-treated groups (n=4 per group). (Scale bar: 47.62 µm). **a** lower row, showed the lack of non-specific staining from the secondary antibodies (see "Materials and methods")

IL12 is known to trigger intra-tumor recruitment of activated NK cells and cytotoxic T lymphocytes [21, 29, 34–37]. To verify the role of IL12 in causing recruitment of NK cells and CTL that would cause enhanced elimination of tumors, we neutralized the IL12 receptor-mediated signaling in these immune cells by peripheral treatment with IL12p40 antibody [24, 29].

IL12Ab treatment abrogates TriCurin-evoked infiltration of natural killer (NK) cells into TC-1 tumors. C has also been reported to activate NK cells in tumors [16]. Cognizant of these studies, we investigated the possibility of TriCurin-evoked, intra-tumor recruitment of activated NK cells (in addition to M1 TAM polarization) as a mechanism for its anti-tumor activity [21]. Based on flow cytometry data from Vehicle, TriCurin, and TriCurin+IL12Ab groups, TriCurin evoked a 376% increase in infiltrating activated (NKp46+) NK cells, which was eliminated in the Tri-Curin+IL12Ab group NKp46+ fluorescence (UL quadrant. red ellipse) within the tumor, thus confirming infiltration of NK cells into the TC-1 tumors in response to TriCurin treatment (Fig. 5a–e). Furthermore, based on immunohistochemical data, the 5-day treatment with TriCurin caused



Fig. 5 IL12 Ab treatment abrogate infiltration of natural killer (NK) cells into TC-1 tumors. Cells from TC-1 tumor implanted mice with 5-day TriCurin (plus normal rat serum, see "Materials and methods"), TriCurin+IL12Ab and Vehicle (PBS) treatments were dispersed, fixed, and permeabilized, the cells immunostained using the activated NK cell-specific NKp46 antibody, and then analyzed by flow cytometry. **a-d** IF from single-stained NKp46+events (red ellipse, UL quadrant) was considered from the three groups, expressed as mean \pm S.E. (Vehicle: red, TriCurin: black, TriCurin+IL12Ab: blue) (Vehicle, n=4; TriCurin, n=4; TriCurin+IL12Ab, n=3). **a**, **b**, **d**, **e** TriCurin treatment affords a 376% increase in NKp46 IF (with respect to Vehicle-treated, *p=0.019). **a**, **c**, **d**, **e** TriCurin+IL12Ab displayed an NKp46 IF, which was comparable to that of the Vehi-

TriCurin-induced IL12 (Supplementary Fig. 2) in causing

displayed an NKp46 IF, which was comparable to that of the Vehia 346% increase in activated (NKp46+) NK cells in the TC-1 tumors (Fig. 5f, g) [38]. In contrast, infiltration of activated (NKp46+) NK cells was virtually eliminated in the TriCurin + IL12Ab group, thus confirming the role of

cle group (with respect to TriCurin-treated, $\Delta p = 0.02$). **f** upper, middle, and lower rows, and **g** TC-1 tumor sections from Vehicle-, TriCurin-, and TriCurin+IL12Ab-treated mice were single-stained with the NKp46 antibody. The Vehicle-treated tumor tissue displayed minimal NKp46 fluorescence, but the TriCurin-treated mice showed a 346% increase in NKp46-staining (with respect to the Vehicle), confirming the recruitment of activated NK cells (* $p = 1.25 \times 10^{-3}$). Tri-Curin+IL12Ab treatment reversed this recruitment of NKp46+NK cells to the level in the Vehicle group (with respect to TriCurintreated, $\Delta p = 1.0 \times 10^{-3}$). Four randomly chosen sections per mouse were used for imaging and the data obtained were expressed as (mean±S.E.M.), from Vehicle-treated (n=4), TriCurin-treated (n=4), and TriCurin+IL12Ab (n=3) groups. (Scale bar: 47.62 µm)

this intra-tumor recruitment of activated NK cells (Fig. 5f, g). Interestingly, C is also known to cause enhanced expression of IFN γ from tumor-associated immune cells (lymphocytes like NK cells and CTL), which, in the case of TriCurin, could prolong the M1 TAM phenotype [17, 19, 29, 34, 38].

IL12 Ab treatment eliminates TriCurin-evoked infiltration of Cytotoxic T lymphocytes into TC-1 tumors. CTL are known to be highly tumoricidal and C has been known to promote intra-tumor infiltration of activated CD8+CTL to cause tumor elimination [17, 19, 20]. In addition, M1-macrophage-derived IL12 has been known to promote the activation and infiltration of CTL [35-37]. Therefore, we next investigated if TriCurin treatment was capable of causing intra-tumor infiltration of activated CD8+CTL and if IL12 regulated this process (Supplementary Fig. 2). As revealed by immunohistochemistry for CD8+CTL, the 5-day treatment with TriCurin triggered a 633% increase in activated (CD8+) CTL in the TC-1 tumors (Supplementary Fig. 3a, b). In addition, data from the TriCurin+IL12Ab group revealed the lack of tumor-infiltrating activated (CD8+) CTL, despite TriCurin treatment, thereby indicating that the IL12 plays a major role in causing the intra-tumor recruitment of activated CTL (Supplementary Fig. 3a, b).

IL12 Ab treatment partially reverses TriCurin-induced apoptosis of E6+ tumor cells and tumor size reduction. In our prior studies, intra-tumor injection of TriCurin into HaRas+, HPV16 E6+, and E7+TC-1 cell-implanted mice, every 72 h for 10 days caused an 80-90% decrease in tumor growth [8]. Here, we examined if the oncoimmunotherapeutic effect of TriCurin in recruiting/activating M1 TAM, NK cells, and CTL in 5 days was also associated with a concomitant reduction in tumor load. Furthermore, we asked if neutralization of NK cells and CTL by IL12 Ab infusion influences the effect of Tri-Curin [21, 29, 34–37]. Five days of intra-tumor TriCurin infusion (every 24 h) caused a 61% decrease in tumor growth, whereas application of IL12 antibody (i.p.) along with TriCurin (intra-tumor) caused a partial reversal of the TriCurin-triggered inhibition of tumor growth (41% decrease) (tumor volumes were determined using water displacement) (Fig. 6a, b). Based on flow cytometry, the reduction in tumor load was associated with a flow cytometry analysis which showed a 68% inhibition of E6 expression in these tumor cells (LR quadrant: red ellipse) (Fig. 6c, d, f, g). The TriCurin + IL12Ab group showed only a 38% inhibition of E6 in these tumor cells, verifying that the neutralization of NK cells and CTL causes 30% less elimination of these tumor cells by (Fig. 6c, e-g). Based on immunohistochemistry, the tumor load reduction was concomitant with an inhibition of the oncoprotein E6 (54% decrease) (Fig. 6h, i) and activation of caspase 3 (383% increase) (Fig. 6h, j) in the tumor cells. In contrast, the TriCurin + IL12Ab group revealed a 31% inhibition of the oncoprotein E6 (Fig. 6h, i) and 67% increase in active-caspase 3 (Fig. 6h, j). Thus, neutralization of NK cells and CTL with the IL12Ab impacted tumor elimination by causing 23% less inhibition of E6 and 316% less activation of caspase 3. This is consistent with our previous in vitro observation that TriCurin treatment for 6 h causes suppression of E6, increased acetylation-mediated activation of p53, and elevation of activecaspase 3 in cultured TC-1 cells [8].

Prolonged TriCurin treatment triggers P-NF-kB and P-STAT1-mediated M2 to M1 polarization of TAM, recruitment of activated NK cells, and suppression of E6+ cells in HNSCC xenograft tumors. To translate the novel findings from our TC-1 model into a more clinically relevant human tumor model, HPV16+ HNSCC cells UMSCC47 were implanted into the flanks of athymic *nude/nude* (NCr) mice (xenograft model); and after the tumors were palpable, the immuno-modulatory effect of intra-tumor TriCurin injection for 5 weeks (3 doses per week) was assessed [7].

Immunohistochemical analysis revealed that the Vehicle-treated TAM were iNOS^{low}, ARG1^{high}, and Iba1+M2 macrophages. In contrast, similar to the 5-day treatment, prolonged TriCurin treatment also caused a major shift in polarity of the Iba1+TAM to the iNOS^{high}, ARG1^{low} M1 form (Supplementary Fig. 4a). We observed an 89% decrease in ARG1 (Supplementary Fig. 4a, b) and a 684% increase in iNOS (integrated fluorescence) (Supplementary Fig. 4a, c).

Our previous results (Fig. 2) and other reports have shown that both TriCurin as well as C are a potent suppressors of activated STAT3 in M2 TAM and that STAT3 suppression causes activation of STAT1, leading to the formation of the M1 phenotype [13, 28]. Also the findings from our TriCurin-treated TC-1 tumors (Figs. 3, 4) and other reports have revealed that the co-activated transcription factors STAT1 and NF-kB (p65) are likely to trigger the expression of the M1-linked enzyme iNOS, which produces NO that is known to cause tumor elimination [12, 13, 26, 30–32]. Immunohistochemical analysis of the Iba1+TAM in the Tri-Curin-treated HNSCC-implanted xenograft tumors revealed elevated levels of co-localized, P-STAT1 (993% increase), and activated P-p65 (93% increase) in the TriCurin-treated Iba1+TAM (Supplementary Fig. 5a–c).

Given the evidence of interaction between M1 TAM and activated NK cells in the tumor microenvironment (Supplementary Fig. 2, Figs. 5, 6), we also probed for tumorinfiltrating activated NK cells in these xenograft tumors [29, 34, 39]. Immunostaining revealed elevated levels of intratumor NKp46+NK cells (441% increase) in the TriCurintreated tumors (Supplementary Fig. 6a–b). This recruitment of activated NK cells is expected to result in stabilization of the M1 TAM phenotype, thereby causing elimination of tumors by the coordinated action of TAM and NK cells [19, 21, 29, 38, 40]. As expected, the intra-tumor activation/ recruitment of M1 TAM and NK cells was associated with the suppression in E6+ tumor cells (Supplementary Fig. 6a) and an 86% reduction in tumor size, as reported earlier [7]. These results were consistent with our previously reported



Fig. 6 IL12Ab treatment partially reverses TriCurin-induced apoptosis of E6+tumor cells and reduction in tumor load. a Volumes of extricated tumors from Vehicle (PBS)-treated, TriCurin-treated, and TriCurin+IL12Ab-treated mice were measured by the water displacement on the day of sacrifice (day 6). Two representative tumors from each group are shown here. b Even after the 5-day treatment, the TriCurin group (six mice per group) showed a dramatic decrease in tumor size (61% relative to Vehicle-treated) (n=6) (* $p=2.54 \times 10^{-5}$). The TriCurin+IL12Ab group (n=3)exhibited a smaller decrease in tumor size (41% relative to Vehicletreated, ** $p = 8.4 \times 10^{-3}$) ($\Delta p = 5.8 \times 10^{-3}$ relative to TriCurintreated) (mean ± S.E.M). c-f Tumor cells from 5 days of TriCurin, TriCurin+IL12Ab, and Vehicle treatment were dispersed, fixed, permeabilized, immunostained using the HPV+tumor cell-specific E6 antibody, and analyzed by flow cytometry. IF from singlestained E6+ events (red ellipse, LR quadrant) was obtained from the three groups (Vehicle: red, TriCurin: black, TriCurin+IL12Ab: Blue). **g** Relative to the Vehicle group (n=5), the TriCurin group

in vitro data showing suppression of E6, increase in p53 levels, and induction of apoptosis in HNSCC cells following TriCurin treatment [7].

(n=5) showed a 68% decrease in E6 IF (*p=0.01) and the Tri-Curin + IL12Ab-treated mice (n=3) showed a 38% decrease in E6 IF (**p = 0.04) ($\Delta p = 0.02$ relative to TriCurin-treated), **h** upper, middle, and lower rows, i and j tumor sections from these three groups also were subjected to immunohistochemistry to assess caspase 3 (Cspse3) activation and E6 expression. The Vehicle group showed high E6 expression (green) and negligible active-caspase 3 (red). Relative to the Vehicle group, the TriCurin group showed a 54% suppression of E6 (* $p = 1.2 \times 10^{-3}$) (i) and a sharp increase in active-caspase 3 (383% increase) (* $p = 4.0 \times 10^{-4}$) (j). Relative Vehicle-treated, the TriCurin+IL12Ab group showed only 31% suppression of E6 $(**p=8.8\times10^{-3})$ ($\Delta p=0.03$ relative to TriCurin-treated) (i). Relative to Vehicle-treated, the TriCurin+IL12Ab group showed 67% upregulation of active-caspase 3 upregulation (**p=0.04) ($\Delta p=2\times 10^{-3}$ relative to TriCurin-treated) (j). Four randomly chosen sections per mouse were used for imaging and data quantified from Vehicletreated (n=4), TriCurin-treated (n=4) and, TriCurin+IL12Abtreated (n=3) groups. (Scale bar: 47.62 µm)

Discussion

This project involved intra-tumor injection of TriCurin, which is expected to cause direct apoptosis of a number of tumor cells. However, due to rapid degradation of C in vivo, the concentration of TriCurin-derived C in the body is expected to drop quickly. Interestingly, our in vivo pharmacokinetic studies [Mukherjee et al., unpublished] using a lipid-encapsulated formulation of TriCurin yielded plasma concentrations of C in the nano-molar range (610–210 nM), which is not high enough to directly kill TC-1 and UMSCC47 cells, as the IC50 values of TriCurin for these cells are much higher (13 μ M+ and 3.22 μ M+, respectively) [7, 8]. Based on our observation that injected TriCurin causes a dramatic reduction in tumor load, we expect that in addition to eliciting direct tumor cell death immediately after intra-tumor injection, TriCurin would elicit its anti-tumor activity also by stimulating the immune cells, which are known to eliminate tumors [12, 13, 16, 19, 20, 41]. Our current study tests this postulate by demonstrating that TriCurin, indeed, causes intra-tumor recruitment of M1 TAM, NK cells, and CTL which are known to eliminate tumor cells [21, 26, 29, 30, 38].

Our data show that TriCurin treatment causes activation/ recruitment of M1 TAM, NK cells, and CTL into pre-clinical HPV+ cervical (TC-1 implanted mice) and activation/ recruitment of M1 TAM and NK cells in HNSCC (xenograft) tumors (Fig. 6) [7]. Analysis of these TriCurin-treated tumors (Fig. 1, Supplementary Fig. 2 and Supplementary Fig. 4) reveals a major shift in polarity of ARG1^{high}, iNOS^{low}, IL10 high, IL12low M2 TAM into the ARG1low. iNOShigh, IL10^{low}, and IL121^{high} M1-type [12]. This repolarization is concomitant with repression of activated STAT3 and induction of activated STAT1 and NF-kB (p65) in the TAM (Figs. 2, 3, 4 and Supplementary Fig. 5). Activated STAT1 is known to cooperate with activated NF-kB (p65) to trigger the M1 phenotype, which is marked by the induction of IL12 and iNOS which should trigger toxic NO production by the TAM (Fig. 1, Supplementary Fig. 2, and Supplementary Fig. 4) [12, 13, 28, 30–32]. We also demonstrate TriCurinmediated, intra-tumor recruitment of activated NK cells and CTL (Fig. 5, Supplementary Fig. 3, and Supplementary Fig. 6), which are expected to contribute to the observed tumor load reduction (Fig. 6 and Supplementary Fig. 6) [7, 16, 21]. The IL12-mediated NK cell and CTL recruitment and activation are attenuated in mice pretreated with an IL12-neutralizing antibody (Supplementary Fig. 2, Supplementary Fig. 3, and Fig. 5). This recruitment of CTL and NK cells may simultaneously cause IFNy-mediated observed stimulation of STAT1 in macrophages and M1-type polarization of TAM, thereby enabling the activated NK cells, CTL, and the M1 TAM to act as a lethal triad against cancer cells. Corroboratively, IL12Ab-mediated abrogation of intratumor recruitment of activated NK cells and CTL partially eliminated the tumoricidal activity of TriCurin (Fig. 6) [13, 16, 19, 21, 29, 33, 34, 36, 38, 40].

Our data also indicate that TriCurin causes this shift in polarity by silencing the M2 TAM and activating/recruiting

a discrete population of M1 TAM while maintaining a constant number of overall intra-tumor Iba1+ TAM (Fig. 1i, j, k) [12]. Interestingly, NKp46+ NK cells have been reported to eliminate M2 macrophages while causing IFN γ -mediated activation and amplification of MHC class I^{high} M1 macrophages [42]. Based on the previous findings of other groups and the data presented in this manuscript, we propose a working model in which injected TriCurin elicits a switch in TAM phenotype from a tumor-promoting M2-type into a tumoricidal M1-type. Furthermore, founded on our IL12 blocking data, we postulate that TriCurin-induced M1 TAM-derived IL12 is responsible for triggering intra-tumor recruitment of NK cells and CTL and elimination of the HPV+ cervical cancer cells (Fig. 6) [7, 8].

Treatments for HNSCC include chemotherapy and/or radiation, which are fairly toxic to the body and they deplete the tumoricidal immune cells [5, 6, 43]. Cancer immunotherapy using chimeric antigen receptor (CAR) T-cell treatment and regulators of T-cell activation (checkpoint inhibitors) has recently come into prominence but with limitations and side effects [22, 23]. Thus, there is an acute need for novel immunotherapeutic strategies to better manage the growing number of HPV+ tumors. TriCurin is highly efficient in stimulating the immune system against cancer cells and can be used as a safe immunotherapeutic agent to turn the immune system against HPV+ tumors.

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Author contributions PB, SM, QP, and LP conceived and planned the experiments. SM, RH, RW, DA, AF, SS, and LP carried out the experiments. All the authors contributed to the interpretation of results. SM and PB took the lead in writing the manuscript. All authors provided critical feedback and helped in shaping the final manuscript.

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Compliance with ethical standards

Conflict of interest Probal Banerjee has a pending patent application "Activity Enhancing Curcumin Compositions and Methods of Use", PCT/US14/67819 pending. The remaining authors declare no conflict of interest.

Ethical approval and ethical standards All procedures performed in studies involving animals were in accordance with the ethical standards of the Institutional Animal Care Committees (IACUC) at the College of Staten Island (approval # 11–008) and The Ohio State University Medical Center (approval # 2009A0172).

Animal source Adult C57BL/6 female mice (2–6 months old) used for the TC-1 tumor experiments were bred and handled at the College of Staten Island (CUNY) [8]. Athymic nude (NCr) mice were purchased from Charles River Laboratories (Wilmington, MA) for the Head and Neck Squamous Cell Carcinoma (HNSCC) UMSCC47 tumor xenograft model and housed at The Ohio State University animal facility [7]. Both the strains mentioned above were bred and handled in accordance to the consent of respective Institutional Animal Care Committees (IACUC) at the College of Staten Island and The Ohio State University Medical Center. All animal protocols were approved by the respective Institutional Animal Care Committees (IACUC) at the College of Staten Island and The Ohio State University Medical Center.

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PERCEIVED STRESS SCALE

by Sheldon Cohen

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PERCEIVED STRESS SCALE by Sheldon Cohen

The *Perceived Stress Scale* (PSS) is the most widely used psychological instrument for measuring the perception of stress. It is a measure of the degree to which situations in one's life are appraised as stressful. Items were designed to tap how unpredictable, uncontrollable, and overloaded respondents find their lives. The scale also includes a number of direct queries about current levels of experienced stress. The PSS was designed for use in community samples with at least a junior high school education. The items are easy to understand, and the response alternatives are simple to grasp. Moreover, the questions are of a general nature and hence are relatively free of content specific to any subpopulation group. The questions in the PSS ask about feelings and thoughts during the last month. In each case, respondents are asked how often they felt a certain way.

Evidence for Validity: Higher PSS scores were associated with (for example):

- failure to quit smoking
- failure among diabetics to control blood sugar levels

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- greater vulnerability to stressful life-event-elicited depressive symptoms
- more colds
- **Health status relationship to PSS:** Cohen et al. (1988) show correlations with PSS and: Stress Measures, Self-Reported Health and Health Services Measures, Health Behavior Measures, Smoking Status, Help Seeking Behavior.
- **Temporal Nature:** Because levels of appraised stress should be influenced by daily hassles, major events, and changes in coping resources, predictive validity of the PSS is expected to fall off rapidly after four to eight weeks.
- **Scoring:** PSS scores are obtained by reversing responses (e.g., 0 = 4, 1 = 3, 2 = 2, 3 = 1 & 4 = 0) to the four positively stated items (items 4, 5, 7, & 8) and then summing across all scale items. A short 4 item scale can be made from questions 2, 4, 5 and 10 of the PSS 10 item scale.
- Norm Groups: L. Harris Poll gathered information on 2,387 respondents in the U.S.

			,
Category	N	Mean	S.D.
Gender			
Male	926	12.1	5.9
Female	1406	13.7	6.6
Age			
18-29	645	14.2	6.2
30-44	750	13.0	6.2
45-54	285	12.6	6.1
55-64	282	11.9	6.9
65 & older	296	12.0	6.3
Race			
white	1924	12.8	6.2
Hispanic	98	14.0	6.9
black	176	14.7	7.2
other minority	50	14.1	5.0

Norm Table for the PSS 10 item inventory

PERCEIVED STRESS SCALE

The questions in this scale ask you about your feelings and thoughts during the last month. In each case, you will be asked to indicate by circling *how often* you felt or thought a certain way.

Name Date _			_		
Age Gender (<i>Circle</i>): M F Other					
0 = Never 1 = Almost Never 2 = Sometimes 3 = Fairly Often	4 = Ve	ry Of	ften		
1. In the last month, how often have you been upset because of something that happened unexpectedly?	0	1	2	3	4
2. In the last month, how often have you felt that you were unable to control the important things in your life?			2	3	4
3. In the last month, how often have you felt nervous and "stressed"?			2	3	4
4. In the last month, how often have you felt confident about your ability to handle your personal problems?	0	1	2	3	4
5. In the last month, how often have you felt that things were going your way?			2	3	4
6. In the last month, how often have you found that you could not cope with all the things that you had to do?	0	1	2	3	4
7. In the last month, how often have you been able to control irritations in your life?			2	3	4
8. In the last month, how often have you felt that you were on top of things?	0	1	2	3	4
9. In the last month, how often have you been angered because of things that were outside of your control?			2	3	4
10. In the last month, how often have you felt difficulties were piling up so high that you could not overcome them?	0	1	2	3	4



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<u>References</u>

The PSS Scale is reprinted with permission of the American Sociological Association, from Cohen, S., Kamarck, T., and Mermelstein, R. (1983). A global measure of perceived stress. *Journal of Health and Social Behavior, 24,* 386-396.

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