



PA28 γ , an Accomplice to Malignant Cancer

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OPEN ACCESS

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Specialty section:

This article was submitted to
Molecular and Cellular Oncology,
a section of the journal
Frontiers in Oncology

Received: 18 July 2020

Accepted: 12 October 2020

Published: 30 October 2020

Citation:

Lei K, Bai H, Sun S, Xin C, Li J
and Chen Q (2020) PA28 γ , an
Accomplice to Malignant Cancer.
Front. Oncol. 10:584778.
doi: 10.3389/fonc.2020.584778

PA28 γ is a nuclear activator of the 20S proteasome, which is involved in the regulation of several essential cellular processes and angiogenesis. Over the past 20 years, many amino acid sites and motifs have been proven to play important roles in the characteristic functions of PA28 γ . The number of binding partners and validated cellular functions of PA28 γ have increased, which has facilitated the clarification of its involvement in different biological events. PA28 γ is involved in the progression of various diseases, and its aberrant overexpression in cancer is remarkable. Patients with low levels of PA28 γ expression have a higher survival rate than those with high levels of PA28 γ expression, as has been shown for a wide variety of tumors. The functions of PA28 γ in cancer can be divided into five main categories: cell proliferation, cell apoptosis, metastasis and invasion, cell nuclear dynamics that have relevance to angiogenesis, and viral infection. In this review, we focus on the role of PA28 γ in cancer, summarizing its aberrant expression, prooncogenic effects and underlying mechanisms in various cancers, and we highlight the possible cancer-related applications of PA28 γ , such as its potential use in the diagnosis, targeted treatment and prognostic assessment of cancer.

Keywords: PA28 γ , cell proliferation, apoptosis, prognosis, treatment

INTRODUCTION

The proteasome system is an indispensable protein degradation system that has the responsibility of degrading the majority of the proteins in eukaryotes (1, 2). It can selectively act on misfolded, damaged, degenerative and nonfunctional proteins and turn them into peptide fragments (3), thus it regulates various molecular processes (4). Usually, the proteasome system comprises four main factors, namely, the 20S core and three proteasome activators (PA700/19S, PA28/11S, and PA200) (5).

The PA28 family has three members—PA28 α , PA28 β , and PA28 γ , and there are several differences among them. First, PA28 α and PA28 β are only found in vertebrates, while PA28 γ has been found in both vertebrates and invertebrates and is more highly conserved (6). Second, PA28 α and PA28 β share 50% of their amino acid sequence, while PA28 γ shares only 25% of the sequence with the other two members (7). Third, PA28 α and PA28 β exist in the cytoplasm in the form of a heteroheptamer, but PA28 γ exists primarily in the nucleus in the form of a homoheptamer (8). In addition, characterization of genomic clones for copies of PA28 α and PA28 β are not clear whereas PA28 γ is probably encoded by a single-copy gene (9). Another difference is that the expression levels of both PA28 α and PA28 β can be enhanced by interferon- γ (IFN- γ) induction, and they take part in the formation of the hybrid proteasome 19S-20S-11S while there's no clear evidence that PA28 γ can form hybrid proteasomes (5). In contrast, PA28 γ is not sensitive to IFN- γ , and it binds to the 20S proteasome to initiate protein degradation in an ATP/ubiquitin-independent manner (8). Moreover, PA28 γ promotes cell proliferation and anti-apoptosis and is closely associated with the occurrence and development of cancer, which implies that the PA28 γ /20S proteasome complex may be a target of anticancer therapy.

Clearly, PA28 γ is a proteasome activator with special characteristics, and here, we concisely demonstrate the origination of PA28 γ considering its function and regulatory mechanisms.

THE CHARACTERISTICS OF PA28 γ

PA28 γ , also known as REG γ , 11S γ , Ki antigen or PSME3, is encoded by the PSME3 gene (10). The human PA28 γ gene is mapped to chromosome 17q12-21 (8). PA28 γ is highly evolutionarily conserved in species such as tick, zebrafish, mouse, cattle and human beings (9, 11). The structure of PA28 γ monomer is speculated to be composed of four helices, and seven monomers will form a homoheptamer (12, 13). As speculated, there is a nine-residue sequence between helix 2 and helix 3, which is called activation loop. This sequence is the

Abbreviations: ATM, ataxia telangiectasia-mutated gene; ATP, adenosine triphosphate; Bcl-2, B-cell lymphoma-2; cAMP, cyclic adenosine monophosphate; CBP, cAMP response element binding protein; CCL2, chemokine (C-C motif) ligand 2; CRC, colorectal cancer; Daxx, death domain associate protein; DNA, deoxyribo nucleic acid; DSF, disease-free survival; ER α , estrogen receptor α ; FLASH, FLICE-associated huge protein; Gly102, glycine 102; HCC, hepatocellular carcinoma; HCV, hepatitis C virus; HUVECs, human umbilical vein endothelial cells; IFN- γ , interferon- γ ; IL-6, interleukin-6; Lys195, lysine 195; MDM2, murine double minute 2; MEKK3, mitogen-activated protein kinase/extracellular signal-regulated kinase kinase kinase 3; miR-7, micro RNA-7; NF- κ B, nuclear factor kappa-B; NLS, nuclear localization sequence; NSCLC, non-small-cell lung cancer; OS, overall survival; OSCC, oral squamous cell carcinoma; O-GlcNAc, O-linked β -N-acetylglucosamine; PA200, proteasome activator 200; PA28, proteasome activator 28; PA28 α , proteasome activator 28 α ; PA28 β , proteasome activator 28 β ; PA28 γ , proteasome activator 28 γ ; PA700, proteasome activator 700; PI3K, phosphatidylinositol-3-OH kinase; PIAS1, protein inhibitor of activated STAT, 1; PSME3, proteasome activator subunit 3; RanBPM, Ran binding protein in the microtubule-organizing center; SIRT1, Sirtuin-1; SLE, systemic lupus erythematosus; SRC-3, steroid receptor coactivator; TCGA, The Cancer Genome Atlas Program; UDP-GlcNAc, uridine 5'-[3-(acetamido-2-deoxy- α -D-glucopyranosyl) dihydrogen diphosphate]; VEGF, vascular endothelial growth factor.

proteasome binding site and is vital for proteasome activation. A mutation in the activation loop N151Y, can suppress the action of the protein and inhibit proteasome activation by the nonmutated PA28 γ . Another mutant, PA28 γ (K195R), affects the acetylation of the lysine 195 (Lys195) residue by the cAMP response element binding protein (CBP), which can be restored by sirtuin 1 in mammals. Moreover, between helix 1 and helix 2, from Pro64 to Gly102, the sequence is called a homolog-specific insert. The insert can vary according to different homologs but has been highly conserved throughout evolution. The nuclear localization sequence (NLS) is in the insert. It may function by coupling proteasomes with nuclear components. Furthermore, in the sequence, the substitution of Lys188 with a negatively charged residue could enable PA28 γ to activate three proteasome catalytic subunits (7) (**Figure 1A**). In addition, the evolutionary tree showed that the region containing multiple functional sites is very conserved among multiple species, which region is amino acid sequence from 145 to 199 of PA28 γ (**Figure 1B**).

Autoantibodies against PA28 γ was first found in the serum of systemic lupus erythematosus (SLE) patients and was named the Ki antigen (14). However, the other biological functions of PA28 γ are gradually eliminated. Early in 1989, Nikaido et al. deduced that PA28 γ might be closely linked to cellular fission (15). Later, a study discovered that PA28 γ -knockout mice showed considerable declines in their growth rates and body sizes compared with those of the control group. The embryonic fibroblasts of the knockout mice were hindered in the S stage of the cell cycle (13, 14). In conclusion, PA28 γ is closely associated with cell division and DNA synthesis.

In recent years, studies have shown that transcript variants are closely correlated with the occurrence and development of tumors. So far, five transcript variants of PA28 γ have been discovered. Among them, the newest to be identified was predicted and confirmed in our previous work. Compared with the other four isoforms of PA28 γ , the fifth isoform missing sixth and fifth exons, it can encode the protein with a truncated form that retains the conserved residues (16). Further investigation is warranted to explore whether there are more transcript variants and their involvement in tumors formation and growth.

THE REGULATION OF PA28 γ IN CANCERS

Aberrant Expression of PA28 γ in Cancers

Early in 2003, PA28 γ was discovered to be abnormally overexpressed in papillary adenocarcinoma samples and anaplastic carcinoma, but its level was relatively low in multinodular goiters (17). Recently, several studies have evaluated the clinical significance of PA28 γ through the use of large clinical cohorts. Debo Chen et al. found that the expression of PA28 γ was closely connected with the differences in the TNM stages of colorectal cancer (CRC) tissues (18). For oral squamous cell carcinoma (OSCC), our team reached similar conclusions—the level of PA28 γ was correlated with overall survival (OS) and disease-free survival (DSF) (19, 20).

To eliminate the deviations in results caused by the heterogeneity of previous studies, we investigated the association between PA28 γ and a variety of malignant tumors by analyzing PA28 γ mRNA abundance in multiple human cancer tissues paired with normal

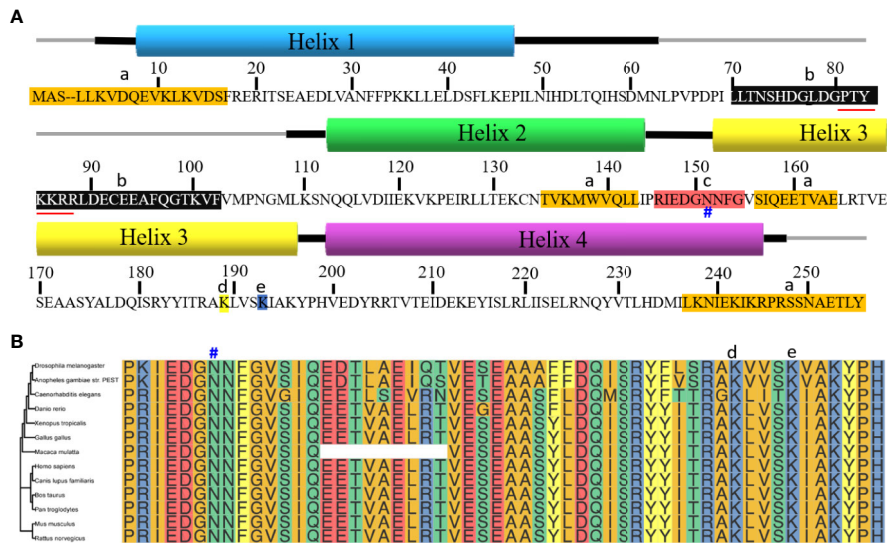


FIGURE 1 | Sequence alignment of PA28 γ . **(A)** PA28 γ is composed of four helices. The thick lines next to the helices are the flanking sequences. a. Sequences highlighted in orange indicate those sequences that are different from the PA28 α and PA28 β . b. Homolog-specific insert is between helix 1 and helix 2 in the black background. It's evolutionarily conserved and contains the nuclear localization sequence (marked with red underline), which binds the proteasome to other molecules. c. Activation loop is the sequence between helix 2 and helix 3 and is highlighted in red. N151Y (marked with #) blocks protein activation by binding to them, preventing them from binding to their normal counterparts. d. Lys188 (highlighted in yellow) enables PA28 γ to stimulate all three proteasome catalytic sites. e. PA28 γ (K195R) (highlighted in blue) can be acetylated mostly on its lysine 195 (Lys-195) residue by the CREB-binding protein (CBP), a modification that can be reversed by sirtuin 1 (SIRT1) in mammalian cells. Acetylation can influence the interaction between the monomers. **(B)** The evolutionary trees among multiple species with amino acids 145 to 199 of PA28 γ . Multi-sequence alignment uses CLUSTAL 2.1 with default parameters, R packages ggtree and ggmsa were used for drawing graphics and evolutionary trees. N151 marked with #, Lys188 marked with d, and K195 marked with e above the corresponding amino acids.

tissues using the TCGA database. The results showed that most of the cancer samples had higher levels of PA28 γ than the adjacent tissues except in kidney chromophobe and kidney renal clear cell carcinoma. Survival analysis of a wide variety of tumors revealed that the level of PA28 γ was correlated with OS and DSF (Figure 2). In conclusion, the expression of PA28 γ is significantly increased in cancer tissues, and PA28 γ expression in malignant tumors is closely related to their prognosis, suggesting that PA28 γ plays an important role in the processes of cancer progression.

Post-Translational Modification of PA28 γ

PA28 γ may undergo molecular modification when involved in various functions, typically acetylation. PA28 γ can be acetylated at the K195 site. The cAMP response element binding protein (CBP), is responsible for modifying PA28 γ by acetylation, and the deacetylase SIRT1 can block the CBP acetylation of PA28 γ (21). Moreover, phosphorylation is another common modification. MEKK3, an upstream molecule of PA28 γ , can increase the expression of PA28 γ and directly modify PA28 γ by initiating the phosphorylation of it. In addition, PA28 γ can be SUMOylated both of *in vitro* and *in vivo* by SUMO-1, SUMO-2, and SUMO-3. The SUMO conjugation of PA28 γ could cause increased stability of this proteasome activator and mediate its cytosolic translocation (22). Thus, these reports suggested that the post-translational modification of PA28 γ is vital importance to its function.

THE FUNCTION AND MECHANISM OF PA28 γ IN CANCER PROGRESSION

Hitherto, it was commonly recognized that PA28 γ plays multifaceted roles in the cellular processes associated with malignant tumors. Closely related to its function, PA28 γ can interact with many molecules. Here, we emphatically summarized the mechanisms into four categories such as regulate cell cycle and apoptosis, regulate tumorigenesis, promotion of angiogenesis, and promotion of DNA repair (Figure 3).

The Mechanism of PA28 γ Regulate the Cell Cycle and Apoptosis

PA28 γ could promotes tumor cell proliferation by affecting the cell cycle. Increasing evidence indicates that PA28 γ is more highly expressed in tumor tissues than it is in normal adjacent tissues. It reportedly is highly expressed and plays an essential part in the proliferation of human laryngeal carcinoma cells (23), oral cancer cells (16), and prostate cancer cells (24), and leads to enhanced pathogenesis of the respective cancer. Cell nuclear dynamics, especially for DNA, constitute an essential stage during cell division. When PA28 γ is knocked down, melanoma cell growth is inhibited and arrested in the G1 phase. Furthermore, the results showed that the DNA content in the G1 phase is increased but correspondingly is reduced in the G2

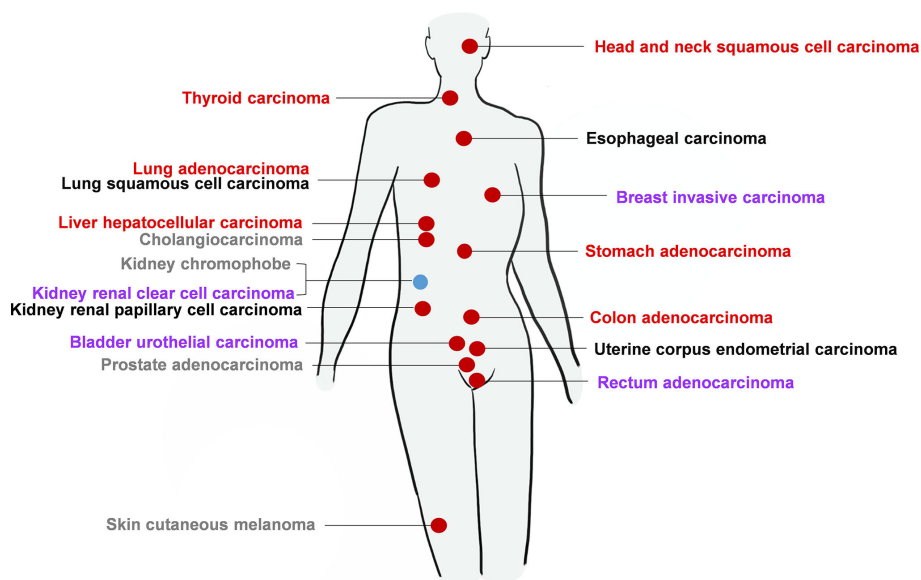


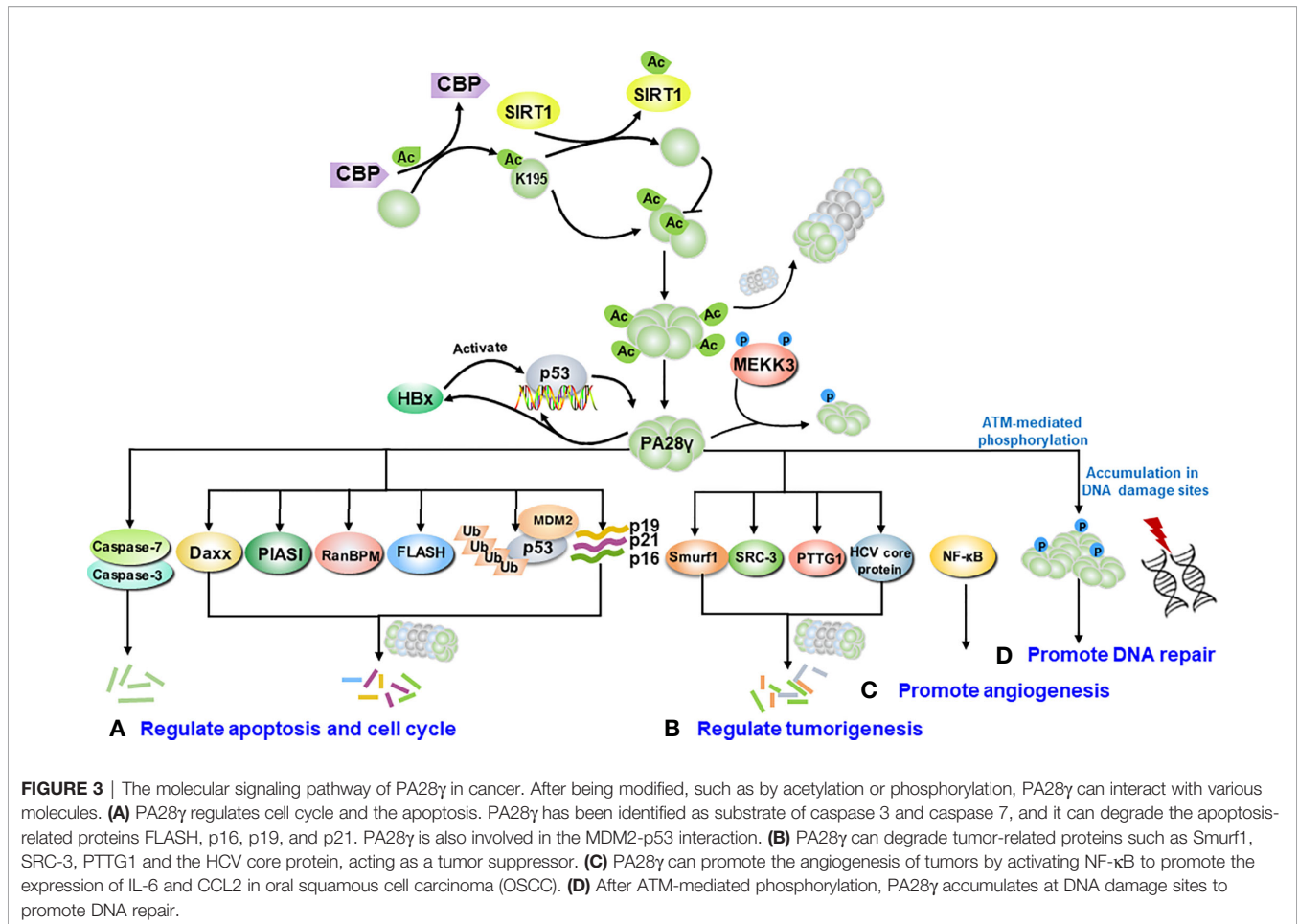
FIGURE 2 | The expression of PA28 γ and its relationship with cancer prognosis for a clinical cohort. According to the TCGA database, in most kinds of cancers, the level of PA28 γ expression increases compared with that in normal tissues, which indicates that the level of PA28 γ may be related to cell proliferation or malignancy. In some of the most common and serious cancers, such as lung carcinoma, breast invasive carcinoma, and head and neck squamous carcinoma, a higher level of PA28 γ is associated with a shorter lifetime for the tumor patients. The red circle indicates increased levels of PA28 γ in the tumor compared with that in normal tissue. The Blue circle indicates decreased levels of PA28 γ in the tumor compared with that in normal tissue. The Red fonts indicate a negative trend in the expression of PA28 γ and the lifetime of the tumor patients, according to the survival curve with $P < 0.05$. Purple fonts indicate a negative trend in the expression of PA28 γ and the lifetime of the tumor patients according to the survival curve, but $P > 0.05$. Black fonts indicate no obvious negative trend in the expression of PA28 γ and the lifetime of the tumor patients according to the survival curve with $P > 0.05$. Gray fonts indicate that there is no current or relative evidence linking survival rate to the expression of PA28 γ .

and S stages in PA28 γ -knockdown melanoma cells compared to DNA content in the cells of the control group, as determined based on the average percentage of cells in the G1 phase (25). Moreover, scientists have discovered that PA28 γ has the capability to degrade other intact tumor cell proliferation-related proteins, such as p16, p12, p19, p21 (26–30). Apoptosis of cancer cells is related to PA28 γ , which primarily suppresses normal apoptosis. For instance, there are study demonstrated that after knocking down PA28 γ , the cells of two different prostate cancer lineages showed a higher apoptosis ratio. The levels of a series of important molecules in cells were also significantly altered, such as p21, cyclin D1 and Bcl-2 (24). Moreover, In two different hepatocellular carcinoma cell lines, when PA28 γ was downregulated by drug, the apoptosis rate significantly increased and the proportion of cells in the G2 phase dramatically decreased, which is found to be of potential in clinic (31).

Studies have indicated that PA28 γ participates in the regulation mechanism of the apoptosis-related star molecules p53 (32) (Figure 4). The p53 gene is the most frequently mutated anti-oncogene in human cancers, and most well-known functions are promoting cell cycle arrest and apoptosis (33, 34). MDM2 as an ubiquitin E3 ligase is the main negative regulator of p53 and affects the stability and function of p53 (35). It can induce the monoubiquitination of p53 and promote the nuclear export of the p53 protein. MDM2 also promotes the

ubiquitination of p53, leading to the degradation of the p53 protein (36–38). Growing evidence suggests that PA28 γ acts as a cofactor during the MDM2-p53 interaction, and the PSME3 is also the target gene of p53 (36). The accumulation of p53 can lead to the overexpression of PA28 γ , which enhances the interaction between p53 and MDM2, promoting the degradation of p53. In this way, a negative feedback pathway is formed, which is conducive to ensuring the stability of p53 content. Cells deficient in PA28 γ are sensitized to stress-induced apoptosis, suggesting that PA28 γ plays a key role in the regulation of apoptosis, possibly by mediating the function of p53 *via* this MDM2-dependent pathway. In addition, scientists have also discovered that mutant p53 and wild-type p53 competitively bind to the sites of PSME3 to promote its accumulation along with the accumulation of mutant p53; consequently, tumor formation is promoted. p21, as a downstream gene of p53, is a broad-acting cyclin-dependent kinase inhibitor that can act as both a tumor suppressor and an oncogene. Therefore, it is assumed that PA28 γ also plays a bidirectional role in tumor pathogenesis.

Taken together, the findings on the degradation of p53 and p21 shed light on the roles of PA28 γ in the cell cycle and cancer. Moreover, PA28 γ interactions with other proteins, including binding partners, that are associated with apoptosis, such as RanBPM, PIASI, FLASH, Daxx and SRC-3, MEKK3, p53 (39–41).



The Mechanism of PA28 γ Regulate Tumorigenesis

It is worth mentioning that, as we explain above, we have confirmed the high levels of PA28 γ expression in malignant tissues and the inverse relationship between PA28 γ content and survival time for cancer patients, and researchers have also verified that some PA28 γ mechanisms promote tumorigenesis. However, in this regard, other evidence proves that PA28 γ has two functions: it can degrade tumor-related proteins in some cases and/or play an antitumor role. SRC-3 is an oncogenic protein from the SRC family, which is a therapeutic target for breast cancer, prostate cancer and ovarian cancer (42, 43). In a study that undermined the traditional idea suggesting PA28 γ can only degrade short peptides, PA28 γ was first demonstrated to interact with SRC-3 and degrade this endogenous protein both *in vitro* and *in vivo* (44).

Furthermore, malignant metastasis and the invasion of tumors are induced when PA28 γ is at an abnormally high level. The motility and invasion capabilities of the cells decrease significantly after PA28 γ is knocked down. High expression in breast cancer patients is closely associated with positive estrogen receptor alpha (ER α) status, leading to poor clinical prognosis (45). Correlation between nuclear PA28 γ expression and invasion and relapse in hepatocellular carcinoma (HCC) (46).

Viral infection, especially infection with hepatitis C virus (HCV), is influenced by PA28 γ . HCV is a major cause of chronic liver diseases, including steatosis, cirrhosis and hepatocellular carcinoma. The HCV core protein has long been proven able to bind with PA28 γ not only in cell culture but also in the livers of HCV core transgenic mice, and overexpression of PA28 γ leads to proteolysis of HCV core protein (27). Moreover, knocking down PA28 γ enhances the degradation of core proteins in a ubiquitin-dependent way, impairs virus production, and leads to HCV core protein accumulation in the nucleus, thereby disrupting the development of both hepatic steatosis and HCC (47). The HCV core can induce transcriptional activation of PA28 γ expression, in turn regulating its own protein level through a feedback loop that involves PA28 γ in either ubiquitin-dependent or independent way (48). The association between PA28 γ and human T-cell leukemia virus type 1 has also been proven (21).

The Mechanism of PA28 γ Promote Angiogenesis

PA28 γ also has an impact on tumor angiogenesis. It contributes to tumor growth and is regarded as an important feature useful for evaluating the prognosis of cancer. Previously, PA28 γ was reported as a novel angiogenic factor because it could ablate VEGF (vascular endothelial growth factor)-induced

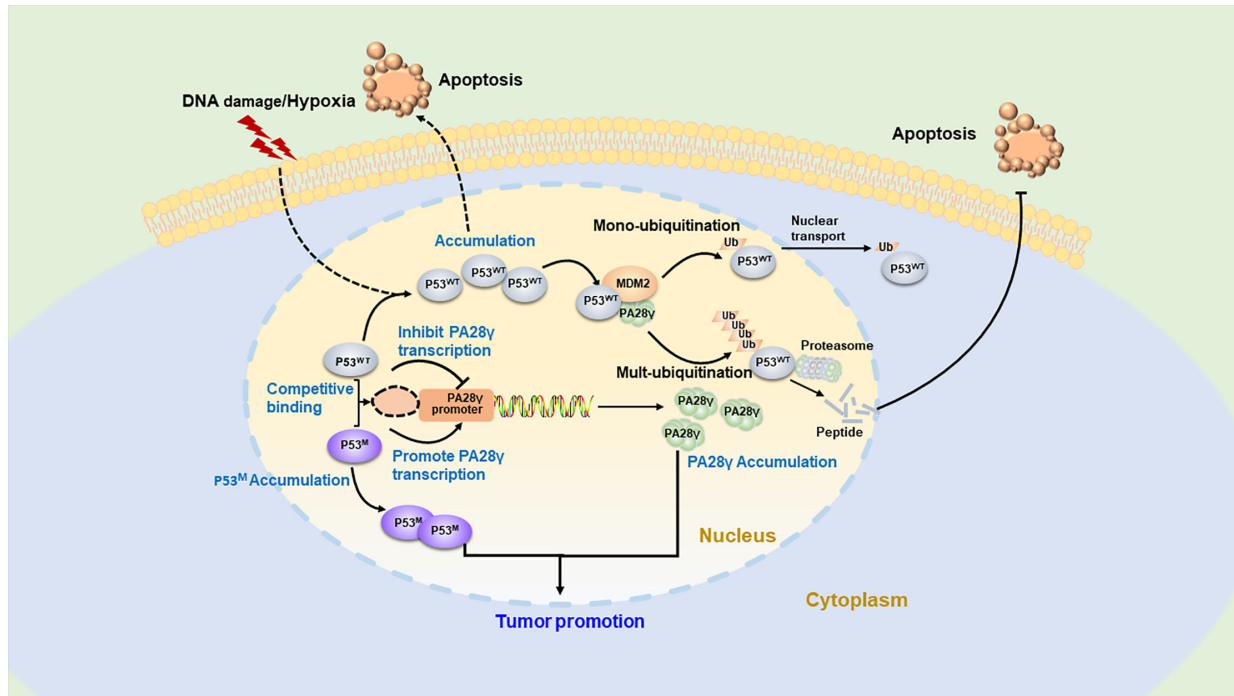


FIGURE 4 | The regulatory feedback mechanism between PA28 γ and P53. Overexpressed wild-type p53 can enhance the activity of the PA28 gene to upregulate PA28 γ , while PA28 γ can promote MDM2-mediated ubiquitination of p53, leading to the nucleation or degradation of p53. This is the negative feedback regulatory mechanism between p53 and PA28 γ . In addition, mutant p53 can compete with wild-type p53 to bind to the site of PA28 γ to promote PA28 γ expression, thus inducing tumorigenesis.

angiogenesis (49). Tumor-associated angiogenesis is of great importance in the metastasis and recurrence of tumors. In our previous study, we analyzed the expression of PA28 γ in OSCC and found that the molecule could promote tube formation of Human Umbilical Vein Endothelial Cells (HUVECs) *in vitro* and accelerate tumor-induced angiogenesis in xenograft mouse models *in vivo* (50). We then found that the expression of PA28 γ could promote the expression and secretion of IL-6 and CCL2 in OSCC cells by regulating the activation of NF- κ B, thus promoting the angiogenesis of endothelial cells (50).

In addition, after phosphorylation by ATM, PA28 γ is recruited to damage sites to boost DNA double-strand break repair *via* proteasome-mediated protein degradation. This ATM-PA28 γ -proteasome axis is required for timely DNA repair (51).

THE POSSIBLE APPLICATION OF PA28 γ IN CANCER PROGNOSIS AND TREATMENT

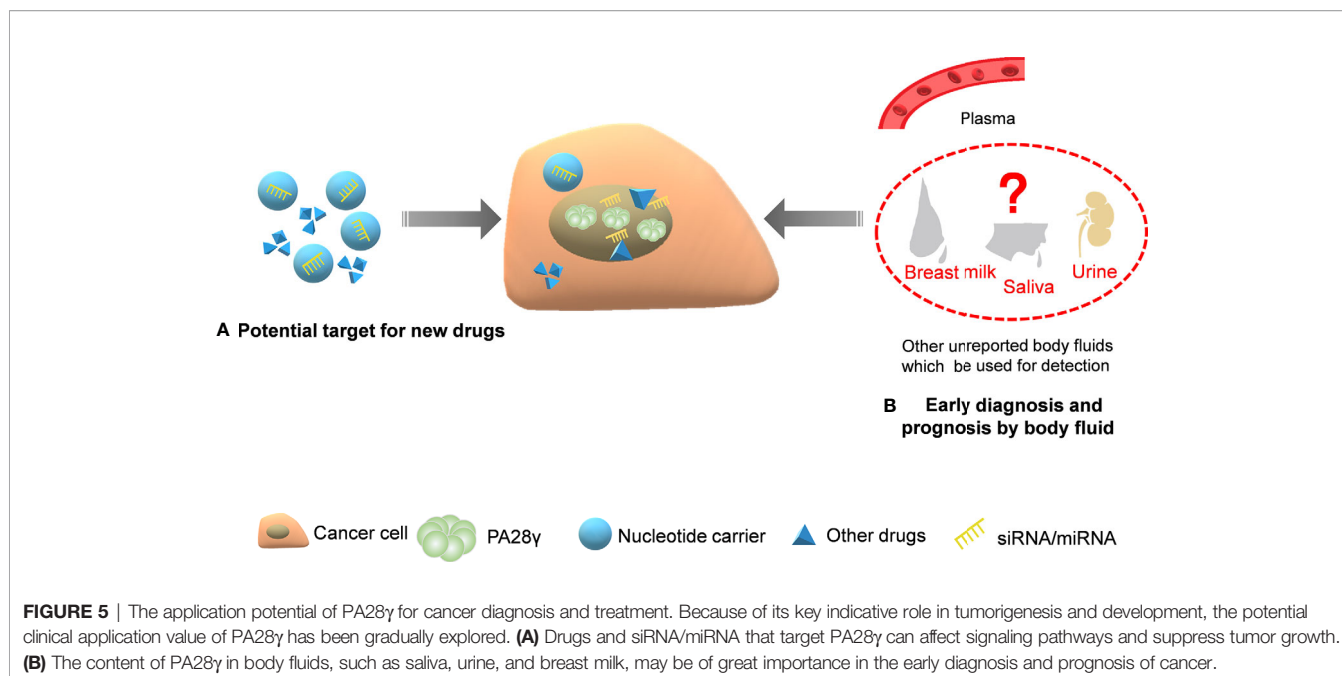
As demonstrated, PA28 γ can affect different cell cycle inhibitors, is involved in important signaling pathways in tumor cells and is proven to play a part in the growth, metastasis, invasion, and angiogenesis of tumors. Consequently, PA28 γ may hold the potential to act as a novel diagnostic biomarker, a therapy target and prognosis predictor (Figure 5).

The Application of PA28 γ for Early Diagnosis

Currently, to develop minimally invasive or even noninvasive tools through blood or other body fluids for the early diagnosis of tumors, more and more researchers are focusing on discovering stable and reliable biomarkers. We believe that PA28 γ has such potential for diagnostic applications. The upregulation of PA28 γ in the serum of patients with colorectal cancer compared to that of healthy volunteers and patients with other bowel disease can be detected by a highly sensitive immunoassay, proving that PA28 γ is able to act as a serum marker for CRC (18, 52). Theoretically, considering the functions of PA28 γ in the cellular processes of cancer as described above, similar results may also be found for other kinds of carcinoma. Nevertheless, investigations on the application of PA28 γ as an early-diagnostic biomarker are lacking. Additionally, before clinical application, the stability, sensitivity, and specificity of PA28 γ will need to be examined carefully. Consequently, the clinical use of PA28 γ requires more patience and hard work.

The Application of PA28 γ for Therapeutic Targeting

To date, several important intercellular molecules, complexes, and pathways have been reported to be influenced by the ubiquitin-independent and ATP-independent degradation induced by the PA28 γ proteasome. Among those, most



correlate closely with various tumor activities. Drugs targeting PA28 γ are likely to act on the signaling pathway of PA28 γ to affect the pathophysiology and development of malignant tumors. For example, researchers found abnormal downregulation of miR-7 in non-small-cell lung cancer (NSCLC) could promote cell proliferation, colony formation, and cell cycle progression, and cyclin D1 expression was lower when miR-7 levels were increased or PA28 γ levels were decreased (12). In another study, after knocking down PA28 γ , the level of p21 expression was increased, while the levels of cyclin D1 expression was decreased (24). These results may indicate that the miR-7/PA28 γ /p21/cyclin D1 pathway may exist in cancer cells and that high levels of PA28 γ may induce tumors to acquire a malignant phenotype. Taking advantage of the signaling pathway, the application of PA28 γ in clinical treatment can be divided into two orientations, as explained below.

To support our hypothesis, we need to validate that PA28 γ is at a low level in a patient, a state that can be the results of one of two functions: inhibiting its formation and or promoting its degradation. With regard to the first aspect, some investigators have already been able to inhibit PA28 γ in ALVA41 prostate cancer cells, a natural amino monosaccharide, glucosamine, may downregulate PA28 γ providing UDP-GlcNAc substrates for O-linked β -N-acetylglucosamine(O-GlcNAc) protein modification (53). A medicine named Tetrandrine could also downregulate PA28 γ expression in different hepatocellular carcinoma cell lines. Tetrandrine can promote apoptosis and regulate the cell cycle by targeting PA28 γ (31).

The Application of PA28 γ for Prognosis

As a biomarker, PA28 γ plays not only a role in preoperative diagnosis but also as a prognostic indicator. High levels of PA28 γ

expression indicate metastasis and poor prognosis for patients with breast cancer. The disease-free and overall survivals indicators with low corresponding PA28 γ expression are obviously more positive than they are for people with high PA28 γ expression levels, demonstrating the possibility of utilizing PA28 γ as a prognostic factor (45, 54). Similarly, PA28 γ is a good predictor of the risk of death for patients with OSCC (19). However, currently, the potential of PA28 γ as a biomarker is not particular popular, and its biomarker function has not been verified in some other tumors. More importantly, to date, there is no definitive criterion for abnormal expression, which requires numerous clinical trials in the future. Currently, the extraction and purification of PA28 γ from serum and tissues are relatively widespread, which requires invasive methods for its detection, and we assume that it would be better if PA28 γ could be tested in saliva or urine.

PERSPECTIVES

Since PA28 γ was discovered decades ago, a great deal of advances have been made in elucidating its characteristics and functions. Its novel expression patterns and diverse functions that promote pathological progress in cancers are relatively clear. The crucial roles in progress of carcinogens to the development of cancer have defined PA28 γ as a promising therapeutic candidate. However, the exact role of PA28 γ in cancer hasn't yet been fully excavated. To date, the protein structure of PA28 γ has not been resolved yet, and there are no commercial post-translational modification antibodies, such as phosphorylated antibodies, acetylated antibodies, and glycosylated antibodies. Limited by this, although some investigations have suggested that PA28 γ can also participate in the tumor suppression process, the underlying mechanism

still unknown, highlighting the need for further innovation in the field.

In terms of exploring the potential biomedical applications, accumulating evidence suggests that PA28 γ holds great potential for use in early diagnosis, prognosis evaluation, and targeted therapy. However, as we describe above, the clinical utilization of PA28 γ could be a new research direction for the many years to come. Thus far, numerous barriers need to be overcome, such as determining the means for accurate measurement, methods to prevent harm during assessments, and most importantly, a reliable criterion for determining effectiveness. All in all, sustained and systematic efforts (e.g. novel methods used in various pre-clinical cancer models) in the future are necessary for greater development and utilization of PA28 γ .

DATA AVAILABILITY STATEMENT

The datasets generated and analyzed during the current study are available in the PubMed repository, www.ncbi.nlm.nih.gov/pubmed.

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AUTHOR CONTRIBUTIONS

KL, HB, and QC wrote the manuscript and designed the figures. SS and CX collected the related references and edited the manuscript. JL provided guidance and revised this manuscript. All authors contributed to the article and approved the submitted version.

FUNDING

This project was supported by the National Natural Science Foundation of China (numbers 81672675, 81872211, 81602375 and 81621062), the MoE III Project from China Higher Ed (grant number B14038), the CAMS Innovation Fund for Medical Sciences (CIFMS, 2019-I2M-5-004).

ACKNOWLEDGMENTS

We thank Lin Zeng (NewCore BioDataStudio in Shanghai) for sequencing data analysis.

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Conflict of Interest: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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