

New Insights into the PTB-Associated Splicing Factor (PSF) and Peroxisome Proliferator-Activated Receptor gamma (PPAR γ) in Colorectal Carcinogenesis

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Abstract

PTB-associated Splicing Factor (PSF) is a multifunctional protein involved in transcription repression, pre-mRNA processing, and DNA repair. Transcriptional repression by PSF is mediated by its interaction with nuclear hormone receptors. However, the physiological context of PSF in regard to nuclear receptor signaling is still unclear. In this review, our recent study identified PSF as a novel PPAR γ -interacting protein and demonstrated that PSF is involved in several important regulatory steps of colon cancer cell proliferation. Recently, the aberrant expression of PSF in tumor cells has been implicated in resistance to drugs that are commonly used in cancer therapy. Therefore, it might be possible to develop and to optimize drugs that inhibit PSF and correct abnormal splicing, resulting in enhanced tumor cell migration, invasion, and proliferation. In this review, we summarize current understanding of the mechanisms underlying the PSF-PPAR γ axis and its role in the control of colorectal carcinogenesis.

An Overview of PSF and PPAR γ

PTB-associated splicing factor (PSF), one of the major nuclear proteins [1] in eukaryotic cells, consists of a single polypeptide chain of 76 kDa (Figure 1A). PSF is highly basic because the amino terminus is rich in proline and glutamine residues [2]. Notably, the amino acid composition of the entire ORF comprises 16% proline and 7% glutamine residues. A recent study revealed that PSF belongs to a family of putative tumor-suppressor proteins [3] that contain an RNA-binding domain (RBD) and a DNA-binding domain (DBD). The NH₂-terminal region of PSF was shown to bind response sequences for Retinoid X Receptor (RXR) [4]. Members of the type II nuclear hormone receptor subfamily (including PPAR γ) bind to their response sequences with or without ligand [5]. In the absence of ligand, the DNA-bound receptors repress gene expression to different degrees [6]. Thus, PSF is a highly complex protein that may be an important component of the transcriptional repression of many different genes via different mechanisms. Recently, Wang et al. reported that PSF plays a central role in the reversible regulation of mammalian cell proliferation and tumorigenesis [7]. Alteration in the expression of PSF and its binding partners therefore has potential as a therapeutic strategy against cancer [3,8].

PPAR γ is a nuclear receptor that plays an essential role in lipid and glucose homeostasis [9,10]. PPAR γ is comprised of four functional parts (Figure 1B): the N-terminal A/B region, which contains a ligand-independent transcription-activating motif, AF-1; the C region binds response elements; the D region, which binds to various transcription cofactors; and the E/F region, which has an interface for dimerizing with retinoid X receptor α (RXR α), an AF-2 ligand-dependent transcription-activating motif, and a Ligand-Binding Domain (LBD) [11]. Recent reports indicate that PPAR γ is over-expressed in many types of cancer, including colon, lung, breast, ovary, and stomach cancer, suggesting that regulation of PPAR γ affects cancer pathogenesis [9,12-14]. While previous studies have demonstrated that some PPAR γ agonists inhibit the growth of cancer cells, many reports show that PPAR γ ligand-mediated growth inhibition varies depending on the cancer cell type. In colon cancer cells, the growth-suppressing effect of PPAR γ ligands evident in *in vitro* studies was not clearly confirmed by *in vivo* studies.

For example, PPAR γ deficiency enhanced colon tumorigenesis in APC^{Min} mice, while another study reported that a synthetic PPAR γ agonist, rosiglitazone, induced colon carcinogenesis [15]. The discrepancy in results may be due, in part, to PPAR γ -dependent and -independent pathways [16].

PSF Directly Interacts with PPAR γ

Many biological functions involve the formation of protein-protein complexes. Our recent study using the HT-29 colon cancer cell line showed that PSF directly interacts with PPAR γ [17]. Following affinity purification, tagged PPAR γ was separated using SDS-PAGE. The identities of the proteins in the various bands were then determined using matrix-assisted laser desorption/ionization (MALDI)-time-of-flight (TOF) MS. This strategy identified several candidate proteins that might interact functionally with PPAR γ [17]. One of the candidates, PSF, is most likely a PPAR γ -interacting protein. Furthermore, we demonstrated that the mammalian two-hybrid assay is a very powerful technique with which to study pair-wise interactions between proteins [18]. The assay utilizes two GAL4-based transcription activation domains of *Saccharomyces cerevisiae*: the DNA-binding domain and the transcription activation domain of the herpes simplex virus VP16 protein [19]. We demonstrated the use of a PSF-PPAR γ mammalian two-hybrid system to study protein-protein interactions. The interaction of chimeric Gal4-PSF deletion mutants with VP16-PPAR γ was assessed using a mammalian two-hybrid reporter gene assay. Loss

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Received May 02, 2013; Accepted May 22, 2013; Published May 25, 2013

Citation: Tsukahara T, Matsuda Y, Haniu H (2013) New Insights into the PTB-Associated Splicing Factor (PSF) and Peroxisome Proliferator-Activated Receptor gamma (PPAR γ) in Colorectal Carcinogenesis. J Cancer Sci Ther 5: 209-211. doi:10.4172/1948-5956.1000208

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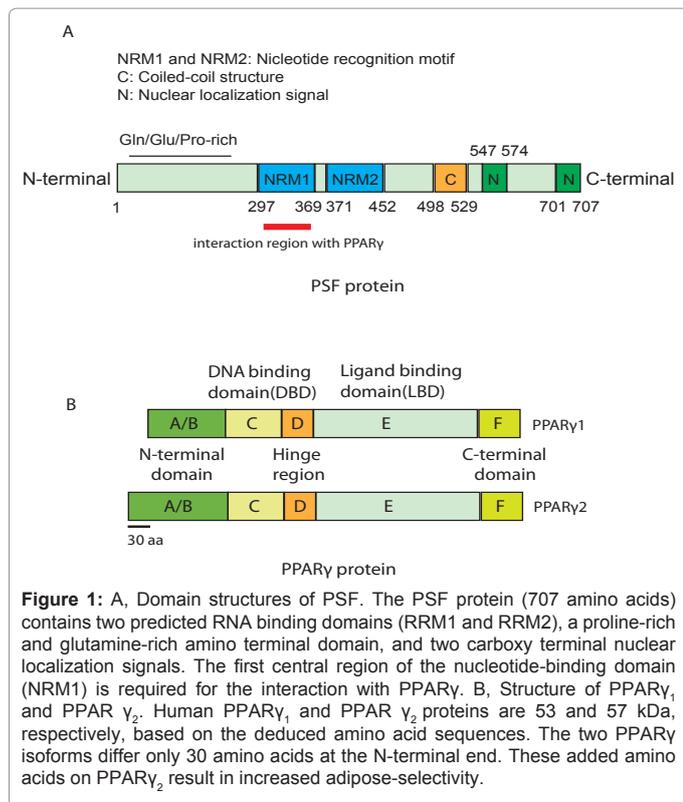


Figure 1: A, Domain structures of PSF. The PSF protein (707 amino acids) contains two predicted RNA binding domains (RRM1 and RRM2), a proline-rich and glutamine-rich amino terminal domain, and two carboxy terminal nuclear localization signals. The first central region of the nucleotide-binding domain (NRM1) is required for the interaction with PPAR γ . B, Structure of PPAR γ_1 and PPAR γ_2 . Human PPAR γ_1 and PPAR γ_2 proteins are 53 and 57 kDa, respectively, based on the deduced amino acid sequences. The two PPAR γ isoforms differ only 30 amino acids at the N-terminal end. These added amino acids on PPAR γ_2 result in increased adipose-selectivity.

of amino acids 1–290 of PSF had no effect on the interaction. Thus, the N-terminal domain is not essential for the interaction between these proteins. Loss of amino acids 291–370 of PSF disrupted the interaction between PSF and PPAR γ . Deletion of amino acids 371–450, 451–662, and 452–707 of PSF also disrupted the interaction with PPAR γ . Thus, our results identified the first nucleotide-binding domain (amino acids 291–370) as an important molecular site for PPAR γ binding [17].

PSF Knockdown and its Phenotype

Adenocarcinomas are the most common type of gastrointestinal cancer, but there are many other forms [20,21]. Cell lines established from human colorectal carcinomas may provide useful tools with which to study the biology of gastrointestinal cancer and to develop and test new therapeutic strategies [22–24]. Our recent study showed that the proliferation of DLD-1 and Caco-2 cells, which express a low level of PPAR γ , was significantly inhibited by knockdown of PSF, whereas the proliferation of HT-29 and LOVO cells, which express a higher level of PPAR γ , was inhibited weakly or not at all. Interestingly, in DLD-1 cells, but not in HT-29 cells, PSF knockdown also induced morphological changes associated with apoptosis, i.e., cell shrinkage and condensation of nuclear chromatin [17]. Our recent work demonstrated that knockdown of PSF induced dramatic cytoplasmic vacuolization 48 and 72 h after siRNA transfection in 30 and 40% of cells in culture, respectively. Cell vacuolation increased in frequency and size, occupying increasingly larger areas of the cytoplasm, in a time-dependent manner. The reason why cytoplasmic vacuoles were present in only DLD-1 cells remains unclear. In electron micrographs, smaller vacuoles in some cancer cells appeared to be distended mitochondria [25]. However, it is unclear if this is a step of apoptosis or necrosis or a distinct form of colon cancer cell death. Our recent work suggested that cytoplasmic vacuolation and apoptotic changes correlated with the dysfunction of mitochondria [17]. We identified candidate proteins

potentially involved in the PPAR γ -PSF interaction and in apoptosis. As expected from a previous study [17], many of these proteins play a role in apoptosis (annexin and VDAC2) and cytoskeletal interactions (tubulin, MYH9, and filamin A) and act as molecular chaperones (HSP90 and T complex protein) (summarized in Figure 2). Interestingly, in DLD-1 cells, voltage-dependent anion-selective channel protein 2 (VDAC2) was upregulated. VDAC2 forms a channel through the mitochondrial outer membrane that allows the diffusion of small hydrophilic molecules [26,27]. VDAC2 has also been implicated in apoptosis, forming an open pore that allows the release of cytochrome *c* from the inner mitochondrial membrane [28]. We investigated VDAC2 mRNA and protein expression in DLD-1 cells after PSF knockdown. Real-time PCR and western blot analysis confirmed that VDAC2 and Bax were upregulated under PSF knockdown conditions in DLD-1 cells [17]. Furthermore, Sharathchandra et al. recently reported that annexin A2 and PSF interact with tumor suppressor protein p53 [29]. p53 levels were reduced after knockdown of annexin A2 and PSF. Annexin A2 is a calcium- and phospholipid-binding protein that is found on various cell types [30,31] and is upregulated in various cancers. It plays multiple roles in apoptosis, proliferation, migration, and invasion [32,33]. Annexin A2 might be useful as a biomarker for the diagnosis and treatment of colon cancer. Together, these studies indicate that VDAC2 and annexin A2 have potential as therapeutic targets to inhibit colon cancer progression.

Conclusions

Targeting specific molecules has become important for developing new cancer treatments. Herein, we reviewed our current understanding of the cellular and molecular interactions between PPAR γ and its target in colon cancer. We provided a general overview of the broad therapies directed at PPAR γ expression or its binding partners that may lead to novel approaches to treat colon cancer. The effect of PSF on PPAR γ targets and the contributions of these targets to PSF-mediated cellular processes require further investigation. This study supports the potential use of PSF and its targets in the development of drugs targeting colon cancer and possibly other types of cancer. Such studies may open up new avenues for colon cancer research and therapeutics.

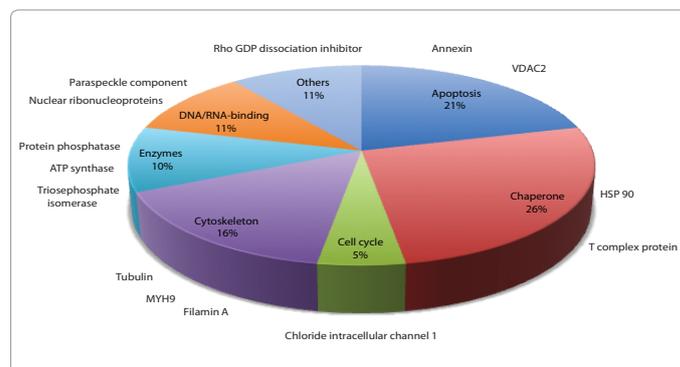


Figure 2: Upregulated proteins in DLD-1 cells after siRNA knockdown of PSF. DLD-1 cells were transiently transfected with control siRNA or siRNA targeting PSF. MS/MS analyses were performed using the AB SCIEX TOF/TOFTM 5800 System (AB SCIEX, Foster City, CA, USA). Protein identification was performed through ProteinPilotTM software (AB Sciex, Framingham, MA, USA) using the UniProt database. We identified 25 distinct proteins whose levels were significantly altered following PSF knockdown in DLD-1 cells [34]. On the basis of these results, we suggest that PSF activity may influence protein translation, the cell cycle, apoptosis, and cytoskeleton dynamics.

Acknowledgments

This work was supported by research grants from the Astellas Foundation for Research on Metabolic Disorders (to Tamotsu Tsukahara), Grant-in-Aid for Takeda Science Foundation (to Tamotsu Tsukahara), and Grants-in-Aid for Scientific Research (C) 22591482 (to Tamotsu Tsukahara) from the Japan Society for the Promotion of Science (JSPS).

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