

Activated Translation of HIF-1 α mRNA as a Key Mechanism in Oncogenesis of Pancreatic Ductal Adenocarcinoma and Other Malignant Diseases

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ABSTRACT

Molecular targeted therapies against KRAS mutant pancreatic ductal adenocarcinoma (PDAC) remain insufficient. The most serious causes are supposed to be bypass activation of the PI3K/AKT/mTOR signaling pathway and crosstalk between mTOR and hypoxia inducible factor (HIF). This short review is aimed at clarifying the involvement of activated translation of HIF-1 α mRNA in oncogenesis of KRAS mutant PDAC in association with CA9 activation. Over 90% of PDAC harbors KRAS mutations, and it is supposed that activated translation of HIF-1 α mRNA is induced by 1. mutant KRAS binding to PI3K, 2. translation activation of HIF-1 α mRNA by mTORC1 in the activated PI3K/AKT/mTOR signaling or 3. by ERK1/2 in the activated KRAS/RAF/REK/ERK signaling. Activated HIF-1 α finally activates CA9 via hypoxia responsive element (HRE). In this sense, activated translation of HIF-1 α mRNA is a key mechanism in oncogenesis of KRAS mutant PDAC. In KRAS mutant intraductal papillary mucinous neoplasm of the pancreas (IPMN) and adult T-cell leukemia/lymphoma (ATL), the same mechanism is suggested to play a crucial role in oncogenesis. In addition, CA9 inhibitors can offer novel molecular targeted therapies against these therapy resistant PDAC, IPMN and ATL.

Keywords: KRAS; PDAC; IPMN; ATL; PI3K; Translation; HIF; CA9

Abbreviations: ATL: Adult T-cell Leukemia/lymphoma; ERK: Extracellular Signal-Regulated Kinase; HIF-1 α : Hypoxia Inducible Factor-1 α ; HRE: Hypoxia Responsive Element; mTORC1: mechanistic Target of Rapamycin Complex 1; NF- κ B: Nuclear Factor- κ B; PI3K: Phosphatidylinositol 3-Kinase

Introduction

Therapy resistance is a serious problem in clinical oncology. Pancreatic ductal adenocarcinoma (PDAC) harbors genetic alterations of KRAS (93%), TP53 (72%), CDKN2A (32%), SMD4 (32%), RNF43 (7%), ARID1A (6%) or others [1]. Various mechanisms of therapy resistance in molecular targeted therapies against PDAC such as resistant mutations [2,3], bypass signaling activation [4,5] or phenotypic plasticity of endothelial-to-mesenchymal transition (EMT) [6,7] have been suggested [8-10]. For instance, insufficient results by inhibitors against effectors in the KRAS/RAF/ MEK/ extracellular signal-regulated kinase (ERK) signaling pathway [8,11] can be ascribed to bypass activation of the phosphatidylinositol 3-kinase (PI3K)/AKT/ mechanistic target of rapamycin (mTOR) signaling pathway [4,5,12]. In addition, it is indicated that translation of mRNA is activated by mTORC1

(mTOR complex 1) [13-15] or ERK1/2 [13,15]. Furthermore, it is suggested that hypoxia inducible factor (HIF)-1 α is involved in oncogenesis of PDAC [16,17], while it is well known that HIF-1 α activates transcription of carbon anhydrase IX (CA9) [18,19]. Finally, CA9 is supposed to be involved in oncogenesis of PDAD [20,21].

This short review is aimed at clarifying the involvement of activated translation of HIF-1 α mRNA in oncogenesis of KRAS mutant PDAC in association with CA9 activation. First, we briefly summarize this complicated interaction in PDAC between the mutant KRAS signaling and the PI3K/ATK/mTOR signaling pathway around activated translation of mRNA HIF-1 α , resulting in CA9 activation, because this is crucial in oncogenesis of PDAC. Second, activation of HIF-1 α and CA9 in intraductal papillary mucinous meoplasm of the pancreas (IPMN) and adult T-cell leukemia/lymphoma (ATL) is concisely shown.

Translation of mRNA

Eukaryotic mRNA translation consists of four phases, initiation, elongation, termination, and ribosome recycling [13], and the first initiation is rate-limiting [22]. mRNA has two characteristic structures, 5' 7-methylguanosine (m7G) cap [23] and 3' poly(A) tail [24], and translation initiation of mRNA is processed in eight phases [13,15,25]: 1. Formation of the ternary complex of eukaryotic translation initiation factor 2 (eIF2), GTP and initiating methionyl tRNA (Met-tRNAi); 2. Formation of the 43S pre-initiation complex (PIC) that consists of the ternary complex (eIF2/GTP/Met-tRNAi), a 40S ribosomal subunit, eIF1, eIF1A, eIF3 and eIF5 [26]; 3. Activation of mRNA by the eIF4F complex, composed of eIF4E (a mRNA-cap binding component), eIF4G (a scaffolding protein) and eIF4A (an ATP-dependent RNA helicase) [14], with assistance of eIF4B and poly(A)-binding protein (PABP) [27]; 4. Attachment of the 43S PIC to the activated mRNA; 5. Scanning of the 5' UTR of mRNA in 5' to 3' direction by 43S PIC; 6. Recognition of start codon (AUG) and formation of the 48S initiation complex; 7. Joining of 60S ribosomal subunit to the 48S initiation complex with assistance of eIF5B-GTP and concomitant release of eIF2-GDP and other factors such as eIF1, eIF3, eIF4B, eIF4F and eIF5; 8. Hydrolysis of eIF5B-GTP and release of eIF1A and eIF5B-GDP from the 80S initiation complex of ribosome. Then elongation phase starts.

Activated translation of mRNA by mTORC1

PI3K activated by its ligand successively activates AKT and mTORC1 [28]. Activated mTOR1 phosphorylates 4E-binding protein 1 (4E-BP1). Phosphorylated 4E-BP1 is released from eIF4E, leading to the association of eIF4E with eIF4G, and finally the assembly of the mRNA-cap binding eIF4F complex is induced [13-15]. The activated eIF4F complex activates translation of mRNA. mTOR1 also activates S6Ks, which then activates eIF4B. Activated eIF4B enhances the mRNA-unwinding activity of eIF4A as a component of the mRNA-cap binding eIF4F complex, leading to activation of mRNA translation [29].

Activated Translation of mRNA by ERK1/ERK2

In the KRAS/RAF/MEK/ERK signaling pathway, activated ERK1/2 phosphorylate RSKs [13,15], which then activate eIF4B, leading to activation of mRNA translation [29]. ERK1/2 also phosphorylate MNKs, and activated MNKs then phosphorylates eIF4E in the eIF4F complex [15], resulting in activation of mRNA translation.

Activated Translation of HIF mRNA and Activation of CA9 in PDAC

Mutant KRAS in PDAC activates its downstream effectors RAF, MEK1/2 and ERK1/2 [8,11]. Activated ERK1/2 phosphorylate vari-

ous targeted molecules [30], but RSKs and MNKs are important because these finally activate translation of mRNA of numerous targeted genes. Of these, HIF-1 α is the most important because HIF-1 α is involved in oncogenesis of PDAC [16,17,31]. In addition, CA9 is activated by HIF-1 α via hypoxia responsive element (HRE) in the promoter region of CA9 [18,19] (Table 1), and inhibitors of CA9 suppress cell proliferation of PDAC cells [16,17,20,21]. In this sense, CA9 is one of the final effectors in PDAC oncogenesis [20,21] and CA9 inhibitors are suggested to be promising molecular targeted therapies against PDAC [12,21]. In addition, mutant KRAS in PDAC activates the bypass PI3K/AKT/mTOR1 signaling pathway. Mutant KRAS activates PI3K α by direct binding to a RAS-binding domain of p110 α in PI3K [32] (Table 1). Activated PI3K then activates successively its downstream effectors AKT and mTORC1. As indicated above, mTORC1 activates translation of HIF-1 α mRNA via 4E-BP1 and eIF4B, leading to activation of CA9 in PDAC.

IPMN

A precursor lesion pancreatic intraepithelial neoplasia (PanIN) progresses into PDAC [4], but there is another precursor IPMN [33]. IPMN harbors KRAS (up to 80%) and/or GNAS (about 70%) mutations, and coexistence of both KRAS and GNAS is found in over 30% [34-36]. Since poor prognosis of malignant IPMN is comparable to that of PDAC [33] and due to high mutation rate of KRAS in IPMN, involvement of HIF-1 α and CA9 in malignant progression and oncogenesis of IPMN is quite possible [37] (Table 1), as in PDAC [16,17,20,21].

ATL

ATL is a hematological malignancy [38] caused by human T-cell leukemia virus type 1 (HTLV-1) [39,40]. In the multistep oncogenesis model of ATL [41], final oncogenic progression is completed by additional events in host cells, not by the HTLV-1-derived Tax [42,43] nor HBZ [44]. In this regard, constitutive activation of nuclear factor- κ B (NF- κ B) [45,46] is the most important among the additional events at the final stage of ATL oncogenesis, because NF- κ B molecules directly activate transcription of HIF-1 α [47,48], leading to activation of CA9 (Table 1). Furthermore, activated expression of AKT is observed in ATL cell lines [49,50] and primary ATL cells [49], while expression of HIF-1 α is activated in ATL cell lines as well as primary ATL cells [49]. In addition, expression of CA9 is confirmed in primary ATL cells [51] and high expression of CA9 in ATL cell lines is correlated with tumorigenicity [51]. These data can support crosstalk between the PI3K/AKT/mTOR signaling pathway and HIF-1 α /CA9 via activated translation of HIF-1 α mRNA (Table 1).

Table 1: Activation of PI3K and HIF-1 α /CA9 in KRAS mutant PDAC/IPMN and ATL.

Diseases	Activation of PI3K	Activated translation of HIF-1 α mRNA	Activation of CA9
KRAS mutant PDAC/IPMN	Binding of KRAS to PI3K	by mTORC1 and/or ERK1/2	HRE of CA9 by HIF-1 α
ATL	Activated transcription of PI3K by NF- κ B	by mTORC1	HRE of CA9 by HIF-1 α

Conclusion

Activated translation of HIF-1 α mRNA is a key mechanism in oncogenesis of KRAS mutant PDAC in association with CA9 activation. In KRAS mutant IPMN and ATL, the same activated translation of HIF-1 α mRNA is suggested to play a crucial role in oncogenesis. In ATL, another crosstalk between NF- κ B and the HIF-1 α /CA9 signaling is indicated to be significant in multistep oncogenesis of ATL. In addition, CA9 inhibitors can offer novel molecular targeted therapies against these therapy resistant PDAC, IPMN and ATL. To realize novel therapies, further studies are required.

Conflicts of Interests

The author declares that there is no conflict of interests.

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