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Role of cyclin-dependent kinase inhibitors in pituitary tumorigenesis : an updateMd. Golam Hossain*, Takeo Iwata*, Noriko Mizusawa*, Zhi Rong Qian[‡], Shozo Yamada[†], Toshiaki Sano[‡], and Katsuhiko Yoshimoto*Department of *Medical Pharmacology, and [‡]Department of Human Pathology, Institute of Health Biosciences, the University of Tokushima Graduate School ; and [†]Department of Hypothalamic and Pituitary Surgery, Toranomon Hospital, Tokyo Japan

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SUMMARY

Human pituitary adenomas are common and potentially serious neoplasms that account for 10-15% of all intracranial neoplasms. In spite of extensive investigations, the molecular basis of human pituitary tumorigenesis remains elusive. The cell cycle is driven by protein complexes composed of cyclins and cyclin-dependent kinases (CDKs). CDK inhibitors (CKIs) serve as negative regulators of cell cycle. CKIs include two distinct families : the INK4 family comprising p16^{INK4A}, p15^{INK4B}, p18^{INK4C}, and p19^{INK4D} and the Cip/Kip family including p21^{CIP1}, p27^{KIP1}, and p57^{KIP2}. Dysregulation in CKIs are recognized as critical factors in tumorigenesis. In recent years, extensive studies have demonstrated that mutations, underexpression, and DNA methylation of the CKIs genes were frequently observed in various types of human cancers. However, the role of CKIs in human pituitary tumors has been elucidated to a limited extent. Here we review the potential role of CKIs in human pituitary adenomas concentrating on gene mutations, promoter methylation, and mRNA or protein expression levels.

Key words : pituitary adenomas, CKIs, INK4 family, Cip/Kip family, mutations, promoter methylation

Introduction

Human pituitary adenomas are the most commonly encountered intracranial neoplasms. Although pituitary adenomas are benign, it is associated with significant morbidity due to its critical location and oversecretion of pituitary hormones¹⁾. A large number of studies have been conducted to elaborate the molecular and pathological basis of pituitary tumorigenesis. However, the mechanisms of tumorigenesis of human pituitary adenomas are largely unknown.

The cell cycle is a tightly regulated process and is controlled at different stages by specific cyclins and cyclin-dependent kinases (CDKs). A critical point in the cell cycle is the G₁/S transition checkpoint frequently aberrated in human cancers^{2,3)}. CDKs are inhibited by CDK inhibitors (CKIs) which play a crucial regulatory role at G₁/S transition. To date, two families of CKIs based on their structural and functional similarities have been described. The INK4 family comprising p16^{INK4A} (CDKN2A), p15^{INK4B} (CDKN2B), p18^{INK4C} (CDKN2C),

and p19^{INK4D} (CDKN2D) shows their negative regulatory activity by binding to CDK4 and CDK6 and opposing their association with cyclin D. The Cip/Kip family including p21^{Cip1} (CDKN1A), p27^{KIP1} (CDKN1B), and p57^{KIP2} (CDKN1C) shows a broad spectrum of inhibitory effects on cyclin/CDK complexes including cyclin D/CDK4, cyclin E/CDK2, and cyclin A/CDK2³.

Recent studies showed that dysregulation of CKIs contributed to progression of various tumors, suggesting that CKIs act as a tumor suppressor^{4,5}. However, the role of CKIs in human pituitary tumors has been elucidated to a limited extent. We review the recent findings of CKIs associated to human pituitary tumorigenesis, with a particular focus on expression, mutations, and promoter methylation profile of CKIs. We also discuss the functional significance of collaborative roles of CKIs.

CKIs and their knock-out mice

The discovery of p16^{Ink4a} and p21^{Cip1} highlighted the importance of CKIs as tumor suppressors. The analysis of CKI-deficient mice further accelerated the deeper understanding of the role of CKIs in cancer research (Table 1). In human, the p16^{INK4A}/p14^{ARF}/p15^{INK4B} locus on chromosome 9p21 is frequently implicated in a wide spectrum of tumors⁶. Deletion of this locus inactivates simultaneously the two members of INK4 family, p16^{INK4A} and p15^{INK4B}, and the entirely unrelated protein, p14^{ARF}.

p16^{Ink4a} null mice develop lymphomas and sarcomas with low penetrance⁷. The major phenotype observed in p15^{Ink4b} knock-out mice was angiosarcomas with a long latency and low frequency, indicating that p15^{Ink4b} has limited tumor-suppressing activities⁸. In human, the p18^{INK4C} gene is located on chromosome 1p32, a region frequently altered in a variety of cancers⁹. Deletion of the p18^{Ink4c} gene in mice results in the frequent development of widespread organomegaly, pituitary hyperplasia and adenomas as well as other neoplasias such as pheochromocytoma, B-cell lymphoma, angiosarcoma, thymic lymphoma, and renal cell carcinoma^{8,10}. These observations indicate that p18^{Ink4c} is a tumor suppressor

Table 1 : Major phenotypes of CKIs knock-out mice

Target	Major phenotype	References
<i>INK4 family</i>		
p16 ^{Ink4a}	Lymphomas and sarcomas with low penetrance	(7)
p15 ^{Ink4b}	Angiosarcomas with long latency	(8)
p18 ^{Ink4c}	Similar to phenotypes seen in mice lacking p27 ^{Kip1}	(8, 10)
p19 ^{Ink4d}	Fertility inspite of testicular atrophy	(11)
<i>Cip/Kip family</i>		
p21 ^{Cip1}	Histiocytic sarcomas, hemangiomas, and lymphomas	(13)
p27 ^{Kip1}	Hyperplasia in several organs and develop adenomas of intermediate lobe of the pituitary gland	(15-17)
p57 ^{Kip2}	Die immediately after birth due to dyspnea resulting from cleft palate, abdominal muscle defects or skeletal abnormalities	(18, 19)
<i>INK4 family ; Cip/Kip family</i>		
p15 ^{Ink4b} ; p18 ^{Ink4c}	Similar to phenotypes of single knock-out mice	(8)
p18 ^{Ink4c} ; p19 ^{Ink4d}	Male infertility	(54)
p18 ^{Ink4c} ; p21 ^{Cip1}	Pituitary adenomas and neuroendocrine hyperplasia	(21)
p18 ^{Ink4c} ; p27 ^{Kip1}	Tumors with shorter latency in endocrine glands including the pituitary	(21)
p19 ^{Ink4d} ; p27 ^{Kip1}	Die of neurological defects such as bradykinesia, proprioceptive abnormalities, and seizures	(12)
<i>CKIs ; others</i>		
p27 ^{Kip1} ; Men1	No noticeable synergistic stimulation of tumor growth	(22)
p18 ^{Ink4c} ; Men1	Accelerated rate with an increased incidence of tumor development in the pituitary, thyroid, parathyroid, and pancreas	(22)
p18 ^{Ink4c} ; p53	Medulloblastomas	(55)

at least in mice. Meanwhile, deletion of the p19^{Ink4d} gene does not give rise to tumors even after long observations¹¹. However, mutant mice lacking both p19^{Ink4c} and p27^{Kip1} develop disorders such as bradykinesia, proprioceptive abnormalities, and seizures¹².

Although the role of p21^{Cip1} deficiency in the development of sarcomas and lymphomas has been defined¹³, its role in pituitary tumor progression is not clear. Very recently, Chesnokova, *et al.* generated triple mutant mice (Rb^{+/-} ; Pttg^{-/-} ; p21^{-/-}) and showed that p21^{Cip1} deficiency restored abrogated pituitary tumor formation in Rb^{+/-} ; Pttg^{-/-} knock-out mice, indicating the potential role of p21^{Cip1} in pituitary tumor growth¹⁴. p27^{Kip1} deficient mice display striking features of tumor development in several organs including pituitary glands¹⁵⁻¹⁷. The p57^{Kip2} knock-out mice lead to developmental disorder

ders such as cleft palate and gastrointestinal abnormalities^{18, 19} ; however, the role of p57^{Kip2} as tumor suppressor is largely obscure. Very recently, Jin, *et al.* demonstrated that the prostates of p57^{Kip2} knock-out mice developed prostatic adenocarcinomas²⁰.

Functional collaboration or redundancy between distinct CKIs confers higher level of regulatory roles in inhibition of tumor progression (Table 1). Although mice lacking two INK4 proteins, p15^{Ink4b} and p18^{Ink4c}, do not develop an accelerated rate of tumors⁸, but collaboration of INK4 family members with Cip/Kip family members confers decreased rate of tumor development. For example, mice lacking either p18^{Ink4c} or p27^{Kip1} slowly develop pituitary adenomas^{8, 10, 15-17}, whereas mice carrying simultaneous deletion of p18^{Ink4c} and p27^{Kip1} develop pituitary adenomas with more accelerated rate²¹. Generation of all four INK4 knock-out mice should be of value to better understand the INK4 family in pituitary tumor development. Interestingly, p18^{Ink4c}; Men1 double knock-out mice develop endocrine tumors with more accelerated rate than that of each knock-out mice²².

The above findings denote the important role of p18^{Ink4c} in the development of pituitary adenomas. The analyses of double null mice clearly indicate the func-

tional cooperation of CKIs in inhibition of pituitary tumor development (Table 1).

Mutations of the CKI genes are infrequent in pituitary tumors

Although the p15^{INK4B} gene concomitant with the p16^{INK4A} gene is usually deleted in a large variety of tumors²³, mutations of the p15^{INK4B} gene in human tumors are infrequent^{24, 25}. A more frequent mutations and deletions of the p16^{INK4A} gene were reported in various malignancies²⁶. However, we and others confirmed that the p16^{INK4A} gene mutations are infrequent in pituitary tumors^{25, 27} (Table 2). The p18^{INK4C} gene mutations were rare in human cancers^{28, 29}. We showed that p18^{INK4C} mutations were absent in human pituitary adenomas. Very recently, van Veelen, *et al.* reported the presence of somatic inactivating missense mutations of p18^{INK4C} in human medullary thyroid carcinomas and pheochromocytomas³⁰.

Although the majority of pituitary adenomas are sporadic, some arise as a familial syndromes. Out of CKIs, the p27^{KIP1} gene is the only identified gene responsible for heritable pituitary tumors. A germline non-

Table 2 : Mutations, promoter methylation, and expression status of the CKI genes in pituitary adenomas

CKIs	Mutations	Promoter hypermethylation	Expression (mRNA or Protein)	References
<i>INK4 family</i>				
p16 ^{INK4A}	No mutations ^{25, 46} , LOH (6%) ²⁵	52% in all subtypes and 71% of non-functioning adenomas ⁴¹⁻⁴³	Loss of protein (62%) and mRNA (93%) expression in all subtypes, especially loss of protein expression in non-functioning adenomas (79%) ^{42, 43, 46}	(25, 41-43, 46)
p15 ^{INK4B}	No mutations ²⁵ , LOH (6%) ²⁵	32-36% of adenomas ^{39, 40}	No reports	(25, 39, 40)
p18 ^{INK4C}	*No mutations	*5% of adenomas	Low mRNA levels in ACTH adenomas (92%) and non-functioning adenomas (83%) ^{*, 56}	(*our results, 56)
p19 ^{INK4D}	No reports	No reports	No reports	
<i>Cip/Kip family</i>				
p21 ^{CIP1}	No reports	No reports	Elevated protein expression : GH (71%) and PRL adenomas (81%) ^{14, 49} Decreased protein expression : non-functioning adenomas (81%) ^{14, 49}	(14, 49)
p27 ^{KIP1}	No mutations ^{33, 34}	No reports	Decreased protein expression : ACTH (66%), GH (64%), PRL (56%), TSH (63%), and non-functioning adenomas (62%) ⁵⁰⁻⁵²	(33, 34, 50-52)
p57 ^{KIP2}	No reports	No reports	No reports	

LOH, loss of heterozygosity ; ACTH, corticotroph ; GH, somatotroph ; PRL, lactotroph ; TSH, thyrotroph

sense mutation in the p27^{KIP1} gene was identified in a multiple endocrine neoplasia type 1-suspected patient with growth hormone (GH)-secreting pituitary adenoma and parathyroid tumors³¹. An inactivating p27^{KIP1} germline mutation was also detected in a Dutch patient with hyperparathyroidism, a corticotroph (ACTH) pituitary adenoma, and a neuroendocrine carcinoid tumor³². These results confirmed the potential role of p27^{KIP1} in genesis of pituitary adenomas. However, several studies revealed infrequent mutations of p27^{KIP1} in sporadic pituitary adenomas^{33, 34}, suggesting that mutations of CKIs play a limited role in human pituitary tumorigenesis.

Promoter methylation of the CKI genes in pituitary adenomas

Epigenetic inactivation by promoter methylation is one of the important mechanisms of gene silencing in human cancers³⁵. Promoter methylation implicated in aberrant gene expression is a hallmark of human pituitary tumorigenesis³⁶. Hypermethylation-associated down-regulated mRNA expression of the p15^{INK4B} gene appears to be a common event in human lymphoid tumors and mouse T-cell lymphomas^{37, 38}.

Ogino, *et al.* reported that the p15^{INK4B} gene promoter was hypermethylated in 36% of pituitary adenomas³⁹. But they did not demonstrate the effect of promoter hypermethylation on p15^{INK4B} expression. These results warrant further investigations to establish the correlation between protein or mRNA expression of p15^{INK4B} and promoter hypermethylation of the gene in pituitary adenomas. Promoter hypermethylation is a common mechanism of p16^{INK4A} inactivation in various tumors including pituitary adenomas³⁹⁻⁴³ (Table 2). Methylation-associated silencing of the p16^{INK4A} gene is more frequent in non-functioning pituitary adenomas than other subtypes and is associated with loss of p16^{INK4A} protein expression⁴¹⁻⁴³. These suggest subtype-specific deregulation of the p16^{INK4A} gene in pituitary tumors. It is considered that epigenetic inactivation by methylation is an early event of pituitary tumorigenesis⁴². In contrast, Seemann, *et al.* demonstrated that loss of p16^{INK4A} expression and its promoter methylation were related

to larger tumor size, suggesting that p16^{INK4A} deregulation is achieved during adenoma progression rather than an early event⁴⁴. We showed reduced expression of p18^{INK4C} in both mRNA and protein levels, but absence of promoter hypermethylation in human pituitary adenomas.

Although p27^{KIP1} expression was reported to be down-regulated in pituitary adenomas, promoter hypermethylation as well as methylation-associated down-regulation of Cip/Kip family members were not reported. Collectively, these data indicate that pituitary adenomas have epigenetic changes in p16^{INK4A} of CKIs.

Deregulated expression of CKIs in pituitary adenomas

p15^{INK4B} expression is shown to be down-regulated in mitogen-stimulated lymphocytes⁴⁵. However, the levels of p15^{INK4B} expression in pituitary adenomas remain elusive. Loss of p16^{INK4A} expression is frequent in non-functioning adenomas^{42, 46} (Table 2). In non-functioning pituitary adenomas, we showed reduced mRNA expression of p18^{INK4C}. Ramsey, *et al.* showed a compensatory role between p16^{Ink4a} and p18^{Ink4c} in mice⁴⁷, but we did not observe their compensatory expression in human pituitary adenomas.

p21^{CIP1} deletion or mutation is not a common feature in human tumors⁴⁸. Interestingly, tumor growth triggers elevated expression of p21^{CIP1} in GH adenomas^{14, 49}. Deregulated expression of p27^{KIP1} is frequent in a wide variety of human malignancies and is considered as a prognostic marker for clinical outcome of human cancers⁴. Down-regulated expression of p27^{KIP1} does not result from inactivating mutations of the p27^{KIP1} gene in pituitary as well as other tumors. p27^{KIP1} protein levels are down-regulated by other mechanisms such as proteolytic degradation, cytoplasmic mislocalization etc⁴. Several studies showed that p27^{KIP1} protein expression is down-regulated in pituitary adenomas⁵⁰⁻⁵² (Table 2). The lower levels of p27^{KIP1} protein in ACTH adenomas are of particular interest, because intermediate lobe-derived pituitary tumors developed in p27^{KIP1} knock-out mice¹⁵⁻¹⁷. In ACTH tumors, an accentuated phosphorylation of p27^{KIP1} leading to its increased degradation is

observed⁵³). These results indicate that phosphorylation of p27^{Kip1} may play a role in pituitary tumorigenesis.

Concluding remarks

Each of the INK4 and Cip/Kip family members shows unique pattern of mutations, gene expression, and promoter methylation. However, the collaborative properties suggest diverse roles for the individual CKIs in regulation of pituitary tumorigenesis.

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