Pituitary adenomas are common intracranial tumors, and clinically relevant pituitary adenomas have been estimated to occur in about one in every 1,000 of the population. The vast majority of these adenomas are sporadic; however, there is increasing recognition that pituitary adenomas may also occur in a familial setting, and a recent estimate suggests that 5% of pituitary adenomas are familial in origin. Familial pituitary adenomas can form part of the classic syndromes of multiple endocrine neoplasia type 1 (MEN1) and Carney complex.

However, a number of families have been identified to have isolated familial pituitary tumors and show an autosomal dominant inheritance with incomplete penetrance (the proportion of individuals with the inherited mutation who develop the disease), without the clinical features or genetic abnormalities of the MEN1 syndrome and Carney complex. Over the last decade, these individuals have been classified as having isolated familial somatotropinoma (IFS), familial isolated pituitary adenoma (FiPA), or pituitary adenoma predisposition (PAP), covering overlapping entities.

The first documented report of families with several members affected by acromegaly occurred over 100 years ago. However, the genetic basis of this condition was unknown until 2006, when a Finnish group identified germline mutations in a gene known as AIP (aryl hydrocarbon receptor interacting protein; see Figure 2) while studying large families with acromegaly and prolactinoma in northern Finland. Subsequent work focused on determining the prevalence of AIP mutations in FiPA families and studying the relevance in sporadic pituitary tumors.

FiPA is an autosomal dominant disease with low or variable penetrance (see Figure 3) characterized by a heterogeneous genetic background. FiPA has been identified in more than 170 families, with over 400 individuals described in the literature, including 86 families having familial acromegaly. Within FiPA families there is a heterogeneity of pituitary tumors (see Figure 4), with somatotroph (growth-hormone-secreting) and lactotroph (prolactin-secreting) adenomas being the most common, although other combinations involving non-functioning adenomas, corticotroph (ACTH-secreting), and gonadotroph (gonadotropin-secreting) adenomas have also been reported. Patients with familial disease are on average four to six years younger at diagnosis than sporadic patients. Patients from later generations tend to be significantly younger at diagnosis compared with earlier generations, probably because of increased pituitary disease recognition and surveillance among later generations.

**Clinical Characteristics of AIP Mutation Patients versus Those with No AIP Mutation**

About 20–40% of families with FiPA have a mutation in the AIP gene. Some early-onset—often childhood-onset—acromegaly patients are
also positive for AIP mutations. Mutations of AIP have mainly been found in families with either pure somatotroph adenomas or families with mixed somatotroph and lactotroph adenomas. Interestingly, none of the pure prolactinoma families have AIP mutations, and no AIP mutation has been found in a known FIPA family with at least one member not having either a somatotroph or lactotroph adenoma. Pituitary adenoma tissue has also been studied for AIP mutations in cases where the DNA extracted from blood (germ line) is negative, but has never revealed any AIP mutations.9,13

Tumors with AIP mutations are diagnosed in subjects at significantly younger ages, and are larger than those found in FIPA patients without AIP mutations, as well as those found in patients with sporadic tumors.11,12 Patients with an AIP mutation have a mean age of diagnosis of 25 years compared with 40 years for those without AIP mutations.9,11,12 The youngest patient described as having AIP mutations is six years old (unpublished data), and around two-thirds of patients with AIP mutations are diagnosed at 25 years of age or under.9,11,12 AIP mutation patients have larger pituitary tumors, suggesting more aggressive disease.35 In our cohort, a poor biochemical response to somatostatin analogs (<50% reduction in growth hormone [GH]/insulin-like growth factor 1 [IGF-I]) occurred in eight of the 15 patients with familial acromegaly.

Due to limited genealogical data, the exact penetrance (proportion of individuals with the mutation who develop the disease) of pituitary tumors is difficult to calculate accurately. However, a best estimate emerges from the largest well-studied family with an AIP mutation: one-third of individuals (three of nine subjects with AIP mutations) developed pituitary tumors at the time of the study.14 We find similar penetrance in our largest family with AIP mutations.

**AIP Mutations Described**

The AIP protein was thought to be associated with the receptor of an environmental toxin and with a protein important in cyclic adenosine monophosphate (cAMP) degradation (a second messenger signalling molecule in the cell). Currently, it is unclear which mechanism leads to pituitary tumorigenesis in patients with AIP mutations. Forty-one AIP mutations have been identified to date, including deletions, insertions, segmental duplications, non-sense and missense mutations, and large deletions. Mutations usually disrupt the structure of the end of the protein molecule that plays a major role in the functioning of the molecule. Most studies have used sequencing methods with AIP primers covering just the exons and the area around them. However, a new technique called multiplex ligation-dependent probe amplification (MLPA) reveals large genomic rearrangements in families who previously may have tested negative for germ line AIP mutations by conventional sequencing.15

**Prevalence of AIP Mutations in Familial Isolated Pituitary Adenoma Families**

Out of more than 170 FIPA families described in the literature, 30 families have been reported as having 24 different types of AIP mutations. However, the prevalence of AIP mutations is difficult to assess because not all of the reported FIPA families have been sequenced for AIP mutations, and the vast majority were not tested using MLPA. A best estimate is provided by the three largest FIPA family cohorts,7,9–12 suggesting that 20% of all FIPA families have AIP mutations. Looking only at families with acromegaly, 21 of 53 (40%) families have an AIP mutation.

**Prevalence of AIP Mutations in ‘Apparently’ Sporadic Patients**

Several studies have searched for AIP mutations in sporadic pituitary adenoma patients, i.e. in patients with no family history of
pituitary disease. About 2% of these patients have an AIP mutation in their DNA (27 of 1,100 sporadic pituitary adenoma patients). Most patients with AIP mutations in the ‘apparently’ sporadic cohort have a diagnosis of acromegaly, but there are two reported cases of mutations in patients with Cushing’s disease.

Other Tumors in Familial Isolated Pituitary Adenoma Patients

In our cohort of FIPA families, non-pituitary tumors occur in families with affected patients or obligate AIP mutation carriers: lipomas, breast, thyroid, testicular, renal and bone marrow tumors, anaplastic astrocytomas, primitive neuroectodermal tumors, and ependymomas (also unpublished data). The association of FIPA with adrenal carcinoma has also been reported. However, it is unclear whether any of these tumors are part of the FIPA syndrome; further studies are necessary to clarify this.

AIP Mutations in Other Tissues

The role of somatic AIP mutations has previously been studied in the pathogenesis of common cancers (373 colorectal cancers, 82 breast cancers, and 44 prostate tumor samples) and 79 endocrine tumors (26 thyroid lesions, 19 adrenal lesions, 16 carcinoids, eight parathyroid lesions, four paragangliomas, four pancreatic endocrine tumors, and two adenocarcinoids). No somatic mutations were found, suggesting that AIP is not strongly involved in tumorigenesis in these tumor types.

Tumor-suppressor Role for AIP

Based on clinical data, it has been suggested that FIPAs are caused by a heterozygous germline mutation in a tumor-suppressor gene. Our group has recently captured unique functional data on AIP consistent with a tumor-suppressor role for AIP. Cells were transfected with the AIP gene and showed reduced proliferation. On the other hand, when the cell’s own AIP was knocked out, cell proliferation increased.

Practical Relevance to the Clinical Endocrinologist of These Emerging Data About Familial Isolated Pituitary Adenomas

Identifying AIP mutations in patients and carriers is of great clinical importance. Patients with AIP mutations tend to have a more aggressive disease, and treatment can be extremely challenging if diagnosis is late. Genetic testing of relatives of patients with AIP mutations may lead to earlier pituitary tumor detection, thus allowing treatment at an earlier stage. All patients with a family history of pituitary adenoma and no suspicion of MEN1 and Carney complex should undergo genetic counseling and testing for AIP.

If a mutation is found, family members should be screened for the mutation. Carriers should be tested regularly for clinical symptoms and signs and should undergo biochemical and (if necessary) imaging investigations, given that heterologous tumors can occur within families but keeping in mind that incidental tumors of the pituitary are common. If no AIP mutation is found, all family members with a 50% chance of inheriting the disease should be regularly tested. Currently, we are searching for gene(s) causing the disease in AIP-negative families and would like patients with a family history of pituitary
Conclusions

AIP has been identified as a novel gene involved in the development of FIPA, especially in those cases involving growth-hormone-secreting tumors, and is probably a tumor-suppressor gene. Mutations in AIP have been found in 20–40% of families with FIPA. This number will likely increase if all families are tested for large gene deletions. Patients with AIP mutations are diagnosed at younger ages, and their pituitary tumors tend to be larger and more aggressive and respond less well to somatostatin analogs.

Apparently unaffected relatives who are possible carriers require full clinical and biochemical investigation. As the majority of FIPA patients do not harbor AIP mutations, and the clinical phenotype (primarily the age at onset and the pituitary tumor type) is different in the AIP-mutation-negative families, we think there is a strong possibility that another gene, or genes, may be involved in the pathogenesis of these FIPA cases.  

References

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