AIP and the somatostatin system in pituitary tumours

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Abstract

Classic somatostatin analogues aimed at somatostatin receptor type 2, such as octreotide and lanreotide, represent the mainstay of medical treatment for acromegaly. These agents have the potential to decrease hormone secretion and reduce tumour size. Patients with a germline mutation in the aryl hydrocarbon receptor-interacting protein gene, AIP, develop young-onset acromegaly, poorly responsive to pharmacological therapy. In this review, we summarise the most recent studies on AIP-related pituitary adenomas, paying special attention to the causes of somatostatin resistance; the somatostatin receptor profile including type 2, type 5 and truncated variants; the role of G proteins in this pathology; the use of first and second generation somatostatin analogues; and the role of ZAC1, a zinc-finger protein with expression linked to AIP in somatotrophinoma models and acting as a key mediator of octreotide response.

Introduction

Pituitary adenomas are usually benign tumours of the anterior pituitary, which represent 15.5% of intracranial neoplasms (Ostrom et al. 2015). They are frequently associated with severe comorbidities due to mass effect and/or the hormone hypersecretion, such as hypogonadism, hypopituitarism, visual disturbances, hypertension, diabetes, emotional disturbances, changes in appearance, growth abnormalities and many others (Asa & Ezzat 2002, Aflorei & Korbonits 2014). These endocrine tumours are unicellular in origin, arising from a monoclonal expansion of a genetically mutated cell (Alexander et al. 1990, Herman et al. 1990, Melmed 1994). The primary initiating cause for pituitary tumourigenesis has been found to be a gain-of-function mutation in the GNAS (Landis et al. 1989) and USP8 (Ma et al. 2015, Reincke et al. 2015) genes in a significant proportion of somatotroph and corticotroph adenomas, while amplification in PIK3CA could be a permissive phenomenon (Finelli et al. 2000, Lin et al. 2009, Murat et al. 2012). A few cases of corticotroph adenomas have also been identified with germline variants in the CABLES1 gene (Hernández-Ramírez et al. 2017a).

Several studies using transgenic mouse models have demonstrated that either the inactivation (Jacks et al. 1992, Kiyokawa et al. 1996) or the overexpression (Abbud et al. 2005) of cell cycle regulators may initiate pituitary tumorigenesis. This was supported by the finding that about 80% of the human pituitary adenomas show at least one alteration in cell cycle regulators (Sapochnik et al. 2016). In the pituitary, classic oncogenes are rarely mutated (Ewing et al. 2007), but a growing set of genes have been identified where loss or gain of function leads to pituitary tumourigenesis (Caimari & Korbonits 2016). A familial background can be identified in about 5% of cases either as part of syndromic disease affecting other endocrine organs, including multiple endocrine neoplasia...
type 1 and 4, Carney’s complex, neurofibromatosis (NF1), DICER1 syndrome and syndromes related to succinate dehydrogenase (SDH) genes or affecting only the pituitary as in familial isolated pituitary adenomas (FIPA) (Beckers & Daly 2007, Leontiou et al. 2008, Kopczak et al. 2014, Lecoq et al. 2015).

Particularly, FIPA is characterised by the manifestation of pituitary tumours in two or more members of the same family in the absence of other syndromic clinical features. FIPA can also present as simplex disease. It is a heterogeneous condition, which includes patients with low penetrance inactivating germline mutations in the aryl hydrocarbon receptor-interacting protein (AIP) gene (Vierimaa et al. 2006) in 17% of FIPA families (Hernández-Ramírez et al. 2015) and patients with the recently described X-linked acrogigantism (XLAG) (Trivellin et al. 2014), which comprise germline or somatic duplications involving GPR101 gene in the Xq26.3 region. Nevertheless, most of FIPA families harbour a currently unknown genetic mutation.

AIP mutation-positive patients are characterised by early onset and usually aggressive growth hormone (GH), prolactin (PRL) or GH-PRL adenomas, rarely other types of pituitary tumours and very rarely concomitant hyperplasia. Patients usually present in the second or third decade (Hernández-Ramírez et al. 2015) and are less responsive to somatostatin analogues (SSA) (Daly et al. 2010). Germline mutations in AIP gene has also been described in sporadic pituitary tumour patients, explained by low penetrance rather than de novo mutations in these families (Leontiou et al. 2008, Jaffrain-Rea et al. 2013, Hernández-Ramírez et al. 2015, Matsumoto et al. 2016). AIP mutation-negative FIPA cases present at a similar age of onset than sporadic pituitary adenoma patients (Hernández-Ramírez et al. 2015).

Patient with XLAG display GH, GH-PRL-secreting adenomas, sometimes with neighbouring hyperplasia or have somatotroph or somatotroph & lactotroph hyperplasia without an adenoma. Most of the cases result from de novo germline or embryonic mosaic somatic mutations (Beckers et al. 2015, Daly et al. 2016a,b, Iacovazzo et al. 2016b, Trivellin et al. 2016).

In this review, we summarise the most recent studies on AIP-related pituitary adenomas, paying special attention to the causes of the resistance to treatment in acromegaly. For readability, and because often referring to both human, mouse or rat species together, genes/ mRNA (italicised) and proteins (not italicised) will always be capitalised.

AIP: function and malfunction

AIP encodes a 330 amino-acid 37 kDa protein, which is highly conserved among species and widely distributed in the organism (Trivellin & Korbonits 2011). AIP is a co-chaperone with an N-terminal immunophilin-like domain (Linnert et al. 2012), which is unable to mediate immunophilin responses (Carver et al. 1998, Laenger et al. 2009) and a highly conserved C-terminal domain with three tetratricopeptide repeat (TPR) motifs and a C-terminal α-7 helix (Morgan et al. 2012), which mediate its interactions with a number of partners (Trivellin & Korbonits 2011). According to experimental data, AIP has a long half-life of 32.7 h in humans and 30.4 h in mice, which may indicate that it is an abundant and highly structured protein (Hernández-Ramírez et al. 2016).

AIP is considered to be a tumour suppressor gene in the pituitary, as loss-of-function mutations predispose to pituitary adenomas often with invasive characteristics. Interestingly, sporadic GH-secreting pituitary adenomas with low AIP expression also show markers of increased invasion (Jaffrain-Rea et al. 2009, Kasuki Jomori de Pinho et al. 2011, Kasuki et al. 2012). AIP, a protein with characteristic seven antiparallel alpha helices, has numerous binding partners and loss of some of these interactions may contribute to tumorigenesis.

AIP is a co-chaperone to Hsp90, probably its most important binding partner. As Hsp90 can bind to 60% of the human kinome and 30% of E3 ubiquitin ligases (Schopf et al. 2017, Taipale et al. 2010), there are plenty of proteins whose function AIP, a protein with high and ubiquitous expression (Fagerberg et al. 2014), could theoretically influence.

Aryl hydrocarbon receptor (AhR)

AIP is essential for the stabilization of AhR in the cytoplasm, by the formation of a complex with Hsp90 and p23 proteins, preventing the ubiquitin-mediated degradation of AhR (Kazlauskas et al. 2000); upon ligand binding, AhR experiences a conformational change and is translocated to the nucleus, where it acts as a transcription factor of certain genes, such as P450, a drug-metabolizing enzyme (Fujii-Kuriyama & Mimura 2005). In pituitary adenomas, reduced AhR was associated with low AIP expression (Jaffrain-Rea et al. 2009), particularly AIP mutation-positive samples showed a frequent loss of cytoplasmic and nuclear AhR, while AIP overexpression was associated to AhR nuclear immunopositivity.
Guanine nucleotide-binding proteins (G proteins)

AIP was found to be associated with Gq13, Gaq and possibly regulate the abundance of Gai-2 (Nakata et al. 2009, Tuominen et al. 2015, Ritvonen et al. 2017). These interactions could influence multiple signalling pathways, with the Gai-CAMP pathway being especially relevant regarding somatotroph cells and somatostatin action (see section below).

Cyclic nucleotide phosphodiesterases (PDE)

A superfamily of enzymes that breakdown cAMP and/or cGMP and therefore regulate their abundance in cells (Beavo 1995) may interact with AIP (Hernández-Ramírez et al. 2017b). Particularly, AIP was able to reversibly inhibit the enzymatic activity of PDE4A5 (rat counterpart of human PDE4A4) (Bolger et al. 2003). In humans, PDE4A4 and PDE4A8 enzymes were overexpressed in functioning and non-functioning pituitary adenomas in comparison to normal pituitary tissue (Bolger et al. 2016), and in line with this, both PDE4A5 and PDE4A4 were able to interact with wild-type AIP (Leontiou et al. 2008, Bolger et al. 2016), but they did not interact with mutant variants. Moreover, another PDE, PDE2A3 was suggested to interact with AIP inhibiting the nuclear translocation of AhR, and subsequently the transcription of certain genes (de Oliveira et al. 2007), although further data are needed to strengthen this relationship.

Somatostatin and its receptors

Somatostatin (SST) was isolated in ovine hypothalamus by its ability to inhibit GH secretion (Brazeau et al. 1973). SST is widely distributed throughout the human central nervous system and also in peripheral tissues, where it has a broad range of biological actions including regulation of neurotransmission, inhibition of pituitary and gastrointestinal hormones, pancreatic enzymes and neuropeptides, etc. (Lamberts 1988, Schettini 1991, Martel et al. 2012). SST gene is transcribed to yield the pre–pro somatostatin-encoding mRNA (Shen et al. 1982, Naylor et al. 1983, Shen & Rutter 1984), which is subsequently translated and the protein is processed to give rise to SST, an active peptide of 28 amino acids (Schally et al. 1980, Brown et al. 1981), which is commonly further processed into a shorter active variant of 14 amino acids, generally named SST-14 or simply SST (Epelbaum 1986, Martel et al. 2012).

SST binds with similar affinity to all its 5 receptor subtypes, named SSTR1–SSTR5, which belong to the seven transmembrane domains (TMD), G protein-coupled receptor superfamily class A (Gahete et al. 2010, Theodoropoulou & Stalla 2013). SSTRs were characterised, for the first time in pituitary cells, in the rat GH-PRL-secreting GH4C1 cell line (Schonbrunn & Tashjian 1978), and later, their structure was identified in human, mouse, rat and other species (Patel 1999). SSTRs are encoded by 5 separate genes, which are intronless, share a common YANSCANPVLY motif in the seventh TMD (Olias et al. 2004, Durán-Prado et al. 2009) and give rise to 5 different SSTR variants in humans, including a splice variant of the subtype 2 in mice (Patel 1999, Olias et al. 2004). In addition to the canonical, full-length SSTRs, two novel truncated variants of SSTR5 have been recently identified and characterised in humans, which were termed sstSTMD5 and sstSTMD4, based on the number of TMDs (Durán-Prado et al. 2009). Subsequent studies have demonstrated that these receptors are functional, and they show distinct distribution in normal tissues and present unique ligand-selective signalling properties and subcellular distribution. Specifically, these receptors are infrequently present in normal tissues, and, while sstSTMD5 is present only in a subset of pituitary adenomas, sstSTMD4 is normally present in pituitary tumours (Durán-Prado et al. 2009, Luque et al. 2015).

It has been observed that each SSTR subtype specially evokes one or more particular SST actions, and considering that they are usually co-expressed, it has been proposed that the specific effect is determined by the combined effect of quantity and type of SSTR subtype expressed in each cell, and the particular signalling routes activated in response to SST. The binding of a ligand, either endogenous or synthetic, to the different SSTRs exert a conformational change in the receptor leading to activation of G proteins and the subsequent signalling pathways (Eglen 2005, Ben-Shlomo & Melmed 2010, Shpakov 2012, Theodoropoulou & Stalla 2013). These pathways can be common among SSTRs, such as cAMP, adenylyl cyclase or Ca2+, or different, considering that most of them are receptor, ligand or dose specific. One example is the apoptotic pathway p53/BAX, which is activated mainly through SSTR3 (Sharma et al. 1996, War et al. 2015). As well as the paradoxically stimulatory effect on GH release observed using very low concentration of SST and cortistatin, an endogenous neuropeptide similar to SST (Ibáñez-Costa et al. 2017), in primate pituitary primary cultures, which is mediated exclusively by SSTR5 through adenylyl cyclase/cAMP/protein kinase A
and intracellular Ca\(^{2+}\) pathways (Côrdoba-Chacón et al. 2012). Thus, the specific cascades triggered are complex as (i) SSTRs frequently co-localise; therefore, the final response will depend on the SSTRs’ interaction pattern (Cakir et al. 2010); (ii) they can form homo- and heterodimers (Durán-Prado et al. 2008), not only with each other, but with dopamine receptors, especially the type 2 (DRD2) and δ- and μ-opioid receptors (OPRD1 and OPRM1) (Rocheville et al. 2000, Pleiffer et al. 2002, Baragli et al. 2007, Somvanshi & Kumar 2014); (iii) SSTRs may display a constitutive activity independently from ligand (Acunzo et al. 2008, Ben-Shlomo et al. 2013, Eigler et al. 2014) and (iv) SSTRs, like many other GPCRs, may be regulated by endocytosis, internal trafficking and arrestin-mediated desensitization mechanisms (Hofland & Lamberts 2003, Tulipano et al. 2004, Gatto et al. 2013a).

### Somatostatin analogues and pituitary adenomas

In addition to, or instead of, surgery, several medical therapeutic approaches are available for functioning pituitary adenomas. Lactotroph tumours are generally very sensitive to dopamine agonists aimed at DRD2, such as cabergoline, decreasing PRL secretion and tumour size, achieving the total remission in a high percentage of patients (Colao & Savastano 2011).

SST was first discovered due to its role in decreasing the GH release of ovine somatotrophes. Since somatotroph adenomas causing acromegaly and gigantism are characterized by the expression of SSTRs, especially SSTR2 and SSTR5 at the mRNA level (Taboada et al. 2008, Durán-Prado et al. 2009, 2010, Neto et al. 2009, Gatto et al. 2013b) and protein level (Gatto et al. 2013b, Chinezu et al. 2014, Iacovazzo et al. 2016a), SST was thought to be an important therapeutic agent. However, the clinical usefulness of SST is limited by its short half-life in circulation (less than 3 min) (Patel & Wheatley 1983). Therefore, to overcome this obstacle, synthetic SSAs were developed, such as octreotide and lanreotide, which selectively bind to SSTR2 and can be used to treat neuroendocrine tumours (Bauer et al. 1982, Taylor et al. 1988, Barbieri et al. 2014). In the case of somatotrophinomas, SSAs aimed at SSTR2 are commonly used in the pre- and post-surgical treatment to decrease GH and insulin-like growth factor 1 (IGF1) secretion and tumour size (Melmed 2009, Melmed et al. 2015, Puig Domingo 2015). Additionally, thyrotroph tumours display SSTR2, SSTR3 and SSTR5 (Yoshihara et al. 2007, Gatto et al. 2012) and octreotide is successfully used to treat these tumours, normalizing TSH levels and decreasing tumour size (Caron et al. 2001, Gatto et al. 2012, van Varsseveld et al. 2014).

In a well-conducted study of unselected acromegaly patients treated with octreotide, 25% of the subjects showed a full clinical benefit: decreased tumour size and normalised both GH and IGF1 levels (Mercado et al. 2007). Therefore, resistance or partial resistance is not so rare, even in patients with high SSTR expression on the tumour after surgery (Colao et al. 2011, Theodoropoulou & Stella 2013, Cuevas-Ramos & Flersier 2014). The cause of this lack of response is still unknown. A multi-receptor SSA was developed, pasireotide (Bruins et al. 2002), which can bind SSTR5 (IC50: 0.16 ± 0.01 nmol/L), SSTR2 (1.0 ± 0.1 nmol/L), SSTR3 (1.5 ± 0.3 nmol/L) and SSTR1 (9.3 ± 0.1 nmol/L) with high affinity, with the hypothesis that simultaneous targeting of more than one SSTR may be more effective in the treatment of patients who are not responsive or who escape from SSTR2 agonist treatment.

agonists suggested that SSTR1 agonists might be useful (Zatelli et al. 2004), and moreover, that pasireotide may reduce cell viability in vitro via the inhibition of VEGF (Zatelli et al. 2007). Indeed, the use of pasireotide was proposed for non-functioning pituitary adenoma patients (Colao et al. 2008), as it has been reflected in two clinical trials (NCT01620138 and NCT01283542; https://clinicaltrials.gov).

The use of somatostatin analogues for acromegaly treatment

The clinical use and efficacy of SSA in acromegaly patients has been established (Oberg & Lamberts 2016); however, the intracellular signalling pathways activated and the precise mechanism of effect is still debated.

Some of the approaches used cell lines, either pituitary-derived from murine models, such as GH3, GC, GH4C1 or other cell types, such as CHO-K1 or HEK-293. The responses are variable depending on cell lines as they may miss some key components of SST pathway. For example, GH3 cells do not always express all SSTRs, sometimes not even SSTR2 (Garcia & Myers 1994, Kim et al. 2005) or p27kip in the case of GH3 or GC cells (Qian et al. 2000, Martin-Rodriguez et al. 2015), p27kip being an effector of certain antiproliferative SST-mediated responses (Pages et al. 1999, Hubina et al. 2006, Grant et al. 2008, Zhou et al. 2012, Aoki et al. 2014, Kiseljak-Vassilidades et al. 2015).

Primary cultures of adenomas derived from acromegaly patients are valuable tools to assess SSA response. Samples from clinically responsive patients show better in vitro response than clinically partially responsive patients (Shimon et al. 1997b, Hofland et al. 2004, Murray et al. 2004, Jaquet et al. 2005b, Ibáñez-Costa et al. 2016). The use of specific individual agonists for each SSTR, either peptidic (Shimon et al. 1997a) or non-peptidic (Rohrer et al. 1998) molecules, has provided key information on the control of the regulation of pituitary hormones secretion in the pituitary. Particularly, in somatotrophinomas, the use of SSTR2 and/or SSTR5 agonists was able to decrease GH release (Shimon et al. 1997b, Damila et al. 2001, Saveanu et al. 2001, 2002, 2006, Jaquet et al. 2005a,b, Zatelli et al. 2005, Peverelli et al. 2013), nevertheless, the simultaneous activation of SSTR2 and SSTR5 did not always show a greater effect on GH release than the single activation of the receptors (Shimon et al. 1997b, Zatelli et al. 2005). In octreotide- and lanreotide-resistant somatotrophinomas, an SSTR1-aimed analogue was able to inhibit GH secretion in vitro (Matrone et al. 2004). In mixed GHI-PRL-secreting adenomas, the use of SSTR5-aimed analogues alone (Zatelli et al. 2005, Gruszka et al. 2012) or in combination with SSTR2 agonists (Fusco et al. 2008), were able to decrease prolactin secretion.

Pasireotide is able to decrease GH secretion and alter other functional endpoints in somatotrophinoma cell cultures (Murray et al. 2004, Ibáñez-Costa et al. 2016, Gatto et al. 2017).

In vitro and in vivo studies provided a list of parameters which allows to predict SSA responsiveness of somatotrophinomas, such as receptor expression, GNAS mutation, granulation pattern or MRI characteristics.

Somatostatin receptors

SSTR2 SSTR2 mRNA expression, and/or SSTR2/SSTR5 ratio, has been directly correlated with a reduction in GH/IGF1 levels and tumour size after surgery using SSTR2-aimed drugs (Taboada et al. 2008, Neto et al. 2009). SSTR2, but not SSTR5 expression, is associated with acute response to octreotide (Gatto et al. 2013b). High SSTR2 immunoreactivity was associated with good response to SSA (Ferone et al. 2008, Fougner et al. 2008, Casarborot et al. 2013, Wildemberg et al. 2013, Iacovazzo et al. 2016a). A recent study showed that SSTR2 mRNA levels positively correlated to GH reduction in vitro in response to octreotide, and a trend in response to pasireotide (Gatto et al. 2017). Somatotrophinomas presenting lower SSTR2 mRNA levels and a lower SSTR2/SSTR5 mRNA ratio showed a better response to pasireotide compared to octreotide.

SSTR5 Although SSTR5 is broadly expressed in somatotrophinomas, few data are available from human studies on responsiveness to compounds activating SSTR5, probably due to the recent introduction of pasireotide. The first such study on acromegaly patients resistant to octreotide showed that the expression of SSTR5 may predict responsiveness to pasireotide treatment; the study observed that patients lacking SSTR5 immunoreactivity in their adenoma sample were resistant to pasireotide, but cases with a high SSTR5 staining score had a better IGF1 response (Iacovazzo et al. 2016a). Interestingly, some differences were observed between the actions of octreotide and pasireotide on gene expression regulation when
tested on primary culture of human somatotrophinomas: both octreotide and pasireotide decreased GH mRNA, but only pasireotide was able to alter SSTR2 and SSTR5 gene expression, it decreased SSTR2 and moderately augmented SSTR5 expression. This could potentially contribute to enhance in vivo response to pasireotide (Ibáñez-Costa et al. 2016). Further studies are needed to clarify the effect on first and second generation SSAs on SSTR expression.

**SSTR5 truncated variants** The presence of sstSTMD4 is inversely correlated to the anti-secretory effect of octreotide in vitro (Durán-Prado et al. 2010) and in vivo (Durán-Prado et al. 2010, Luque et al. 2015).

**GNAS mutation**

The recurrent somatic mutations in GNAS gene coding for the α-subunit of the stimulatory G protein Gs, commonly named gsp mutation, have been associated with particular clinical characteristics: smaller and less invading densely granulated tumours, normally appearing in older patients (Landis et al. 1990, Spada et al. 1990, Faglia et al. 1996, Yang et al. 1996, Barlier et al. 1998, Kim et al. 2001, Freda et al. 2007). The implication of gsp mutation in SSA response has been widely discussed (Larkin et al. 2013); nevertheless, a recent meta-analysis revealed that GNAS-positive patients have an approximately 10% greater reduction in GH levels in response to an acute octreotide suppression test (Efstatiadou et al. 2015). Additionally, GNAS positive patients show high levels of SSTR2 mRNA (Taboada et al. 2011) and low levels of sstSTMD4 (Luque et al. 2015).

**Granulation pattern**

Pituitary adenomas have been classified according to their granulation pattern in electron microscopy analysis as densely or sparsely granulated tumours. Cytokeratin staining is used in clinical practice to characterise densely granulated adenomas having cytokeratin staining with perinuclear pattern and sparsely granulated adenomas having dot-like pattern (Obari et al. 2008). Sparsely granulated somatotrophinomas occur in younger patients, are larger and more invasive than densely granulated tumours and typically express SSTR5 but not SSTR2 (Mayr et al. 2013), while densely granulated adenomas present higher levels of SSTR2 and are more responsive to SSA treatment (Obari et al. 2008, Fougner et al. 2012, Kato et al. 2012, Brzana et al. 2013, Larkin et al. 2013).

**MRI T2 signal intensity**

Hypointense GH-secreting adenomas on T2-weighted MRI are frequently densely granulated adenomas and are associated with a better response to SSAs (Hagiwara et al. 2003, Puig-Domingo et al. 2010, Heck et al. 2012, 2016). The level of SSTR5, but not SSTR2, is negatively correlated with T2 intensity (Shen et al. 2016). Hypointense adenomas are smaller than hyper- and iso-intense adenomas, presenting less invasion of cavernous sinuses and optic chiasm compression, but show higher IGF1 levels (Potorac et al. 2015).

**Epigenetic regulation of AIP in SSA response**

MicroRNAs (miRNAs) are small endogenous non-coding RNA molecules (18–25 nucleotides), which may impair protein expression (Barlet 2004, Gadelha et al. 2013a). mir-107 is overexpressed in somatotrophinomas and non-functional pituitary adenomas (Trivellini et al. 2012). mir-107 inhibited AIP expression in vitro but there was no correlation between miR-107 expression and AIP expression in human samples. Another miR, miR-34a was highly expressed in pituitary adenomas with lower AIP protein levels than in high AIP expression adenomas (Denes et al. 2015). In vitro, the overexpression of miR-34a induced an inhibition of endogenous AIP in HEK293 and GH3 cell lines; miR-34a levels were inversely correlated with the response to SSA treatment, miR-34a levels were lower in those patients controlled with octreotide LAR than in uncontrolled patients. The role of miRNAs in SSA response needs further investigations.

**The role of AIP and ZAC1 in SSA response in somatotrophinomas**

Korbonits and coworkers suggested that AIP has a key role in SSA response (Chahal et al. 2012, Gadelha et al. 2013b). Indeed, most of the patients with AIP mutation-positive somatotroph adenomas are, at least partially, resistant to pharmacological treatment with SSAs; nevertheless, the causes of this resistance are complex and may be related to several intracellular characteristics of the mutant tumoural somatotrophs. AIP mutation-positive patients are less responsive to SSTR2-specific SSAs (Leontiou et al.
The abundance of the receptors may be involved; sporadic GH tumours with low AIP protein expression are less likely to be controlled using octreotide (Kasuki et al. 2012) and present lower SSTR2 and SSTR3 and similar SSTR5 levels than tumours with high AIP protein expression (Iacovazzo et al. 2016a), while AIP mutation-positive tumours presented higher levels of SSTR5 than sporadic patients (Chahal et al. 2012).

AIP mutation-positive somatotroph tumours are frequently sparsely granulated adenomas (Leontiou et al. 2008, Hernández-Ramírez et al. 2015) and sparsely granulated pituitary adenomas are known to have poorer response to SSAs (Fougner et al. 2012, Brzana et al. 2013). Patients with GNAS mutations respond better to SSAs (Efstathiadou et al. 2015), while the presence of AIP and GNAS mutations seems to be mutually exclusive in somatotrophinomas (Hernández-Ramírez et al. 2015). Recent studies performed on human and mouse somatotrophinomas demonstrated that AIP is essential to maintain relatively low levels of cAMP in normal somatotrophs, and the lack of AIP causes an accumulation of cAMP through defective Gαi-2 signalling, which leads to a downregulation of phosphorylated extracellular signal-regulated kinases 1/2 (p-ERK1/2) and p-CREB (Tuominen et al. 2015). This point was supported by the fact that low Gai-2 levels were observed in sporadic somatotrophinomas with decreased AIP immunoreactivity, and a positive association between AIP and Gai-2 was found at protein level, which suggests a combined regulation (Ritvonen et al. 2017). AIP expression was associated to higher Gai-2 and lower Ki67.

In vitro Gai-3 silencing revealed that AIP deficiency might lead to cAMP accumulation via Gai-3, although its expression at protein level was not affected by the presence or absence of AIP (Tuominen et al. 2015).

AIP seems to be directly involved in SST signalling pathways: it has been observed that octreotide treatment induced an increase in AIP both at mRNA and protein levels in GH3 cell line; furthermore, patients treated preoperatively with lanreotide showed increased AIP immunostaining in the somatotroph adenomas compared to samples from age-, sex- and tumour size-matched acromegaly patients (Chahal et al. 2012, Jaffrain-Rea et al. 2013). A novel mechanism of action of octreotide was described involving PI3K signalling pathway, which results in an increase in the expression of ZAC1, a zinc finger protein that regulates cell cycle progression (Theodoropoulou et al. 2006). In line with this, octreotide treatment increases ZAC1 mRNA expression (Theodoropoulou et al. 2006, Chahal et al. 2012), which may link AIP to the ZAC1-mediated antiproliferative

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Figure 1
Summary of the proposed model of SSA-AIP-ZAC1 pathway on somatotrophinoma cells. (A) High levels of AIP, AIP (alone or via AHR/ARNT), ZAC1 and p53 directly activate gene transcription; p53 arrests cell cycle, through p21 activation, and increases apoptosis. Octreotide triggers ZAC1/p53 activation through somatostatin receptor 2 (SSTR2) binding and GSK3β pathway. Octreotide increased AIP and ZAC1 expression. G proteins activate the signalling pathway when SSTR2 binds its ligand, such the inhibition of adenylate cyclase (AC), which reduces cAMP levels. In summary, octreotide decreases cell proliferation (green arrow) and activates the apoptotic pathway (pink arrow) through SSTR2 in somatotrophinomas. (B) Low levels or mutated AIP, ZAC1 expression is decreased when AIP is downregulated, and in AIP mutated patients, presumably disrupting the ZAC1/p53 route. Lower SSTR2 has been reported in some studies in AIP-mutated patients, which may also contribute to the lower effect of SSTR2 aimed SSAs. Lack of AIP reduces the expression of Gai-2 subunit, involved in blocking the AC, which could hinder SST signalling. In summary, the lack of AIP impairs the effect of octreotide, leading to a less activation of apoptotic pathways and increasing the activation of cell proliferation. Arrow-headed lines and bar-headed lines indicate activation and inhibition, respectively.
response (Fig. 1A). As octreotide treatment caused elevated AIP and heterologous overexpression of wild-type AIP increased ZAC1 expression, while AIP silencing reduced ZAC1 expression (Fig. 1B; Chahal et al. 2012), these all point to an SST-AIP-ZAC1 pathway. In line with this, a recent study revealed that ZAC1 may be a mediator of octreotide antiproliferative effect on gastric cancer cells (Wang et al. 2017).

ZAC1 is encoded by PLAGL1 gene – it is a seven-zinc finger protein functionally related to p53, including tumour suppressor effects through induction of cell cycle arrest at G1 and apoptosis (Spengler et al. 1997, Varrault et al. 1998, Theodoropoulou et al. 2010). PLAGL1 is an imprinted gene highly expressed during embryonic development (Piras et al. 2000, Valente & Auladell 2001, Valente et al. 2005, Varrault et al. 2006). Postnatally, ZAC1 is highly expressed in the pituitary, mostly in GH and PRL cells in mice, the expression being lower in FSH cells (Pagotto et al. 1999). In humans, GH-, PRL- and ACTH-secreting adenomas express PLAGL1, but its expression in gonadotroph-derived tumours is very low (Pagotto et al. 2000, Theodoropoulou et al. 2009). It is remarkable that PLAGL1 gene is located on the chromosome 6q24–25, a region that has been frequently related to loss of heterozygosity events in breast, ovarian and adrenal tumours (Bilanges et al. 1999, Cvetkovic et al. 2004, Lemeta et al. 2004, 2006), and also in non-functioning pituitary adenomas (Pagotto et al. 2000). It has been reported that high ZAC1 immunostaining is associated to a good prognosis in non-functioning pituitary adenomas (Noh et al. 2009), a type of pituitary tumour that display very low ZAC1 expression compared to normal pituitary or somatotropinomas (Vieria Neto et al. 2013).

**Concluding remarks**

In summary, there are several factors that lead to reduced SSA responsiveness: low SSTR2, low SSTR2/SSTR5 ratio, younger age, male gender, high ststMD4 expression, hyperintense T2 on MRI, sparsely granulation pattern, low AIP expression, no GNAS mutation, higher basal cAMP levels due to a defective Gai-2 signalling, low ZAC1 levels and presumably a disrupted ZAC1-p53 antiproliferative effect in response to SSAs. The molecular mechanisms connecting all these factors are still unclear and further data and better models are required to fully understand the mechanism of effect of SSAs.

**Declaration of interest**

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of this review.

**Funding**

The research leading to these results has received funding from the People Programme (Marie Curie Actions) of the European Union’s Seventh Framework Programme (FP7/2007–2013) under REA grant agreement n° 608765; Rosetrees Trust (M505) and Medical Research Council (MR/M018539/1).

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Received in final form 25 July 2017
Accepted 22 August 2017
Accepted Preprint published online 23 August 2017