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Genetic and genomic mechanisms of primary aldosteronism

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The authors have nothing to disclose.

Abstract

Aldosterone producing adenomas (APA) and bilateral adrenal hyperplasia are the main cause of primary aldosteronism (PA), the most frequent form of secondary hypertension. Mutations in ion channels and ATPases have been identified in APA and inherited forms of PA, highlighting the central role of calcium signalling in PA development. Different somatic mutations are also found in aldosterone producing cell clusters in adrenals from normal subjects and from patients with unilateral and bilateral PA, suggesting additional pathogenic mechanisms. Recent mouse models have also contributed to a better understanding of PA. Application of genetic screening in familial PA, development of surrogate biomarkers for somatic mutations in APA and use of targeted treatment directed at mutated proteins may allow improved management of patients.

1 Primary aldosteronism (PA) is the most frequent form of secondary arterial hypertension with a prevalence of 5% of hypertensive patients in primary care and until 10% of hypertensive 2 subjects in reference centers [1, 2]. PA is due to autonomous aldosterone production by the 3 adrenal gland, the two major causes being the presence of an aldosterone producing adenoma 4 5 (APA) or bilateral adrenal hyperplasia (BAH). In addition to sporadic forms, four different familial forms were described, accounting for approximately 5% of PA cases. PA patients 6 7 exhibit hypertension associated in many cases with hypokalemia. The biochemical diagnosis is based on high levels of plasma aldosterone and low plasma renin, with an increased aldosterone 8 to renin ratio (ARR). The confirmation of PA diagnosis is performed by one of different tests, 9 including oral salt loading or captopril challenge tests, followed by adrenal image and adrenal 10 vein sampling (AVS) to subtype PA as unilateral or bilateral forms [3]. PA subtyping guides 11 the optimal treatment, unilateral adrenalectomy for lateralized APA or long-life drug therapy 12 13 with mineralocorticoid receptor antagonists in the presence of bilateral forms. Due to deleterious effects of aldosterone on blood vessels and heart, patients with PA have an increased 14 15 cardiovascular risk when compared with age, sex and blood pressure matched patients with primary hypertension [4, 5]. 16

Aldosterone is synthetized from cholesterol in the cells of the zona glomerulosa (ZG) of 17 the adrenal cortex by a cascade of enzymatic reactions. The ZG specifically expresses the 18 enzyme aldosterone synthase (encoded by CYP11B2), responsible for the three final enzymatic 19 reactions leading to aldosterone biosynthesis [6]. Aldosterone biosynthesis is tightly regulated 20 to maintain salt and water homeostasis, the two most important factors being angiotensin II 21 (AngII) and extracellular potassium concentration (K⁺) (Box 1). In basal conditions ZG cells 22 23 are maintained in a hyperpolarized state due to the presence of a large number of potassium channels [7] and the Na⁺/K⁺-ATPase. ZG cell membrane depolarization is induced by AngII or 24 increase in plasma K⁺ concentration, causing the opening of voltage-gated Ca²⁺ channels and 25 the increase of the intracellular Ca²⁺ concentration. AngII also stimulates Ca²⁺ release from the 26 endoplasmic reticulum by binding the angiotensin II Type 1 receptor (AT1R) and stimulating 27 the inositol triphosphate pathway. The increase in cytosolic Ca^{2+} activates calcium signaling 28 (via calmodulin and calcium/calmodulin-dependent protein kinases), the main trigger for 29 30 CYP11B2 expression and aldosterone production [8, 9]. Other regulators of aldosterone biosynthesis include ACTH, serotonin, interleukine 6, epidermal growth factor and leptin [10-31 32 13].

In the last decade, following the discovery of *KCNJ5* mutations associated with PA, different studies performing whole exome sequencing identified mutations in genes coding for ion channels and ATPases as responsible for APA and familial PA and highlighted the central role of calcium signaling on PA pathogenesis. These studies allowed the identification of somatic mutations in more than 85% of APA and completely changed the classification of familial forms (Box 2. Clinician's Corner).

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40 Genetics of primary aldosteronism

41 The first genetic defect associated with PA was described almost 30 years ago. A chimeric gene, where the regulatory regions of CYP11B1 are juxtaposed with the coding sequence of 42 CYP11B2, was identified as responsible of familial hyperaldosteronism Type 1 (FH-I) [14, 15] 43 (Table 1). FH-I is an autosomal dominant disease presenting as early-onset hypertension 44 associated with biochemical abnormalities of PA and increased production of 18-45 hydroxycortisol and 18-oxocortisol, which improves with glucocorticoid treatment [16, 17]. 46 The chimeric CYP11B1/CYP11B2 gene leads to ectopic expression of CYP11B2 throughout the 47 48 adrenal cortex, with aldosterone being produced not only in cells from ZG, and with an inappropriate ACTH-dependent regulation of aldosterone biosynthesis following the circadian 49 rhythm of cortisol (Figure 1) [18, 19]. 50

During the last decade, whole exome sequencing (WES) performed on DNA from APA 51 has allowed the identification of somatic mutations in genes coding for ion channels (KCNJ5 52 encoding for the potassium channel GIRK4, CACNA1D coding for the α1 subunit of the L-type 53 54 Ca²⁺ channel Cav1.3) and ATPases (ATP1A1, coding for the α1 subunit of the Na⁺,K⁺-ATPase, and ATP2B3, coding for the plasma membrane calcium-transporting ATPase 3 (PMCA3) [20-55 23]. The frequency of somatic mutations was reported to be approximately 50% in studies 56 performing Sanger sequencing of hot spot regions of APA-driver genes on DNA extracted from 57 frozen pieces of tumor [24, 25]. The recent development of aldosterone synthase (CYP11B2) 58 immunohistochemistry (IHC)-guided next-generation sequencing (NGS) allowed the 59 60 identification of mutations in APA-driver genes in 88% to 93% of APA [26-28].

In parallel, the discovery of germline mutations in genes coding for the same ion channels
 identified in APA and also in *CACNA1H* (coding for the α1 subunit of the T-type Ca2+ channel
 Cav3.2) and *CLCN2* (coding for the chloride channel ClC-2) have complexified the

classification of familial forms of PA [20, 22, 29-32], with four different forms now classified
in FH-I to FH-IV, based on the underlying genetic defect.

All the different somatic and germline mutations increase *CYP11B2* expression and aldosterone biosynthesis by affecting cell membrane potential and/or intracellular ionic homeostasis, resulting in increased intracellular calcium concentration and activation of calcium signaling (Figure 1).

70 KCNJ5 mutations

71 Somatic and germline KCNJ5 mutations were identified in APA and in patients with a 72 familial form of PA (FH-III) [20]. The most prevalent KCNJ5 mutations (p. Gly151Arg, p. Thr158Ala, p. Leu168Arg) are localized near or within the selectivity filter of the channel. 73 74 These mutations cause loss of K⁺ selectivity and increase sodium permeability, resulting in cell membrane depolarization followed by opening of voltage-gated Ca²⁺ channels and stimulation 75 of Ca²⁺ signaling [20, 33, 34] (Figure 1). A small number of *KCNJ5* mutations are localized in 76 regions far from the selectivity filter and could be responsible for decreased abundance of the 77 channel at the plasma membrane [35]. While the impact of GIRK4 downregulation on 78 79 aldosterone production was not observed in cell models [33], a recent study suggested that cell proliferation and apoptosis may be regulated by the level of GIRK4 expression [36]. 80

81 Recurrent somatic KCNJ5 mutations are the most frequent genetic abnormality observed in APA, being identified in approximately 40% of adenomas [24, 37, 38]. Ethnic differences 82 were observed among cohorts, with a higher prevalence of somatic KCNJ5 mutations in patients 83 from East Asian cohorts [35, 39-41]. Different studies have shown that KCNJ5 mutations are 84 more frequent in female and younger patients [24-28, 35, 38, 42, 43], and may also be associated 85 with higher aldosterone levels and larger tumor size in some studies [37, 38] but not in others 86 [28]. KCNJ5 mutations were also suggested to be a marker of better surgical outcome after 87 adrenalectomy [44]. Compared with other mutational groups, APA carrying KCNJ5 mutations 88 present lower percentage of cells expressing CYP11B2 and higher percentage of cells 89 expressing CYP11B1 [28]. A recent study, however, reported no difference in overall 90 91 aldosterone synthase expression as a function of mutational status [45]. In addition, KCNJ5-92 mutated APA exhibit decreased GIRK4 expression in comparison with the adjacent ZG [28, 36, 46, 47]. 93

Germline *KCNJ5* mutations are also responsible for FH-III [20] (Table 1). FH-III was first
 described in 2008 as severe early-onset hypertension associated with hypokalemia, high urinary
 concentrations of hybrid steroids 18-oxocortisol and 18-hydroxycortisol, and massive bilateral

adrenal hyperplasia [48]. Germline *KCNJ5* mutations were found in different FH-III families
presenting variability in the severity of hyperaldosteronism and in the subtype of PA, sometimes
within the same family [49-53].

In vitro studies revealed that mutated GIRK4 may be blocked by high therapeutic doses of the calcium channel blocker verapamil, or by macrolides, decreasing *CYP11B2* expression and aldosterone biosynthesis [54-56]. Clinical studies are currently ongoing, in hypertensive patients with PA, to evaluate the potential clinical use of macrolides on PA subtyping or the identification of somatic *KCNJ5* mutations before surgery [57].

105 CACNA1D and CACNA1H mutations

CACNA1D mutations affect different properties of Cav1.3 channel, delaying the voltage-106 dependent inactivation or inducing opening of the channel at less depolarized potentials. This 107 results in increased Ca^{2+} influx leading to the activation of Ca^{2+} signaling and aldosterone 108 overproduction (Figure 1) [21, 22]. Using CYP11B2 IHC-guided NGS, the prevalence of 109 somatic CACNA1D mutations was 21% in APA from white American patients, 37% in a French 110 cohort, and as high as 42% in APA from African-American patients, being the most frequent 111 genetic abnormality in this population [26-28]. While CACNA1D mutations were associated 112 with smaller tumors in studies using Sanger sequencing to genotype APA [24], this association 113 was not described in a recent study using CYP11B2 IHC-guided NGS [28]. In addition to 114 somatic mutations, de novo germline mutations in CACNA1D were identified in two children 115 exhibiting a severe form of hyperaldosteronism in the first year of life associated with a 116 complex neurologic disorder (Primary Aldosteronism, Seizures and Neurologic Abnormalities 117 (PASNA) [22] (Table 1). 118

Germline CACNA1H mutations are responsible for FH-IV. Mutations modify the Cav3.2 119 channel properties inducing a gain of function, resulting in increased Ca²⁺ influx followed by 120 activation of calcium signaling and overproduction of aldosterone (Figure 1) [29, 30]. The 121 recurrent germline CACNA1H mutation p.Met1549Val was described in five children with 122 123 onset of PA before age 10 years [29]. Micronodular adrenal hyperplasia was observed in the 124 histological analysis of one case [29]. A de novo germline CACNA1H mutation also affecting codon 1549 (p.Met1549Ile) was described in one children with PA associated with multiplex 125 developmental disorder [30]. Germline CACNA1H mutations were also identified in adult 126 patients with a familial inheritance of PA and in one patient with APA, suggesting that 127 CACNA1H mutations may predispose to PA with different phenotypic presentation [30]. 128 Recently, somatic CACNA1H mutations were also observed in a rare subset of APA [58]. 129

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131 ATP1A1 and ATP2B3 mutations

ATP1A1 mutations were identified in 8% to 17% of APA by CYP11B2 IHC-guided NGS 132 [26-28]. The α subunit of the Na⁺,K⁺-ATPase, encoded by ATP1A1, is composed of 10 133 134 transmembrane domains (M1 to M10) and intracellular N- and C- termini. Somatic ATP1A1 mutations are localized in M1, M4 and M9 domains [21, 23, 25, 40, 59]. While mutations in 135 the M1 and M4 domains affect the K⁺ binding pocket decreasing the pump affinity for K⁺, 136 mutations in the M9 domain affect a supposed sodium-specific site of the pump, all mutations 137 138 decreasing the pump activity [60, 61]. The reduced affinity for K⁺ and the loss of pump activity result in cell membrane depolarization and cell acidification, without overt increase of 139 intracellular Ca²⁺ (Figure 1) [60]. However, the role of cytosolic acidification on autonomous 140 aldosterone production is not established. 141

142 ATP2B3 mutations were identified in 1.7% to 10% of APA, with higher prevalence in studies using CYP11B2 IHC-guided NGS [24-28, 43]. PMCA3, encoded by ATP2B3 is 143 144 composed of 10 transmembrane domains (M1 to M10) and intracellular N- and C- termini. All APA-driver ATP2B3 mutations are in frame deletions affecting a "PEGL" motif in the M4 145 domain, a region involved in calcium binding and ion gating [23-25, 43, 62]. Mutations in 146 ATP2B3 decrease pump activity, impairing calcium export and resulting in increased cytosolic 147 calcium concentration and activation of calcium signaling (Figure 1). A second mechanism for 148 autonomous aldosterone biosynthesis was suggested; ATP2B3 mutations may induce a sodium 149 150 leak resulting in cell membrane depolarization and opening of voltage-dependent calcium channels, but may also induce a calcium leak through mutated pumps [63]. 151

152 CLCN2 mutations

Germline CLCN2 mutations are responsible for FH-II (Table 1). FH-II was used to group 153 all familial forms of PA without an established genetic cause, with a diagnosis based on the 154 presence of two or more affected family members [64, 65]. Whole-exome sequencing 155 performed in a large Australian FH-II family identified a germline mutation in CLCN2 156 157 segregating with the disease in 8 subjects [32]. Three other PA pedigrees carried the same 158 mutation and, additionally, four different germline CLCN2 mutations were identified in unrelated patients with early-onset PA [32]. A de novo germline CLCN2 mutation was 159 identified, concomitantly, in a 9 years-old PA patient exhibiting severe hypertension and 160 profound hypokalemia [31]. This mutation changes the properties of ClC-2 leading to increased 161 chloride conductance at resting potentials and chloride efflux followed by cell membrane 162

depolarization, activation of calcium signaling and stimulation of *CYP11B2* expression and
autonomous aldosterone production (Figure 1) [31]. In addition to germline mutations and FHII, a somatic *CLCN2* mutation was reported in one APA [66].

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167 CTNNB1, PRKACA and ARMC5 mutations

Somatic mutations in *CTNNB1*, coding for β -catenin, were identified in 2.1% to 5.1% of 168 APA [43, 67]. CTNNB1 mutations are localized in exon 3 and were previously described in 169 cortisol-producing adenomas and adrenocortical cancer. CTNNB1 mutations are more prevalent 170 171 in women and an association with PA during pregnancy due to aberrant expression of gonadal receptors in APA was suggested [68]. However, it has been shown that the regulation of 172 173 aldosterone production by gonadal hormones may also occur in APA without somatic CTNNB1 mutations [69]. Further studies are necessary to establish the role of CTNNB1 mutations on 174 175 APA development.

Somatic *PRKACA* (encoding the cAMP-dependent protein kinase catalytic subunit alpha)
mutations were identified in two patients with APA, one presenting aldosterone and cortisol cosecretion [70]. *PRKACA* mutations were also described in cortisol producing adenomas and
their roles in autonomous aldosterone production and APA development are unknown.

Finally, germline *ARMC5* (armadillo repeat containing 5) variants, predicted to be damaging, were observed in African-American patients with PA [71]. Germline *ARMC5* variants were also observed in a European cohort of patients with PA, although they were not predicted to be damaging using bioinformatics tools [72]. *ARMC5* mutations were previously identified in primary bilateral macronodular adrenal hyperplasia and associated with hypercortisolism [73]. The link between *ARMC5* mutations and PA remains to be further determined.

187 Animal models of primary aldosteronism

188 Genetic studies have greatly contributed to a better understanding of the mechanisms 189 responsible for PA development, highlighting the role of ion channels and pumps, but also of 190 the Wnt/ β -catenin pathway (Table 2). Remarkably, potassium channels and the Wnt/ β -catenin 191 pathway had been shown previously to play crucial roles in the regulation of aldosterone 192 biosynthesis and homeostasis of the adrenal cortex by specific mouse models.

Invalidation of *kcnk3* or/and *kcnk9*, coding for the two-pore domain potassium channels
Task1 and Task3, resulted in different forms of hyperaldosteronism or low renin hypertension

[74-78]. Simultaneous invalidation of kcnk3 and kcnk9 leads to ZG cell depolarization and PA 195 resistant to salt suppression, without affecting cellular morphology and adrenal zonation [75]. 196 ZG-specific invalidation of both potassium channels resulted in a milder phenotype consisting 197 198 of a moderate increase of plasma aldosterone that was not associated with a reduction of plasma renin or increased ARR; nevertheless, it was sufficient to significantly increase blood pressure 199 [78]. Different phenotypes were observed when Kcnk3 or kcnk9 were invalidated separately. 200 Task3 channel deletion causes salt-sensitive hypertension with low renin [76, 77], associated 201 with ZG cell depolarization, modification of Ca^{2+} signaling and alteration of the physiological 202 regulation of aldosterone, without changes in adrenal morphology. In neonatal mice, Task3 203 204 deletion led to major adrenal dysfunction, associated with increased aldosterone, corticosterone 205 and progesterone levels [79]. Deletion of Task1 resulted in severe hyperaldosteronism 206 remediable by glucocorticoids associated with abnormal expression of aldosterone synthase in 207 the zona fasciculata (ZF), despite normal morphological zonation of the adrenal cortex [74]. Whereas this phenotype was observed in female mice all along their life, it was only observed 208 209 in pre-pubertal male mice, suggesting an androgen-driven upregulation of compensatory mechanisms [74]. In these mice, a subset of genes was closely associated with 210 211 hyperaldosteronism, including *Dkk3* coding for Dickkopf3, a member of the Wnt signaling pathway [80]. Interestingly, invalidation of dkk3 in $kcnk3^{-/-}$ mice resulted in hyperaldosteronism 212 also in male mice, suggesting a role for *dkk3* in the development of PA [80]. 213

After the identification of CLCN2 mutations in patients with FH-II, two different knock-in 214 215 mouse models provided important insight regarding the role of chloride channels in PA development [81, 82]. Deletion of eight N-terminal residues constituting the inactivation 216 217 domain of the Clc-2 chloride channel, where the p.Met22Lys, p.Gly24Asp and p.Tyr26Asn 218 mutations are located [31, 32], resulted in hypertension and hypokalemia in mice, with high aldosterone and low renin levels, recapitulating the major features of PA [81]. Mice harboring 219 220 the heterozygous p.Arg180Gln mutation, mimicking the human p.Arg172Gln mutation found in FH-II [32], present a mild form of PA with increased aldosterone associated with a mild 221 222 elevation of blood pressure, but absence of morphological adrenal abnormalities [82].

Through different mechanisms, the mutations identified in APA converge upon increased calcium signaling to increase aldosterone production. The constitutive expression in mice of a gain-of-function mutant of the AII receptor type 1A (AT1R) led to the development of lowrenin hypertension and relative hyperaldosteronism [83]. More recently, specific activation of Gq signaling in adrenal cortex, using a Designer Receptors Exclusively Activated by Designers Drugs (DREADD) activated by clozapine N-oxide (CNO), was used to establish a mouse model
of PA [84]. CNO treatment results in increase of Cyp11b2 expression and aldosterone levels,
decreased plasma renin concentration and abnormal zonation of Cyp11b2, with ZF cells
expressing both Cyp11b1 and Cyp11b2. In addition, high blood pressure was observed after
CNO treatment in mice submitted to high salt diet.

Whereas these mouse models develop hyperaldosteronism, the presence of tumors was 233 never observed, suggesting that modification of intracellular ion balance is not sufficient to 234 induce both increase of aldosterone production and adenoma development. Activation of the 235 236 Wnt/β-catenin pathway, playing an important role in adrenal development, has been involved in adrenal carcinoma and adenoma [85] and was found in two-thirds of APA [86]. In mice, 237 238 constitutive activation of β -catenin results in adrenal hyperplasia and dysplasia as well as increased cell proliferation. More interestingly, β-catenin activation also led to increased 239 240 aldosterone production and hyperaldosteronism [87]. However, the development of tumors was observed only in rare cases with features of carcinoma rather than adenoma [87]. 241

Recently, retinoic acid receptor α (RAR α) signaling has been identified as involved in 242 nodule formation by transcriptome analysis performed in APA. Some years ago, proteomic 243 analyses have suggested a role of retinoic acid receptor signaling in the early stage of adrenal 244 development [88]. Invalidation of rara expression in mice results in structural disorganization 245 246 of the adrenal cortex characterized by the loss of the radial organization of the ZF and abnormalities in vessel architecture and extracellular matrix, in both male and female mice, 247 with no major modifications of aldosterone production [89]. Beyond the role of rar α in the 248 249 maintenance of the normal adrenal cortex structure and cell proliferation, dysregulation of this signaling may contribute to abnormal cell proliferation in PA [89]. 250

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252 APCC and their role in aldosterone biosynthesis and PA

Until the description of aldosterone producing cell clusters (APCC), expression of *CYP11B2* and aldosterone biosynthesis was thought to occur exclusively in ZG cells under the tight control of different factors, the two majors being AngII and K⁺ (see above). APCC have been described in 2010 [90]. They are located under the capsule and composed of ZG-like cells in the outer part and of columnar ZF-like cells in the inner part. Despite their morphological properties and the fact that Disabled-2, a marker of ZG, is expressed only in the outer part, the entire structure expresses CYP11B2 but not CYP11B1, suggesting that APCC may constitute intermediate structure between ZG and ZF [86, 91]. However, transcriptome profiling of APCC
revealed a greater homology to ZG cells than to ZF cells [92, 93]. APCC are found in normal
adrenals and their number and size are correlated with age, but not with gender [45]. APCC are
also found in adrenal cortex adjacent to an APA and in adrenals from patients with BAH [90,
91, 94].

Genetic analysis of APCC, using CYP11B2 IHC-guided guided NGS on FFPE tissue, 265 266 identified somatic mutations in APA driver genes, including CACNAID, ATPIA1 and ATP2B3, but not KCNJ5, in 35% of APCC from normal adrenals [92]. More recently, the description of 267 268 APCC-to-APA translational lesions (pAATL), composed of a subcapsular APCC-like structure 269 and a micro-APA-like structure and carrying somatic mutations suggested the possibility for 270 APCC to constitute the starting point for the development of APA (Figure 2) [93]. Other evidences, however, support the occurrence of two independent events leading to APA 271 272 development [95]. It has been shown that the adrenal cortex adjacent to an APA may exhibit 273 ZG hyperplasia, increased nodulation and reduced vascularization [86]. Distinct CYP11B2 positive nodules may carry different mutations within the same adrenal [28, 96] and different 274 APCC located in the cortex adjacent to an APA may also carry different somatic mutations, 275 including KCNJ5 mutations [28]. Finally, a patient with lateralized PA and familial 276 277 adenomatous polyposis further supports a two-hit model for APA development. The patients carried a germline APC mutation with loss of heterozygosity in adrenals (first hit), responsible 278 for a macronodular hyperplasia. In one CYP11B2 positive nodule, a somatic KCNJ5 mutation 279 280 was identified, being responsible for autonomous aldosterone production (second hit) (Figure 281 2) [97].

APCC appear also to play a role in the pathogenesis of bilateral forms of PA. In a study 282 investigating adrenals from 15 patients with BAH who underwent adrenalectomy, the number 283 of APCC was significantly higher compared to adrenals from normotensive controls, 284 285 suggesting that APCC, through autonomous aldosterone production, may contribute to the development of PA. Interestingly, sequencing of 99 APCC from the 15 adrenals identified 286 287 somatic mutations in at least one APCC in all but one case; all mutations affected the CACNA1D gene [94]. These results suggest for the first time that the presence of APCC in BAH may be, 288 289 in part, responsible for PA development; however, they need to be confirmed in a larger cohort 290 of patients.

291

292 Concluding remarks

Over the last years, CYP11B2 guided NGS has allowed the identification of somatic 294 295 mutations in APA-driver genes in more than 85% of APA. In addition, the description of germline mutations in genes coding for different ion channels has allowed refining the 296 297 classification of familial forms of PA and the description of de novo early-onset PA. In mechanistic terms, these mutations highlight the central role of plasma membrane potential, 298 intracellular calcium concentrations and activation of calcium signaling in the pathogenesis of 299 PA. However, the sequence of events leading to APA formation as well as the mechanisms 300 301 responsible for bilateral PA remains unknown. Somatic mutations in APA-driver genes were also identified in APCC from normal adrenals and from adrenals with APA. While this 302 303 discovery suggests a possible role of APCC in PA, the identification of different mutations 304 among APA, APCC and micronodules within the same adrenal implies the contribution of 305 additional mechanisms (see Outstanding Questions). Finally, the investigation of different mouse models has largely contributed to our understanding of some aspects of the development 306 307 of hyperaldosteronism. However, none of these models leads to APA development, suggesting that there might be the requirement for additional events to trigger nodulation, which remain to 308 309 be established. New studies identifying surrogate markers of APA mutational status before surgery, associated with the recent description of drugs specifically blocking mutated KCNJ5 310 channels, could open new and exciting perspectives for a better diagnosis and targeted treatment 311 of PA. 312

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Box 1. Regulation of aldosterone biosynthesis

Aldosterone is produced in the zona glomerulosa of the adrenal cortex to maintain blood volume 322 as well as sodium and potassium homeostasis in the body. Aldosterone is synthetized from 323 cholesterol through sequential enzymatic steps catalyzed by different cytochrome P450 324 325 enzymes and hydroxysteroid dehydrogenases. In the zona glomerulosa, the enzyme aldosterone synthase (encoded by CYP11B2) catalyzes the three terminal steps of aldosterone biosynthesis: 326 hydroxylation at position C11 of deoxycorticosterone (DOC) resulting in corticosterone, 327 hydroxylation at position C18 of corticosterone yielding 18-hydroxy-corticosterone and the 328 oxidation of the hydroxyl group at C18, producing aldosterone. 329

Aldosterone biosynthesis is mainly regulated by the renin angiotensin system and plasma 330 331 potassium concentrations. Under basal condition zona glomerulosa cells are hyperpolarized, due to the presence of a large number of K⁺ channels. Both increased extracellular potassium 332 333 concentrations and angiotensin II inhibit K⁺ channels, leading to cell membrane depolarization, opening of voltage gated Ca^{2+} channels, increasing intracellular Ca^{2+} concentrations. 334 Angiotensin II also signals through the Angiotensin II Type 1 receptor via Gaq proteins leading 335 to activation of phospholipase C-β, increase of inositol triphosphate, and mobilization of 336 intracellular Ca²⁺ stores from the endoplasmatic reticulum, increasing intracellular calcium 337 levels. This leads to activation of Ca^{2+} signaling, which increases aldosterone biosynthesis by 338 activating transcription factors, in particular the nuclear receptor subfamily 4 group A (NR4A) 339 members 1 and 2 (NURR77 or NGF1B and NURR1), the cyclic AMP-dependent transcription 340 factor ATF-1 and the cyclic AMP-responsive element-binding protein (CREB), which increase 341 the expression of CYP11B2, coding for aldosterone synthase. Increased Ca^{2+} signaling also 342 enhances early and intermediary steps of adrenal steroidogenesis, including release of 343 344 cholesterol from cytoplasmic stores, activation of the expression of the steroid acute regulatory protein (StAR), which promotes the transfer of cholesterol to the inner mitochondrial 345 346 membrane, and the synthesis of cofactors for p450 cytochrome enzyme.

347 Box 2. Clinician's Corner

Primary aldosteronism (PA) is the most frequent form of secondary arterial hypertension with a prevalence of up to 10% of hypertensive patients. PA patients have a higher cardiovascular risk compared to patients with essential hypertension. The two main causes of PA are unilateral aldosterone producing adenomas (APA) and bilateral adrenal hyperplasia. The diagnosis of PA includes screening, confirmation tests and subtype identification. Treatment is tailored to the underlying cause: adrenalectomy for unilateral disease and drug therapy forbilateral forms.

Familial forms of PA (FH) account for 5% of the cases. They are classified according to 355 the underlying genetic defect. FH-I is caused by a chimeric gene composed of the promoter 356 regions of CYP11B1 and the coding region from CYP11B2. FH-II is caused by germline 357 mutations in the gene CLCN2, coding for the chloride channel ClC-2. Germline mutations in 358 KCNJ5, coding for the potassium channel GIRK4 are responsible FH-III. Finally, germline 359 mutations in CACNA1H, coding for the voltage dependent T-type calcium channel Cav 3.2 are 360 responsible by FH-IV. Germline CACNA1D mutations were associated with a rare form of 361 early-onset hyperaldosteronism associated with neurological abnormalities. 362

Somatic mutations in genes coding for ion channels (*KCNJ5*, *CACNA1D*) and ATPases (*ATP1A1* and *ATP2B3*) were identified in the majority of APA. Their frequency may vary in different populations, with *KCNJ5* being more frequent in cohorts from Asia and *CACNA1D* mutations in cohorts from African ancestry. *KCNJ5* mutations are more frequent in women and young patients. Mutations in *CTNNB1*, coding for β -catenin, were identified in 5% of APA, most frequently in women and possibly associated to pregnancy.

369 Somatic mutations are also found in aldosterone producing cell clusters (APCC), adrenal 370 structures responsible for autonomous aldosterone production, in normal adrenals. Somatic 371 mutations in APCC are also found in the adrenal cortex adjacent to APA and adrenals from 372 bilateral adrenal hyperplasia. APCC may play a role in the development of PA, as well as in the 373 physiology of aldosterone biosynthesis in normal adrenals.

The discovery of the genetic basis of PA opens new perspectives for the development of new and better diagnostic tools and for drug therapy targeting mutated proteins. Also, it allows for genetic screening and counseling in affected families and improved management of mutation carriers.

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595

596 Figure legends

Figure 1. Cellular mechanisms of autonomous aldosterone biosynthesis. In unstimulated 597 598 conditions, zona glomerulosa cells are in a hyperpolarized state, due to the presence of a large number of potassium channels. Cell membrane depolarization, following stimulation of 599 600 aldosterone biosynthesis, leads to opening of voltage-gated calcium channels and activation of calcium signaling, the main trigger for aldosterone biosynthesis. Mutations in different channels 601 602 and pumps have been identified in different forms of familial hyperaldosteronism and APA. Mutations in GIRK4 potassium channels in APA and FH-III lead to sodium entry into the cells 603 instead of extrusion of potassium. Mutations in CLC-2 chloride channels in FH-II and APA 604 increase chloride efflux, and mutations in the α 1 subunit of the Na⁺,K⁺-ATPase, found in APA, 605 are responsible for loss of pump activity, but also lead to proton entry into the cells. These 606 mutations lead to cell membrane depolarization and opening of voltage gated calcium channels. 607 Mutations in the α 1 subunit of the L-type Ca²⁺ channel Cav1.3, found in APA and PASNA, and 608 in α 1 subunit of the T-type Ca²⁺ channel Cav3.2 in FH-IV and APA, result in changes in their 609 610 functional properties, particularly allowing calcium entry at lower membrane potential, whereas mutations in PMCA3 are responsible for loss of pump activity and accumulation of calcium in 611 612 the cells. All these mutations induce an increase of intracellular calcium concentration and 613 activation of calcium signaling, followed by stimulation of CYP11B2 transcription and increase in aldosterone biosynthesis. In FH-I, a chimeric gene in which the coding region of CYP11B2 614 is fused to the regulatory region of CYP11B1 leads to ectopic expression of CYP11B2 615 throughout the adrenal cortex and control of aldosterone biosynthesis mainly by ACTH. 616

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Figure 2: Pathogenic model of aldosterone producing adenoma development. Two 618 different models may explain APA development in the adrenal cortex. (Left panel) "APCC 619 model": occurrence of somatic mutations in different APA driver genes (KCNJ5, CACNA1D, 620 621 ATP1A1, ATP2B3, KCNJ5) lead to the development of aldosterone producing cell clusters (APCC). APCC may develop into APA through the formation of possible APCC-to-APA 622 translational lesions (pAATL). (Right panel) "Two-hit model": Abnormal cell proliferation and 623 nodulation in the zona glomerulosa, due to genetic or environmental factors, may create a 624 propitious environment for the occurrence of somatic mutations in APA driver genes (KCNJ5, 625 CACNA1D, ATP1A1, ATP2B3, CACNA1H, CLCN2). In both hypothesis, activation of calcium 626 signaling, due to the presence of somatic mutations, leads to increased CYP11B2 expression 627 and autonomous aldosterone production. 628

629Table 1. Familial and inherited forms of primary aldosteronism.

Disease	Age of onset	Specific features	Gene	Transmission	Treatment
Familial hyperaldosteronism type I	Variable Often before 20 ys	Cerebrovascular events at young age (<30 ys)	Chimeric CYP11B1/B2	AD	Glucocorticoids, MRA
Familial hyperaldosteronism type II	Variable Young onset in patients with <i>CLCN2</i> mutations	none	CLCN2	AD	MRA
Familial hyperaldosteronism type III	Before 20 ys Variable in mild forms	Massive bilateral adrenal hyperplasia in severe cases	KCNJ5	AD	MRA Bilateral adrenalectomy in severe cases
Familial hyperaldosteronism type IV	Variable Most frequent before 20 ys	Developmental disorder in some cases	CACNA1H	AD	MRA
Primary Aldosteronism, Seizures and Neurologic Abnormalities (PASNA)	Childhood	Seizures and neurological abnormalities	CACNA1D	? (de novo)	Calcium channel blocker

AD: autosomal dominant; MRA: Mineralocorticoid Receptor antagonist

Model	Phenotype	Adrenal Phenotype	Mechanism	Ref
TASK1 inactivation	 Hyperaldosteronism remediable by glucocorticoids Both sexes in young mice Restricted to females in adult mice 	 Cyp11B2 absent in the ZG Ectopic Cyp11B2 expression in the ZF restricted to females in adults. 	More depolarized membrane voltage at resting conditions	[74]
TASK1 and TASK3 inactivation	Overproduction of aldosterone resistant to salt suppressionNormal/low renin	• Cellular morphology and zonation preserved in adult mice (only males)	• Marked depolarization of ZG cells.	[75]
TASK3 inactivation	 Salt-sensitive, low renin, arterial hypertension Abnormalities in the regulation of aldosterone Severe hyperaldosteronism in neonatal knockout mice 	 No changes in adrenal morphology 	 Depolarization of adrenocortical cells. Abnormal Ca²⁺ signaling. 	[76, 79]
TASK3 inactivation	 Salt-sensitive, low renin, arterial hypertension Mild hyperaldosteronism resistant to salt suppression 	 No changes in adrenal morphology 	• More depolarized membrane voltage at resting conditions	[77]
TASK1 and DKK3 inactivation	Hyperaldosteronism remediable by glucocorticoids in both sexes	• Absence of altered functional zonation in male mice	• More depolarized membrane voltage at resting conditions	[80]
Constitutive activation of β -catenin	• Increased aldosterone production independent of renin	• Ectopic expression of Dab2, Beta- catenin and Cyp11b2 in ZF	 Beta-catenin dependent activation of <i>at1r</i> and <i>cyp21</i> Increased expression of Nurr1 and Nur77 leading to <i>Cyp11b2</i> activation 	[87]
ZG Specific inactivation of TASK1 and TASK3	Arterial hypertensionMild hyperaldosteronismMild aldosterone autonomy	NA	NA	[78]

Table 2. Recent mouse models of hyperaldosteronism.

Constitutively open ClC-2	 Marked hypertension High serum aldosterone Low renin activity Hypokalemia 	• No changes in adrenal morphology, increased expression of Cyp11b2 in the ZG	 Increased chloride [conductance in the ZG Cell membrane depolarization Increased cytoplasmic Ca²⁺ concentration Increased <i>Cyp11b2</i> expression 	[81]
Knock-in <i>Clcn2</i> model (homologous to human <i>CLCN2</i> mutation in FH-II)	 Mildly elevated blood pressure Mildly elevated aldosterone levels 	 No changes in adrenal morphology Incomplete suppression of Cyp11b2 expression upon high- salt challenge 	 Increased calcium oscillatory [activity in adrenal cells Increased <i>Cyp11b2</i> expression 	[82]
Specific and inducible adrenal activation of Gq signaling	HypertensionIncreased aldosterone levelsDecreased renin	• Disorganization of adrenal functional zonation	• Gq signaling dependent [<i>Cyp11b2</i> expression in ZF cells	[84]

ZG: zona glomerulosa; ZF: zona fasciculata; NA: not available



Figure 1



