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Loss-of-function mutations in *SOX10* cause Kallmann syndrome with deafness

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Abstract

The SOX10 transcription factor plays a role in the maintenance of progenitor cell multipotency, lineage specification, cell differentiation, and is a major actor in the development of the neural crest. It has been implicated in Waardenburg syndrome (WS), a rare disorder characterized by the association of pigmentation abnormalities and deafness, but *SOX10* mutations cause a variable phenotype that spreads over the initial limits of the syndrome definition. Based on recent findings of olfactory bulb agenesis in WS individuals, we suspected *SOX10* was also involved in Kallmann syndrome (KS). KS is defined by the association of anosmia and hypogonadotropic hypogonadism due to incomplete migration of neuroendocrine GnRH (gonadotropin-releasing hormone)-cells along the olfactory, vomeronasal, and terminal nerves. Mutations in any of the nine genes identified to date account for only 30% of the KS cases. KS can be either isolated or associated with a variety of other symptoms including deafness. This study reports *SOX10* loss-of-function mutations in approximately one-third of KS individuals with deafness, indicating a substantial involvement in this clinical condition. Study of *SOX10*-null mutant mice revealed a developmental role of *SOX10* in a subpopulation of glial cells called olfactory ensheathing cells. These mice indeed showed an almost complete absence of these cells along the olfactory nerve pathway, as well as defasciculation and misrouting of the nerve fibers, impaired migration of GnRH-cells, and disorganization of the olfactory nerve layer of the olfactory bulbs.

Introduction

SOX10 (MIM 602229) belongs to the SOX family of transcription factors, whose members are involved in a multitude of developmental and cellular processes.¹ First identified as a glial cell transcription factor, it was soon revealed as a major player in the development of neural crest (NC) cells. NC cells are a population of multipotent precursor cells that emerge at the borders of the neural tube, migrate extensively throughout the embryo, and differentiate into a variety of cell types including skin pigment cells, and neurons and glia of the peripheral and enteric nervous systems.² SOX10 plays a role in the maintenance of progenitor multipotency, specification, and differentiation of numerous cell types through the regulation of several transcriptional targets.^{1,3-5} Its involvement in Waardenburg syndrome (WS) contributed significantly to the understanding of its function in NC in general and in the melanocytic and enteric lineages in particular.⁶

WS is a clinically and genetically heterogeneous condition that manifests with sensorineural congenital deafness and abnormal pigmentation of the hair, skin, and iris. Four subtypes (WS1 to WS4 [MIM 193500, 193510, 148820, 277580]) as well as neurological variant (PCWH, for Peripheral demyelinating neuropathy-Central dysmyelinating leukodystrophy-Waardenburg syndrome-Hirschsprung disease [MIM 609136]) have been described.⁶ Since 1998, approximately 100 heterozygous point mutations or deletions of *SOX10* have been reported, first in WS4 (WS with Hirschsprung disease/megacolon),⁷ then in its neurological variant,⁸ and finally in WS2 (WS without Hirschsprung disease)⁹ (see also the WS gene mutation database at LOVD [Leiden Open Variation Database]).⁶

To delineate the range of temporal bone abnormalities associated with impaired SOX10 function, we recently performed a study of MRI and/or CT scans of inner ears from 15 WS individuals. Incidentally, this study also revealed an unexpectedly high frequency of olfactory

bulb agenesis (88% of the cases who could be analyzed),¹⁰ a finding that had been described only once before in association with a *SOX10* mutation.¹¹ Notably, one of the male included in our radiological study had previously been reported as having anosmia and hypogonadism.⁹ The association of anosmia and hypogonadotropic hypogonadism is known as Kallmann syndrome (KS [MIM 147950, 244200, 308700, 610628, 612370, 612702]) and explained by a pathological sequence in embryonic development. Premature interruption of the vomeronasal and terminal nerve fibers in the peripheral olfactory system have been shown to result in incomplete migration of the neuroendocrine GnRH (gonadotropin-releasing hormone)-cells along these nerves, precluding them from penetrating into the forebrain and reaching their final destination in the preoptic and hypothalamic region.¹² The prevalence of KS has been estimated at 1/8,000 in males and 1/40,000 in females. Nine genes have been implicated to date, namely *KALI*, *FGFR1*, *FGF8*, *PROKR2*, *PROK2*, *WDR11*, *HS6ST1*, *CHD7*, and *SEMA3A* (MIM 300836, 136350, 600483, 607123, 607002, 606417, 604846, 608892, and 603961, respectively), but mutations in any of these genes have been identified in only approximately 30% of KS individuals.¹³ KS can be associated with a variety of non-olfactory, non-reproductive symptoms including deafness, but the association of KS with deafness has so far received little genetic explanation.

Here, we asked whether persons affected by KS carry mutations in *SOX10*. We found a notable prevalence (about 38%) of *SOX10* mutations in a group of individuals presenting with the clinical association of KS and hearing impairment, thereby shedding new light on this clinical association. We showed that these mutations affect *SOX10* function in vitro. Homozygous *Sox10* mutant mice show an almost complete absence of olfactory ensheathing cells (OECs) along the olfactory, vomeronasal, and terminal nerves, abnormal fasciculation and axonal misrouting of the olfactory neurons, impaired GnRH-cell migration, and disorganization of the olfactory nerve layer of the olfactory bulbs.

Subjects and Methods

Subjects

This study was approved by the national research ethics committee (Agence de Biomedicine, Paris, France). Seventeen cases (9 males and 8 females) presenting with KS plus at least one WS-like feature were investigated, as well as 86 “random” cases (67 males and 19 females) addressed for genetic exploration of KS, including 20 with various non-olfactory, non-reproductive associated anomalies (including eight with cleft lip or palate). Hypogonadism was diagnosed based on clinical and hormonal evaluation, while diagnosis of anosmia/hyposmia was based on the individual’s interview and confirmed by olfactory tests with increasing concentrations of odorant molecules (olfactometry) and/or MRI showing agenesis of the olfactory bulbs. Informed consent for genetic testing was obtained. Genomic DNA was extracted from peripheral blood leukocytes using standard protocols. These individuals did not carry mutations in the coding sequences of previously analyzed genes, specifically, *KALI*, *FGFR1*, *FGF8*, *PROKR2*, and *PROK2*, all involved in KS.

Mutation screening

The coding exons of *SOX10* were analyzed by Sanger sequencing of the PCR products as previously described.⁹ Mutations were named according to the international nomenclature based on RefSeq accession number NM_006941.3 for the *SOX10* cDNA. *SOX10* deletions or rearrangements were sought using QMF-PCR with a method slightly modified from Bondurand et al., 2007.⁹ The three coding exons were amplified in five amplicons sorted in two different reaction mixes. The sequences of the primers used are available upon

request. Individuals carrying a *SOX10* mutation were further tested for the presence of mutations in the other genes involved in KS or in non-syndromic congenital hypogonadotropic hypogonadism, specifically, *CHD7*, *WDR11*, *HS6ST1*, *SEMA3A*, *GNRHR*, *GNRH1*, *TACR3*, *TAC3*, *KISS1R*, and *KISS1*. To confirm the *de novo* occurrence of the mutation, comparison with the parental DNA (when available) was conducted through analysis of six microsatellites located on different chromosomes, using the linkage mapping set (Applied Biosystems, Carlsbad, CA, USA) according to the manufacturer's instructions.

Animals and genotyping

The generation and genotyping of *Sox10^{lacZ}* mice (*Sox10^{tm1Weg}*) have been described previously.¹⁴ Experiments were performed in accordance with the ethical guidelines of the Institut National de la Santé et de la Recherche Médicale. Embryos at E12.5 and E14.5 were obtained from staged pregnancies, fixed in 4% paraformaldehyde (PFA) at 4°C, and frozen in OCT (Optimal Cutting Temperature) compound. Head sections (16 µm thick) were cut using a Leica CM3050S cryostat. Alternatively, embryo heads were fixed in 1% PFA and 0.2% glutaraldehyde and used for X-Gal staining.

Immunostaining and X-Gal staining

X-Gal staining followed standard procedures. Immunostaining of mouse embryo sections was performed as described.¹⁵ The primary antibodies used were anti-SOX10 (N-20 or D-20) (goat, 1/50 Santa Cruz), anti-TUJ1 (mouse, 1/1,000, Eurogentec), anti-BLBP/BFABP (rabbit, 1/5,000, kindly provided by T. Müller),¹⁶ anti-P75 (rabbit, 1/500, Promega), anti-S100 (rabbit, 1/400, Dako Cytomation), anti-GnRH (rabbit, 1/500, Abcam), and anti-β-galactosidase (chicken, 1/500, Abcam). Secondary antibodies were anti-goat-FITC, anti-rabbit-Cy3, anti-mouse-Cy3, anti-goat-AlexaFluor555, anti-rabbit-AlexaFluor488, anti-mouse-

AlexaFluor647, anti-guinea pig-Cy3, and anti-chicken-AlexaFluor488 (1/200, Invitrogen or Jackson ImmunoResearch). TUNEL staining was performed using the In Situ Cell Death Detection kit, fluorescein (Roche) according to the manufacturer's instructions. The total number of GnRH-cells was estimated by counting the GnRH-positive cell bodies in more than two-thirds of the sections, from the vomeronasal organ to the end of their migration pathway. The number of GnRH-cells on the missing slides was scored as the mean of the previous and following ones. Preparations were mounted in Vectashield and examined using an Olympus SZH10 stereo-microscope coupled to the Visilog capture program or a Zeiss Axioplan 2 confocal microscope coupled to the Metamorph software package.

Human tissues

A human fetus was obtained from medically terminated pregnancy at 8 weeks of embryonic development, with parents' written informed consent. After fixation in a 4% formaldehyde solution, the head was embedded in paraffin. Serial sagittal sections (4 µm thick) were cut using a Microm HM340E microtome and collected on Superfrost Plus slides (Thermo Scientific). Immunohistochemistry analysis was conducted as described¹⁷ using the antibodies against SOX10, TUJ1, and S100 cited above. Due to the limited number of slides, double SOX10/S100 staining was performed on the nasal mesenchyme only.

Plasmids

The pECE-SOX10, pCMV-SOX10Myc, pECE-PAX3, pECE-EGR2, pGL3-MITFdel1718, and pGL3-Cx32 vectors have been described previously.¹⁸⁻²⁰ The mutations identified were introduced within the pECE-SOX10 (in the case of c.2T>G mutation) or pCMV-SOX10Myc constructs by site-directed mutagenesis using the QuikChange mutagenesis kit (Stratagene, Netherlands). The pGL3-MPZ construct was kindly provided by J. Svaren.²¹

Cell culture, transfection, and reporter assays

HeLa cells were grown in Dulbecco's modified Eagle's medium supplemented with 10% fetal calf serum and transfected using Lipofectamine Plusreagent (Invitrogen, Carlsbad, CA, USA). Cells were plated on 12-well plates and transfected 1 day later with 0.175 µg of each effector and reporter plasmid for the *MITF* and *Cx32/GJB1* promoter study. In the *MPZ* enhancer study, 0.250 µg of reporter plasmid was used. As far as the competition assays are concerned, increasing amounts of mutant SOX10 plasmids (0.175, 0.350, or 0.525µg) were mixed with a fixed amount of wild-type SOX10 plasmid (0.175 µg) and reporter constructs. In each case, the total amount of plasmid was kept constant by the addition of empty pECE or pCMV-Myc vectors. Twenty-four or 48 hours post-transfection, cells were washed twice with PBS, lysed, and the extracts were assayed for luciferase activity using the Luciferase Assay System (Promega, Madison, WI, USA) as described previously.^{9,19,22} Production of SOX10 was assessed by immunoblot analysis using standard protocols.²³ Quantification was performed using GeneTools v3.05 software. Alternatively, cultures were fixed in 4% PFA for 10 min at room temperature and immunocytochemistry was performed as described above using SOX10 N-20 and D-20 antibodies.

In silico analysis of the mutations

Mutations were analyzed using software packages including Polyphen-2, SIFT, Alamut2.0.2 software for splicing, dbSNP, 1000 Genome Project, and Exome Variant Server. The conformation files for SOX17/DNA were imported from the Protein Data Bank (accession code 3F27) and visualized using the Swiss-Pdb Viewer software.^{24,25}

Results

SOX10 mutations are frequent in individuals with KS and deafness

We first searched for *SOX10* point mutations and deletions in individuals diagnosed with KS, who also presented one or several of the known features of *SOX10*-linked WS. We screened 17 cases (9 males and 8 females) previously found negative for mutations in the main genes involved in KS, 13 of them presenting with deafness (unilateral in three cases), two with pigmentation defects (hair and skin hypopigmentation; early graying in a deaf), two with intellectual disability and one with psychomotor delay (both features that can be found in the neurological variant of WS [PCWH]). Eleven cases also had additional symptoms unrelated to WS.

Six new *SOX10* nucleotide changes were identified in this cohort: a mutation of the initiation codon (c.2T>G, p.?), two nucleotide changes predicting missense mutations within the HMG domain (c.331T>G, [p.Phe111Val]; c.424T>C, [p.Trp142Arg]), a splice site mutation (c.698-1G>C), a single base-pair deletion predicted to result in a frameshift (c.1290del, [p.Ser431Argfs*71]), and finally a nucleotide change predicted to result in a missense mutation located in the transactivation domain (c.1298G>A, [p.Arg433Gln]). These changes were not found in at least 50 control individuals (100 chromosomes) of the same origin and the relevant databases (dbSNP, 1000 Genome Project, Exome Variant Server) did not provide evidence that any of these variations are found in control populations.

Clinical and molecular findings in persons carrying *SOX10* mutations are summarized in Table 1 (cases A to F). All six individuals had anosmia as well as absent or delayed spontaneous puberty. Two males had cryptorchidism, and one also had micropenis. One of them demonstrated early graying of the hair. Interestingly, all but one were deaf. Pedigrees of the two familial cases are represented in Figure S1A. A sample from the clinically affected

mother of case D (anosmia and deafness) (see Table 1 and Figure S1A) was obtained, and cosegregation of the mutation and the disease was confirmed. Parents could also be analyzed for two of the sporadic cases (case B and E) and the mutation was proved to be de novo in both cases.

Five mutations result in impaired SOX10 function

In silico prediction suggested likely pathogenic consequences of all six mutations. The splice site mutation c.698-1G>C was predicted to result in complete loss of the last splice acceptor site using several programs, with consequences similar to previously identified splice site mutations at the same location (c.698-2A>C, c.698-2A>T).^{26,27} The PolyPhen2 and SIFT programs respectively predicted a “likely damaging” and a “not tolerated” effect of the three missense substitutions. Functional effects of the mutations were tested through in vitro analysis.

The p.Phe111Val, p.Trp142Arg, c.1290del, and p.Arg433Gln mutations were tested using a construction allowing production of SOX10 with a Myc tag at its aminoterminal end. After confirmation of the protein production by immunoblot analysis (Figure 1A), we first compared the transactivation capacities of the mutant proteins on *MITF* (Microphthalmia-associated transcription factor) and *MPZ* (Myelin protein zero; P0) promoters/enhancers, alone or in synergy with known SOX10 partner transcription factors, PAX3 (Paired-box 3) and EGR2 (Early growth response 2) respectively (Figure 1B and C).^{19,21} The p.Phe111Val, p.Trp142Arg, and c.1290del mutant SOX10 were unable to transactivate the *MITF* reporter construct alone or in synergy with PAX3, whereas the p.Arg433Gln mutant SOX10 behaved like the wild-type protein. On the *MPZ* enhancer reporter construct, the p.Phe111Val, p.Trp142Arg, and c.1290del mutant SOX10 also lost their transactivation capacities alone and demonstrated variable synergistic activity with EGR2 (specifically, conserved for

p.Phe111Val and p.Trp142Arg, lost for c.1290del). Again, the p.Arg433Gln mutant protein showed no change compared with wild-type SOX10. Together, these findings indicated loss of function of the first three mutations and no pathogenic effect of the p.Arg433Gln mutation in vitro. These findings are consistent with the observation that Arg433 is located in the transactivation domain, where no WS-causing missense mutations have been characterized thus far, while Phe111 and Trp142 are located within the highly conserved HMG domain, as are the amino acid residues modified by the previously identified SOX10 missense mutations.²⁴

Due to its location in the translation initiation codon, the c.2T>G mutation was tested using a *SOX10* construction allowing production of an untagged protein. Although not detected in immunoblot analysis performed under standard conditions (data not shown), the mutant protein was visualized by immunocytochemistry. Use of an antibody directed against the carboxy-terminal portion of SOX10 revealed that a mutant protein was produced and localized within the nucleus, as was the wild-type protein (Figure 1D, D20-Ab). Notably, we failed to detect the mutant protein with another antibody directed against the amino terminus of SOX10 (Figure 1D, N20-Ab), which supports the use of a downstream methionine as an alternative initiation codon. This mutant protein showed either absent or reduced transactivation capacity on the *MITF*, *MPZ*, or *GJB1* (another SOX10 target gene, encoding connexin 32) reporter constructs (Figure 1E). Synergistic activity was lost with PAX3, while it was retained with EGR2 on *MPZ* but not on *GJB1* (Figure 1E).

The six mutations were also tested in a competition assay on the *MITF* promoter. They did not show any dominant negative effect at a ratio of 1:1 and 2:1 to the wild-type protein (Figure S1B). Only at a ratio of 3:1 did the mutations (except p.Arg433Gln) induce a decrease of the luciferase induction.

Functional analysis of *SOX10* missense mutations previously identified in the context of WS allowed us to show that aminoacid substitutions in close contact with the main hydrophobic core of the HMG domain alter subcellular localization of the protein, leading to its accumulation in nuclear foci.²⁴ The hydrophobic core is composed of four highly conserved residues, two tryptophans and two phenylalanines, which are located at the intersection of the three α -helices that compose the HMG domain and maintain their structural shape. The p.Phe111Val and p.Trp142Arg mutations described here both remove one of the hydrophobic core components (Figure 2A). We therefore analyzed the effects of the mutations on the subcellular localization of *SOX10* by immunocytochemistry. Whereas the c.1290del and p.Arg433Gln mutant proteins showed a nuclear localization pattern similar to that observed for the wild-type protein (Figure 2B), the p.Phe111Val and p.Trp142Arg proteins showed partial cytoplasmic relocation (consistent with the location of Phe111 and Trp142 within the bipartite nuclear localization signals (NLS) and the nuclear export signal (NES), respectively) as well as subnuclear accumulation in foci.

Together, these results strongly indicate a pathogenic effect of five mutations among the six identified, all found in individuals presenting with the clinical association of KS and deafness.

SOX10 mutations are rare in KS individuals without hearing impairment

We then aimed to determine whether *SOX10* is also involved in other clinical forms of KS, and particularly in KS without deafness. We screened 86 random KS individuals, including 66 KS cases without associated signs and 20 cases with non-olfactory, non-reproductive additional symptoms, for *SOX10* point mutations or deletions. We identified two additional mutations (c.323T>C, [p.Met108Thr] and c.451C>T, [p.Arg151Cys]) (Table 1, cases G and H; see Figure S1C for case G pedigree) affecting aminoacid residues of the HMG domain. Notably,

the individual who carried the p.Met108Thr mutation showed hypoacusis, whereas the absence of hearing impairment was confirmed in the individual carrying the p.Arg151Cys mutation. Arg151 is located close to the hydrophobic core of the protein (Figure 2C, upper panel) whereas the Met108 residue contacts both the hydrophobic core and the DNA target (Figure 2C, lower panel), and is located in the bipartite NLS of SOX10. Its substitution could thus affect SOX10 structure, binding to DNA and/or nuclear localization as the primary defect. Immunocytochemistry experiments were performed to analyze the subcellular location of the mutant proteins. Both p.Met108Thr and p.Arg151Cys missense mutations resulted in partial cytoplasmic relocalization of SOX10 and subnuclear accumulation in foci (Figure 2D). Luciferase assays confirmed the loss-of-function effect of these mutations on the *MITF* promoter, both alone and in the presence of the cofactor PAX3 (Figure S1D).

The seven likely pathogenic mutations found in this study are shown along with the main functional domains of SOX10 (Figure 2E). Additional screening for mutations in the genes involved in KS or congenital non-syndromic forms of hypogonadotropic hypogonadism was performed in the individuals with a *SOX10* mutation (A to H, Table 1) and only yielded a *SEMA3A* heterozygous missense variant (p.Val435Ile) in case E. This variant has been found at similar frequencies in KS individuals and control subjects, although it has been reported to have some deleterious functional consequences *in vitro*.²⁸

These results indicated that *SOX10* mutations are rare in KS individuals without associated signs and confirmed that the clinical association of KS and hearing impairment is more specific. We then used a mouse model to explore the embryonic defect leading to KS as a result of impaired SOX10 function.

SOX10 is expressed in embryonic olfactory ensheathing cells in mice and humans

OECs, peculiar glial cells involved in the growth and guidance of the olfactory axons, have recently been shown to derive from NC in mouse and chick. SOX10 was used as a marker of NC-derived cells in these studies, and its pattern of expression indeed suggested that it is expressed by OECs.²⁹⁻³¹ As OECs are heterogeneous in the pattern of markers they express,³² we fully characterized the SOX10 expression profile during development of the olfactory structures using antibodies directed against SOX10 and several markers of OECs.

In E12.5 mouse embryo, the olfactory, vomeronasal, and terminal nerve fibers can be seen in the mesenchyme surrounding the olfactory epithelium and converge on the migratory mass, a heterogeneous group of cells located in the fronto-nasal mesenchyme beneath the presumptive olfactory bulbs. OECs are detected all along the nerve pathway, where their cytoplasm ensheathes the axon bundles, and begin to invade the olfactory nerve layer (ONL) of the developing olfactory bulb at this stage (Figure 3A). Immunostaining on coronal sections of E12.5 embryo head (Figure 3A) revealed that SOX10 is coexpressed with the OEC marker BLBP/BFABP, whereas it showed mutually exclusive expression with the neuronal marker TUJ1 (β -tubulin). More specifically, SOX10 (nuclear staining, red) and BLBP were coexpressed along the olfactory, vomeronasal, and terminal nerve pathway, in the fronto-nasal mesenchyme, and in the migratory mass below the presumptive olfactory bulb (Figure 3B and data not shown). SOX10-positive cells also expressed the OEC markers P75/NGFR (note that this marker is not specific to OECs and also labels most cells in the nasal mesenchyme) and S100 along the nerve fibers and in the nasal mesenchyme (Figure 3B). By contrast, they did not express P75 and showed variable S100 immunostaining within the migratory mass (Figure 3B).

At E14.5, the olfactory epithelium has developed. SOX10 demonstrated the same pattern of expression in OECs (defined as BLBP+, P75+, S100+, TUJ1- cells) of the nasal mesenchyme and along the nerve pathway (Figure 3C and data not shown). At this stage, the olfactory bulb

had formed from the rostral telencephalon, and a continuous outer layer of SOX10-expressing cells was observed, which corresponds to the ONL (Figure 3D). These cells were BLBP-positive and P75-negative, while only the outermost cells were S100-positive (Figure 3D and E). Apart from OECs, we observed some SOX10 expression in the nasal glands (Figure S2A and B). We also confirmed the presence of a few non-neuronal SOX10-expressing cells in the olfactory epithelium at this stage (Figure S2C), as previously reported.^{29,31}

Finally, we studied SOX10 expression in the peripheral olfactory system of a human embryo at 8 weeks of embryonic development (equivalent stage to mouse E14.5). Immunostaining experiments revealed that SOX10-expressing cells (nuclear, green) were located along the olfactory, vomeronasal, and terminal nerve trajectory (TUJ1 staining, red) in the nasal mesenchyme (Figure 4A), in the migratory mass, and in the olfactory bulb (Figure 4B).

Double staining of SOX10 with the OEC marker S100 along the olfactory nerves confirmed that SOX10-expressing cells are OECs (Figure 4C).

Together, these results confirmed SOX10 expression in OEC during early development of the peripheral olfactory system in mice and humans.

The Sox10 mutant mouse has olfactory ensheathing cell defects

We then used mice bearing a *Sox10* mutation (*Sox10^{lacZ}*)¹⁴ to explore the embryonic defect leading to KS as a result of impaired SOX10 function. We first performed X-Gal staining to detect β -galactosidase (*lacZ* expression) in heterozygous and homozygous mutant E14.5 embryos. The olfactory bulb had formed in both genotypes, but an abnormal colonization of the olfactory bulb by X-Gal-stained (blue) OECs was apparent in homozygotes (Figure 5A). We then compared β -galactosidase expression with various markers by immunohistochemistry on coronal sections. A general overview of the olfactory system showed that the olfactory, vomeronasal, and terminal nerves had formed in the homozygous

mutant embryos, but OECs (β -galactosidase-positive cells) were almost absent in the nasal mesenchyme and along the nerve pathway (Figure 5B and higher magnification in Figure 5C). Only a few OECs were observed in the upper part of the fronto-nasal mesenchyme, under the migratory mass. By contrast, numerous OECs were present in the migratory mass and the ONL, but they appeared to encircle the olfactory bulbs incompletely, forming a thinner, disorganized, and discontinued layer.

We then determined the expression pattern of OEC markers in the absence of SOX10. In the upper part of the fronto-nasal mesenchyme, the marker profile of the few β -galactosidase-positive cells present in the mutant homozygotes differed from that of cells in heterozygotes, with fainter BLBP and absent S100 labeling in most of these cells, while P75 staining was preserved (Figure 5D). In the olfactory bulb ONL, BLBP staining was preserved, and S100 staining (normally found in the outermost cell layer of the ONL) was lost, but most if not all OECs were now P75-positive (Figure 5E).

In summary, these results indicated an almost complete absence of OECs in the nasal mesenchyme of the *Sox10* homozygous mutant embryos, defective colonization of the olfactory bulbs, and abnormal profiles of the remaining OECs in both the nasal mesenchyme and the ONL of the olfactory bulbs.

To explain these defects, we compared the development of OECs in heterozygous and homozygous *Sox10* mutant embryos at an earlier stage. At E12.5, the absence of OECs in most of the nasal mesenchyme was already visible in the mutant homozygotes (Figure S3A). The migratory mass had formed; however, defective colonization of the olfactory bulb anlage by OECs was already detectable on more rostral sections (Figure S3B). To determine if the absence of OECs in the nasal mesenchyme was due to apoptosis of *Sox10*-defective cells, we counted the number of TUNEL-positive cells in the nasal mesenchyme. We did not find a significant difference in the number of apoptotic cells between heterozygous and

homozygous *Sox10*^{lacZ} embryos (Figure S3C), indicating that the defect responsible for the low number of OECs in the homozygous mutant embryos occurred earlier or by a non-apoptotic mechanism.

The OEC defect impacts the development of olfactory, vomeronasal, and terminal nerves and the migration of neuroendocrine GnRH-cells

OECs ensheath the olfactory, vomeronasal, and terminal nerve fibers and also contribute to axonal pathfinding, fasciculation, and defasciculation.³² We thus looked at the trajectory of these nerve fibers in the *Sox10* mutant embryos. TUJ1 staining on E14.5 heads showed that the nerves had formed in mutant homozygotes despite the almost complete absence of OECs in the nasal mesenchyme (Figure 6A). However, axons were abnormally routed; some of them did not target the olfactory bulb and instead contacted axons from the other side, dorsally to the nasal septum (red arrowhead in Figure 6A). Furthermore, as a result of the absence of OECs, axons were not ensheathed along their most ventral trajectory, and their defasciculation could be observed near the nasal septum (red arrow on Figure 6A; defasciculation is also visible on Figure 5D).

Hypogonadism in KS results from the so-called olfacto-genital fetopathological sequence, whereby incomplete embryonic migration of the neuroendocrine GnRH-cells from the nose to the brain arises from the disruption of vomeronasal and terminal nerve fibers.¹² We therefore analyzed the migration of these cells in the *Sox10* mutant embryo. In E14.5 wild-type and heterozygous embryos, most GnRH-cells had already left the extracerebral nerve pathway and were migrating within the two cerebral hemispheres. In homozygous mutant embryos, GnRH-cells were found to accumulate on the vomeronasal and terminal nerve trajectory in the nasal mesenchyme (Figure 6B and data not shown). GnRH-cell count along the nerve pathway confirmed this observation by showing a significantly larger number of GnRH-cell

bodies in the *Sox10*^{laZ} homozygotes than in wild-type and heterozygous embryos (Figure 6C). Although some GnRH-cells did reach the migratory mass in the homozygous mutant embryos, few cells had penetrated into the forebrain en route to the hypothalamic region (Figure 6D). The overall number of GnRH-cells appeared unchanged (estimated 969 in wild-type, 949 in heterozygous and 937 in homozygous mutant embryos). These results show that the *Sox10* homozygous mutant mice, which have a complete lack of SOX10, also undergo a pathological sequence in embryonic development similar to that responsible for KS. The defects we observed in the *Sox10* homozygous mutant mice are schematized in Figure 7.

Discussion

KS is genetically heterogeneous, with various modes of transmission: autosomal recessive, autosomal dominant with incomplete penetrance, X chromosome-linked, and oligogenic. However, only 30% of cases have mutations in any of the nine genes identified thus far.^{13,28} Deafness is one of various non-olfactory, non-reproductive anomalies that are sometimes found together with KS.¹³ Its prevalence in KS individuals has been estimated at approximately 5%.³³ As our understanding of the molecular basis of KS has progressed, deafness has been reported in individuals with *KALI*, *FGFR1*, *FGF8* or *CHD7* mutations, but these cases remain relatively rare.³⁴⁻³⁸ Taking into account the high prevalence of hearing impairment in the general population, the association of KS with deafness may sometimes be coincidental, as was shown in a family where deafness cosegregated neither with KS nor with the *FGF8* mutation.³⁹ Comparatively, the remarkably

large penetrance of deafness in the KS individuals who carry mutations in *SOX10* appears highly significant.

We characterized seven different *SOX10* mutations in persons affected by KS. As in WS, the mutations were found in the heterozygous state together with a dominant mode of inheritance. Some phenotypic variation was observed. In family D, the mother, who also carries the mutation, suffered from deafness and anosmia but had a normal puberty and spontaneous pregnancy. Although mosaicism cannot be excluded, this finding most likely refers to the usual variability of phenotypic expression that is frequently observed in developmental disorders, and in particular in KS or *SOX10*-linked WS. Stochastic events and modifier genes are often proposed to explain at least part of the phenotypic variability. In this respect, the *SEMA3A* sequence variant that was found in case E may influence the expression of the disease.

In the first part of our study, five mutations were found among 13 individuals with the clinical association of KS and deafness, corresponding to a *SOX10* involvement of 38%. This rate may be slightly overestimated, because a few KS individuals with deafness and already known mutations in other genes had been excluded. However, to date *SOX10* stands as the main gene involved in this specific clinical association.

The hearing loss was sensorineural, profound or total in most cases. The audiograms of cases D and E are shown in Figure S4, illustrating a total loss of hearing on the two ears at all frequencies. In contrast, case G showed a mild sensorineural hearing loss (30 dB at 1000 and 2000 Hz on the left ear, 40 dB from 250 to 1000 Hz on the right ear). A striking finding is the high proportion of females among persons carrying *SOX10* mutations in this series (4 females and 3 males), while KS has been estimated to be three to five times more frequent in males than in females.¹³ However, an approximately 1:1 sex ratio was also found in the group

of KSplusdeafness individuals (7 females out of 13 cases), an observation that needs to be confirmed by further studies.

Seven of the 8 *SOX10* sequence variations identified (four missense substitutions, one frameshift mutation, one splice site mutation, and one mutation of the initiation codon, schematically summarized in Figure 2E) result, or are predicted to result, in an altered production or function of SOX10. We performed transactivation assays on two target genes of SOX10, namely *MITF* and *MPZ*.^{19,21} *MITF* was chosen due to its critical role in melanocyte development, whereas *MPZ* was selected based on its known expression in OECs.⁴⁰ Our results do not support a deleterious effect of the p.Arg433Gln mutation. The other 7 mutations were found to alter subcellular localization and/or transactivation capacities, thus validating their deleterious effect. The four missense mutations located in the HMG domain showed a peculiar aspect of relocalization to nuclear bodies, which we had previously observed for amino acid substitutions in close contact with the main hydrophobic core of the HMG domain.²⁴ Whether these foci are a cause or a consequence of the pathogenic effect is still unclear.

The c.2C>T substitution affects the *SOX10* initiation codon. However, immunostaining of cells transfected with cDNA carrying the mutation, using antibodies directed against the SOX10 amino or carboxy terminus, showed that an in-frame protein is produced. The first in-frame ATG codon corresponds to Met90 and, if used, would produce a protein conserving the HMG and transactivation domains, but lacking most of the dimerization domain.⁴¹ As Met90 is the only in-frame methionine more proximal to the two NLS, this hypothesis is consistent with our observation that the protein produced does not relocalize to the cytoplasm.⁴²

Significantly, one of the KS individuals had early graying and deafness and therefore fulfilled the diagnosis criteria for type 2 WS, but no pigmentation defects were reported for the other cases. For some persons, clinical reevaluation was possible after the identification of the *SOX10* mutation. The absence of WS-like pigmentation disturbance was confirmed in case D

and her mother as well as in case B and C, while case E had lately developed a frontal white forelock at approximately age 25 years. No evidence at this point indicates what makes a given *SOX10* mutation a KS- or WS-causing mutation. As a whole, the mutations we identified here were not typically different from the mutations previously identified in WS except for their relative frequency: we found mostly missense mutations of the HMG domain and few truncating mutations in our group of KS individuals (while most *SOX10* mutations are predicted to result in a truncated protein in WS), a finding that must be confirmed in additional studies. In regard to previous clinical findings in WS (very rare reports of anosmia and hypogonadism/cryptorchidism among almost 100 reported persons with different *SOX10* mutations), as well as the recent observation that 88% of WS individuals with a *SOX10* mutation and inner ear morphological abnormalities also have olfactory bulb agenesis, it remains possible that anosmia and hypogonadism have been underestimated in WS. This phenomenon could possibly be explained in part because people usually do not spontaneously complain of anosmia and by the fact that WS is often diagnosed in childhood.

The involvement of *SOX10* in mouse olfactory development was not suspected until recently, when its expression was reported in OECs.²⁹⁻³¹ Here, we showed that *SOX10* plays a major role in the development of these peculiar NC-derived glial cells. In *Sox10*-null mutant embryos, a large part of the peripheral embryonic olfactory system lacked OECs at the embryonic stages analyzed.

Our results showed that the OEC deficiency occurs prior to E12.5 in the mouse. Based on current knowledge about *SOX10* function in other tissues, the defect likely occurs between the emergence of NC cells from the neural tube and their arrival at the olfactory placode. *SOX10* is thought to play a role in sustaining the survival of multipotent NC cells. In the absence of *SOX10*, a dramatic increase in cell death has been reported for vagal NC cells prior to their entry into the foregut as well as in various other NC derivatives.⁴⁶⁻⁵⁰

The remaining OECs were located in the uppermost part of the fronto-nasal mesenchyme, the migratory mass, and the ONL. They had an abnormal expression profile and formed a discontinued and disorganized layer around the olfactory bulbs, indicating that SOX10 is also probably involved in their identity and function at several locations. Several explanations can be proposed as to why some OECs persisted in the mutant mice. One possibility is that not all OECs are SOX10-dependent. Another hypothesis is a partial functional redundancy between SOX10 and another protein of the SOX family. SOX8, which together with SOX10 and SOX9 forms the E subgroup of SOX transcription factors, is a good candidate based on its expression in the ONL during embryogenesis and the described redundancy between SOXE subfamily members in other tissues.⁴³⁻⁴⁵

Despite the markedly reduced number of OECs, the olfactory, vomeronasal, and terminal nerves had formed in the Sox10-null embryos, as had the olfactory bulbs. This finding may be surprising since OECs not only ensheath and fasciculate the nerve fibers, but also extend processes ahead of the pioneer olfactory axons they ensheath, suggesting that they orchestrate their growth and guidance.^{32,51} However, although the olfactory axons were formed and extended some processes toward the migratory mass and the olfactory bulb in the Sox10-null mutant embryos, we found that they were partially misrouted and defasciculated, thus confirming the role of OECs in these processes.

In the mouse, neuroendocrine GnRH-cells begin to leave the epithelium of the olfactory pit at approximately E11.5. They migrate in close association with growing fibers of the vomeronasal and terminal nerves, then penetrate into the rostral forebrain and continue their migration toward the hypothalamus along the terminal nerve or a branch of the vomeronasal nerve.⁵² In E14.5 Sox10-null embryos, the latest embryonic stage we could examine, GnRH-cells accumulated outside the brain, along the vomeronasal and terminal nerve pathway, in the regions devoid of OECs. Few GnRH-cells were seen in the forebrain of these mice, which

could reflect an impaired or delayed migration. To the extent that mice and humans are comparable, it remains to be determined whether the defective GnRH-cell migration in this particular genetic form of KS is primarily due to the absence of OECs on the vomeronasal and terminal nerve trajectory or to the defective structure of these nerves, as previously suggested in other genetic forms.¹²

All the abnormalities we found in the *Sox10* mutant mouse were observed in homozygous embryos, and embryonic lethality of these mice precludes further testing of late olfactory development and fertility. In the normal ONL, OECs contribute to the defasciculation, sorting, and refasciculation of axons and are therefore crucial to olfactory bulb glomeruli formation and the establishment of the olfactory topographic map.³² They are also involved in the renewal of olfactory receptor neurons and their axonal growth throughout life. Accordingly, it is tempting to speculate that the defect in the number and function of OECs in the *Sox10* mutant mouse could have drastic consequences on the maturation of the olfactory bulbs and the ability of olfactory nerve fibers to renew throughout life. The use of a conditional knock-out mouse model to avoid lethality would be of interest to explore the late consequences of the absence of SOX10 in the peripheral olfactory system.

SOX10 mutations have been found in the heterozygous state in both KS and WS individuals. No reproduction defect has been reported in the *Sox10* heterozygous mutant mice, suggesting that both olfaction and GnRH neurosecretion are not strongly affected, although it remains possible that subtle, as yet unrecognized defects in OECs have some functional consequences in adult mice. By contrast, depigmentation and megacolon are found in heterozygous mice as in WS4 individuals. Such differences in sensitivity to genetic diseases between mice and humans are not rare. Alternatively, oligogenicity has been described in KS and mutations in unknown genes may contribute to the disease in some instance. Notably, the inner ear morphological defects associated with *SOX10* mutations are also quite

marked and have a high penetrance in humans, while they are much less evident in the *Sox10* homozygous mouse mutant.^{10,53}

Sox10 is expressed in the melanocytic intermediate cells of the cochlear stria vascularis, which produce the endocochlear electric potential essential to the hearing process.⁵⁴ It is also widely expressed during early inner ear development before being restricted to the cochlear and vestibular ganglia and to supporting cells of the sensory epithelium. In addition to a specific role in glial development of the ganglia, SOX10 has been shown to promote the survival of cochlear progenitors during otocyst formation and differentiation of the organ of Corti.⁵³⁻⁵⁵ In the *Sox10* homozygous mutant mice, the structure and cellular organization of the organ of Corti appear normal, but the cochlear duct is shortened, with no apparent malformation of the vestibule.⁵³ In humans, apart from the cochlear degeneration thought to take place in WS in the absence of intermediate cells of the stria vascularis, a proportion of WS individuals with *SOX10* mutations had an enlarged vestibule, agenesis or hypoplasia of semi-circular canals, and an abnormally shaped cochlea.¹⁰ Together, these results suggest that the high penetrance of deafness among persons who carry *SOX10* mutations is likely the consequence of several different defects in the development of the inner ear.

MRI or CT scans of the temporal bone have been performed in 4 of the 7 individuals.

Abnormal images were not found in case B (not all the temporal bone structures could be analyzed but the semi-circular canals were present and normally shaped). A vestibulo-cochlear dysplasia was reported in case D. The temporal bone CT scan of case C showed a bilateral hypoplasia of the lateral and posterior semi-circular canals as well as a vesicular vestibule on one side and an enlargement of the vestibular aqueduct on the other side. The CT scan of case E showed bilateral enlargement of the vestibule and hypoplasia of the lateral semi-circular canals. Interestingly, the association of semi-circular canal hypoplasia or agenesis with olfactory bulb agenesis and hypogonadotropic hypogonadism is also found in

CHARGE syndrome (Coloboma, Hear defects, Choanal atresia, Retardation, Genital and Ear anomalies) due to mutations in *CHD7*.⁵⁶ Individuals affected by typical CHARGE syndrome are not difficult to distinguish from persons carrying *SOX10* mutations, but in individuals affected by mild forms of CHARGE syndrome, who do not show all the cardinal signs of the disease, this condition may be difficult to differentiate in the absence of a complete clinical description.⁵⁶⁻⁵⁸ From now on, the existence of semi-circular canal hypoplasia or agenesis in a person affected by KS should be considered an indication for both *CHD7* and *SOX10* molecular analyses. Isolated or minor isolated signs of CHARGE syndrome, such as coloboma, heart defects, but also facial asymmetry, middle or external ear malformations, hypoplastic vestibule may point towards *CHD7*, while some depigmentation features or enlarged vestibule may point to a *SOX10* defect.

Our findings implicate NC-derived OECs in the pathogenesis of KS, thus defining the *SOX10*-related genetic form of the disease as a new neurocristopathy. The peripheral olfactory nervous system is unique in that it renews throughout life, a property attributed to the presence of the OECs, which makes them strong candidates for cell-mediated repair of a variety of neural lesions.^{32,51} Despite this major medical relevance, the consequences of the absence or depletion of OECs in the peripheral olfactory system have been poorly characterized. In this respect, the *Sox10* knock-out mouse may prove to be a valuable model. In summary, we characterized a new role of *SOX10* in human pathology, 14 years after the cloning and first implication of this gene in WS. We found *SOX10* loss-of-function mutations in individuals demonstrating the clinical association of KS with hearing impairment and more rarely in individuals demonstrating KS without associated signs. From now on, *SOX10* is the first gene to test for the presence of mutations in the KS plus hearing impairment association. Based on a mouse model study, we suggest that this particular genetic form of KS results from

a previously unreported primary defect affecting OECs during early embryonic development of the peripheral olfactory system.

Supplemental data

Supplemental data include four figures, S1, S2, S3 and S4.

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Web resources

1000 genome project: <http://www.1000genomes.org/>

dbSNP: <http://www.ncbi.nlm.nih.gov/projects/SNP/>

exome variant server: <http://evs.gs.washington.edu/EVS/OMIM:>

<http://www.ncbi.nlm.nih.gov/omim>

Polyphen-2: <http://genetics.bwh.harvard.edu/pph2/>

SIFT:<http://sift.jcvi.org> WS gene mutation database at LOVD:

http://grenada.lumc.nl/LOVD2/WS/home.php?select_db=SOX10

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Figure titles and legends

Figure 1. Functional analysis of the mutant SOX10 proteins

(A) Immunoblotting analysis showing wild-type (wt) or mutant SOX10 proteins using an antibody directed against the carboxyterminal portion of the protein.

(B and C) Luciferase reporter gene analysis. HeLa cells were co-transfected with the wild-type (wt) or mutant SOX10 expression vector and a reporter construct containing the *MITF* promoter (B) or *MPZ* intronic enhancer (C) and known SOX10 cofactors expression vectors, i.e., PAX3 (B) or EGR2 (C). Reporter gene activation is presented as luciferase fold induction relative to the empty vector. Results are the mean \pm s.e.m of at least three different experiments, each performed in duplicate.

(D) Detection and localization of the c.2T>G mutant protein. HeLa cells transfected with wild-type (left panels) or mutant c.2T>G (right panels) SOX10 constructs. Nuclei were counterstained with TO-PRO-3 iodide (blue). Transfected cells were immunostained with anti-SOX10 antibodies (red) directed against either the aminoterminal (N20) or the carboxyterminal (D20) of the protein, as indicated. The merged images are presented below. A higher magnification of SOX10 labeling is also shown in gray (bottom panels).

(E) Luciferase reporter gene analysis. HeLa cells were co-transfected with the wild-type (wt) or mutant c.2T>G SOX10 expression vectors and a reporter construct containing the *MITF* promoter (left panel), *MPZ* intronic enhancer (central panel), or the *GJB1* promoter (right panel) and the PAX3 (left panel) or EGR2 (central and right panels) expression vector. Reporter gene activation is presented as fold induction relative to the empty vector. Results are the mean \pm s.e.m of at least three different experiments, each performed in duplicate.

Figure 2. Subcellular localization of the mutant SOX10 proteins and summary of all SOX10 mutations found in this study

(A) Three-dimensional representation showing the location within the HMG domain of the residues affected by the identified missense mutations. Three-dimensional view of the HMG domain of SOX17 (backbone in red) that forms three α -helices (white ribbons), bound to its DNA target (blue). Upper panel: the four residues that form the hydrophobic core are shown in yellow. Lower panel: the residues corresponding to Phe111 and Trp142 of SOX10, both belonging to the hydrophobic core, are indicated in green and pink, respectively.

(B) Subcellular localization of wild-type and mutant proteins by immunostaining. HeLa cells transfected with wild-type (left panels) or mutant (other panels) SOX10 constructs. Nuclei were counterstained with TO-PRO-3 iodide (blue). Transfected cells were immunostained with anti-SOX10 antibodies (red). Images shown are with the D20 antibody, but similar results were obtained with N20 directed against the amino terminus of the protein. The merged images are presented below. A higher magnification of SOX10 labeling is also shown in gray (bottom panels).

(C) Three-dimensional representation of the location of the HMG domain residues affected by the missense mutations identified in “random” KS individuals, as in (A). Upper panel: the residue corresponding to Arg151, in contact with the hydrophobic core, is indicated in green. Lower panel: the residue corresponding to Met108, in contact with the DNA target, is indicated in green.

(D) Subcellular localization of the Arg151Cys and Met108Thr mutant proteins by immunostaining, as in (B).

(E) Schematic representation of the SOX10 protein and mutations found in this study.

D: dimerization domain; K2: K2 domain; HMG: HMG domain; TA: transactivation domain.

Figure 3. SOX10 expression in the mouse embryonic olfactory system

(A) Doubleimmunolabeling of E12.5 embryo head (coronal sections) forSOX10 (red), the neuronal marker TUJ1 (blue),or the OEC marker BLBP (green). The boxed regions are the migratory mass and the nasal mesenchyme magnified in (B).

(B) Higher magnification of the vomeronasal nerve (left panel), nasal mesenchyme (middle panel), and migratory mass (right panel). Triple labeling forSOX10 (red), the neuronal marker TUJ1 (blue), and anOEC marker (green;BLBP, P75,or S100 as indicated). The dotted lines represent the limit between the olfactory epithelium and the mesenchyme.

(C) Double labeling of E14.5 embryos olfactory epithelium and mesenchyme (coronal sections) forSOX10 (red), the neuronal marker TUJ1 (blue), or the OEC marker BLBP (green).

(D) Triple labeling of E14.5 embryo olfactory bulbs (coronal sections) forSOX10 (red), the neuronal marker TUJ1 (blue), or the OEC marker BLBP or P75 (green) as indicated. The boxed regions in the medial ONL are magnified in (E).

(E) Higher magnification at the level of the medial ONL. Triple labeling forSOX10 (red), the neuronal marker TUJ1 (blue), and an OEC marker (green;BLBP, P75, or S100 as indicated).

M: mesenchyme; MM: migratory mass; OB: olfactory bulb; OE: olfactory epithelium; VNO: vomeronasal organ.

Figure 4. SOX10 expression in the human embryonic olfactory system

(A and B) Immunostaining of the head of a human fetus at 8 weeks of embryonic development (sagittal sections), at the level of the nasal mesenchyme (A) or migratory mass and olfactory bulb (B). Double labeling for SOX10 (green) and the neuronal marker TUJ1 (blue),and counterstaining with DAPI (blue).

(C) Immunostaining showing an olfactory nerve at higher magnification. Double staining for SOX10 (green) and the OEC marker S100 (red) and counterstaining with DAPI.

M: mesenchyme; MM: migratory mass; OB: olfactory bulb; OE: olfactory epithelium.

Figure 5. OEC defect in the E14.5 *Sox10* mutant mice

(A) Whole-mount X-Gal staining of the head in heterozygous (*Sox10*^{lacZ/+}, left panel) and homozygous (*Sox10*^{lacZ/lacZ}, right panels) mutant embryos, facial view. The skin was removed to allow visualization of the olfactory bulbs, indicated by the black arrowheads.

(B) General overview of the olfactory system upon triple labeling for β -galactosidase (green), the neuronal marker TUJ1 (blue), and the OEC marker BLBP (red) in *Sox10* heterozygous (left panel) and homozygous (right panels) mutant embryos.

(C) Higher magnification of the regions boxed in (B), showing the presence of OECs ensheathing the vomeronasal nerve fibers in the heterozygous *Sox10* mutant embryos and the absence of these cells in the homozygous embryos.

(D and E) Higher magnification of the nasal mesenchyme (D) or ONL (E) immunostained for an OEC marker (BLBP, P75, or S100; red), β -galactosidase (green), and the neuronal marker TUJ1 (blue), as indicated in the figure, in *Sox10* heterozygous (left panels) and homozygous (right panels) mutant embryos.

MM: migratory mass; NS: nasal septum; OB: olfactory bulb; OE: olfactory epithelium.

Figure 6. Abnormal nerve fasciculation, axonal pathfinding, and GnRH-cell migration in *Sox10* mutant mice

(A) TUJ1 (upper panel) and β -galactosidase (middle panel) immunostaining and merged image (lower panel) over the nasal septum at a similar level of heterozygous (*Sox10*^{lacZ/+}) and homozygous (*Sox10*^{lacZ/lacZ}) mutant E14.5 embryos, as indicated. The arrow and arrowhead in

the homozygote indicate the defasciculation of sensory axons and their misrouting over the nasal septum, respectively.

(B) GnRH-cells along the vomeronasal nerve trajectory in wild-type (left panel) and homozygous *Sox10* mutant (right panel) E14.5 embryos. The GnRH immunostaining is in red, and DAPI staining is blue. Insets show higher magnifications.

(C) Box plots showing quantification of the number of GnRH-cells along the trajectory of the vomeronasal nerve in wild-type, heterozygous, and homozygous mutant mouse embryos. Each dot corresponds to the number of GnRH-positive cell bodies counted on one side of a section. The top and bottom of each box represent the 25th and 75th percentiles, respectively. The middle line is the median. Statistical significance was tested with Student's ttest. n.s., not significant; *** indicates a P value <0.0001.

(D) DAPI (upper panel) and GnRH (lower panel) staining of sections at the level of the preoptic area in the wild-type (left), heterozygous (center) and homozygous (right) E14.5 embryos.

OB: olfactory bulb; VNO: vomeronasal organ; NS: nasal septum; OE: olfactory epithelium.

Figure 7. Summary of the defects observed in the *Sox10* mutant embryo

(A) Schematization of the cut planes (a and b) drawn in (B) on the head of an E14.5 mouse embryo.

(B) Summary of the defects observed in the *Sox10* homozygous mutant embryos (*Sox10^{lacZ/lacZ}*, right panel) compared to wild-type embryos (left panel). The OECs are shown in green, the nerve fibers in blue, and the GnRH-synthesizing cells in red.

OE: olfactory epithelium; OB: olfactory bulb; POA: preoptic area; VNO: vomeronasal organ.

Table 1. Phenotypes of the KS individuals carrying *SOX10* mutations

| Case | Age (year) | Gender | Occurrence | FSH (UI/L) basal-peak | LH (UI/L) basal-peak | E2 (pg/ml) | T (ng/ml) | Spontaneous puberty | Sense of smell | Olfactory bulb (MRI) | Hearing | Other clinical signs | Mutation (DNA) | Mutation (protein) | In silico evidence | In vitro evidence |
|---|------------|--------|---|-----------------------|----------------------|------------|-----------|---------------------|----------------|----------------------|---------------------|--|---------------------|--------------------|--------------------|-------------------|
| Clinically selected KS individuals | | | | | | | | | | | | | | | | |
| A | 26 | M | familial | 0.2-2.0 | 0.4-2.1 | | <1.7 | no | anosmia | agenesis | unilateral deafness | micropenis, cryptorchidism, white hair (22 years old) | c.2T>G | p.? | pathogenic | pathogenic |
| B | 18 | F | sporadic | 2.8-ND | 0.3-ND | | <10 | no | anosmia | agenesis | prelingual deafness | ptosis | c.331T>G (de novo) | p.Phe111Val | pathogenic | pathogenic |
| C | 39 | F | sporadic | <0.5-ND | 0.87-ND | | 42 | no | anosmia | ND | prelingual deafness | obesity (BMI=51) | c.424T>C | p.Trp142Arg | pathogenic | pathogenic |
| D | 25 | F | familial (anosmia + deafness in mother) | 2.1-7.9 | 0.8-8 | | 20 | delayed | anosmia | agenesis | prelingual deafness | | c.698-1G>C | p.spl? | pathogenic | |
| E | 20 | M | sporadic | | | | | delayed | anosmia | ND | prelingual deafness | cryptorchidism <i>SEMA3A</i> : p.Val435Ile (+/-) | c.1290del (de novo) | p.Ser431Argfs*71 | pathogenic | pathogenic |
| F | 20 | M | sporadic | | | | | | anosmia | ND | normal | intellectual disability, dysmorphism, polymalformation | c.1298G>A | p.Arg433Gln | pathogenic | not pathogenic |
| Random KS individuals | | | | | | | | | | | | | | | | |
| G | 33 | M | familial? (a brother likely anosmic) | 0.8-0.9 | 0.41-0.6 | | 0.23 | no | anosmia | ND | hypoacusis | ptosis | c.323T>C | p.Met108Thr | pathogenic | pathogenic |
| H | 19 | F | sporadic | <1-4.4 | 0.5-8 | | <0.1 | no | anosmia | agenesis | normal | macroscelia | c.451C>T | p.Arg151Cys | pathogenic | pathogenic |

Age is indicated at time of DNA sampling, usually age of diagnosis. The following abbreviations were used: BMI, body mass index; E2, estradiol; FSH, follicle stimulating hormone; LH, luteinizing hormone; MRI, magnetic resonance imaging; ND, not determined; nt, nucleotide; T, testosterone. Normal range: FSH/LH: 2-20 UI/L; E2: >20 pg/mL; T: 2-10 ng/mL.