Genetic causes of optic nerve hypoplasia

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ABSTRACT
Optic nerve hypoplasia (ONH) is the most common congenital optic nerve anomaly and a leading cause of blindness in the USA. Although most cases of ONH occur as isolated cases within their respective families, the advancement in molecular diagnostic technology has made us realise that a substantial fraction of cases has identifiable genetic causes, typically de novo mutations. An increasing number of genes has been reported, mutations of which can cause ONH. Many of the genes involved serve as transcription factors, participating in an intricate multistep process critical to eye development and neurogenesis in the neural retina. This review will discuss the respective genes and mutations, human phenotypes, and animal models that have been created to gain a deeper understanding of the disorders. The identification of the underlying gene and mutation provides an important step in diagnosis, medical care and counselling for the affected individuals and their families. We envision that future research will lead to further disease gene identification, but will also teach us about gene–gene and gene–environment interactions relevant to optic nerve development. How much of the functional impairment of the various forms of ONH is a reflection of altered morphogenesis versus neuronal homeostasis will determine the prospect of therapeutic intervention, with the ultimate goal of improving the quality of life of the individuals affected with ONH.

INTRODUCTION
The optic nerve, which is composed of retinal ganglion cell axons and supporting glial cells, transmits visual information from the retina to the brain. Optic nerve hypoplasia (ONH) is a non-progressive congenital abnormality characterised by underdevelopment of the optic nerve. Typically, the anomalous optic nerve head appears pale and small, with a pale or pigmented peripapillary halo or double-ringed sign that is visible with ophthalmoscopy. ONH typically occurs bilaterally (80% of all cases). The severity of visual impairment varies between cases. Some eyes with ONH have no light perception, while others have acceptable levels of functional vision. Severe bilateral ONH can be diagnosed within the first few months of life. Affected patients typically manifest early-onset sensory nystagmus (involuntary, rapid eye movements), followed by strabismus (inability to align the eyes simultaneously) often related to the visual impairment due to defective communication between eye and brain. Individuals with unilateral ONH are often diagnosed at an older age, compared with those with bilateral ONH, due to preserved vision in the one normal eye.

The first recorded case of ONH was documented in 1884 in a small child by Magnus.1 Magnus noticed a small, pale optic nerve in a boy with nystagmus and a high degree of amblyopia. However, some researchers considered Briere’s report to be the first case in 1877.2 He described a 7-year-old girl who was born blind, with no optic disc, but normal choroid and central retinal vessels. Some commentators have suggested, however, that the presence of retinal vessels must imply an entrance and exit for them, and thus, given the instrumentation of the period, the disc(s) may have been missed. The first schematic illustration of optic disc appearance of ONH was done by Schwarz in 1915.3 To date, ONH is the second leading cause of blindness and is the most common congenital optic nerve anomaly in the USA.4 The reported prevalences of ONH range from 2 to 17.3 per 100,000,5 with a considerable rise in prevalence starting in the 1980s. The cause of this increase remains disputed; however, it may be due to heightened physician awareness and improved observation and thus diagnosis of the disorder. Given that most ONH cases are isolated within their respective families, research into the causal factors of ONH has focused on environmental effects. Many environmental risk factors for ONH have been reported, including maternal alcohol abuse during pregnancy, young maternal age, primiparity, maternal use of recreational drugs, anticonvulsants or antidepressants.6 However, familial cases of ONH also exist,7 8 suggesting genetic aetiologies. With the recent advancement in molecular diagnostic technology, mutations in an increasing number of genes have been reported to cause ONH.

Although rare, the description of ONH may sometimes be confused with optic atrophy,9 especially when serial examinations have not been done, and the examiner cannot appreciate whether there has been a progression or degeneration over time. Optic atrophy is a condition in which the optic nerve tissues had developed normally and either are damaged and/or degenerate secondarily.

Although ONH can occur as an isolated finding, it is seen much more frequently as part of a syndrome. ONH is usually accompanied by other anterior segmental defects of the eye (MIM 607108),10 structural abnormalities of the brain, hypopituitarism (MIM 184429),11 developmental delay/intellectual disability, and autism spectrum disorders.12 This review will focus on the genetic mutations that are currently known to cause ONH. Herein, we will define ONH broadly as any optic disc that shows decreased neuronal area and small optic nerves, congenitally. The reviews of the more narrowly defined septo-optic dysplasia (SOD), also known as de Morsier syndrome, can be found elsewhere.6 11

To date, variants in genes involved in transcription regulation, chromatin remodelling,
α-dystroglycan glycosylation, cytoskeleton and scaffolding protein, RNA splicing, and the MAP kinase signalling pathway, have been associated with ONH. In the first part of the review, we will introduce the basic functions of the genes involved, the clinical features of the affected individuals and the animal models used to study the respective disorders. In the second part of the review, we will delineate the common developmental pathway shared by some of the key transcription factors in eye development.

Transcription factors

HESX1

HESX1 homeobox 1 (HESX1) encodes a homeobox protein, which plays an important role in normal forebrain development and the early determination and differentiation of the pituitary gland in murine models. Dattani et al reported the first genetic mutation in HESX1 (homozygous p.R160C) in a familial case (siblings from a consanguineous family) of SOD. Subsequent novel heterozygous HESX1 mutations were identified in patients with ONH, one of whom had intellectual disability. In the study of Dattani et al, remaining controversial, subsequent novel heterozygous HESX1 mutations were identified in patients with ONH diagnosed with combined pituitary hormone deficiency or SOD. In addition, HESX1 constitutive knockout mice (Hesx1−/−) show substantial perinatal and postnatal lethality and display variable anterior central nervous system (CNS) defects and pituitary dysplasia. Anophthalmia, microphthalmia, defective olfactory development, and abnormalities in the corpus callosum, hippocampal commissures and septum pellucidum were described in Hesx1−/− mice, while the milder phenotype was found at very low frequency in Hesx1+/− mice (1%).

PAX6

Paired box gene 6 (PAX6) encodes a transcription factor that is involved in eye morphogenesis. It was first implicated in human aniridia, but later found to be involved in other eye anomalies, including microphthalmia, cataracts, foveal hypoplasia and ONH (MIM 607108). Although ONH is not common in individuals with PAX6 mutations, Azuma et al reported heterozygous PAX6 mutations (p.Q205X, p.S292I and p.M381V) in three individuals with ONH, one of whom had intellectual disability. In the same study, they also identified heterozygous PAX6 mutations (p.Q378R and p.T391A) in two patients with optic nerve agenesis. Hingorani et al summarised ophthalmologic evaluations in 43 individuals with variable anomalies of the iris, carrying heterozygous mutations in PAX6. They reported nystagmus and foveal hypoplasia as the most common clinical findings, present in 41 and 37 individuals, respectively. In comparison, ONH was found in 10 individuals in this cohort, most of whom carried frameshift mutations. Given that PAX6 is also a master regulator of neurogenesis, abnormalities other than ocular defects have also been reported, including developmental delay, cognitive impairment, autism, epilepsy and structural brain abnormalities of white matter, mostly the corpus callosum.

To date, more than 40 PAX6 mutant mouse models are available (Mouse Genome Informatics (http://www.informatics.jax.org/)), most of which have phenotypes affecting the eyes/vision, the nervous system, craniofacial development, and/or mortality. One of the first characterised PAX6 mouse models is the Sey/Sey (Small eye) mouse. Sey/Sey pups are born without both eyes and nasal cavities, manifesting a high prevalence of perinatal mortality due to breathing problems, associated with the absence of the nose. Later studies showed the homozygous knockout animals also had forebrain defects. Heterozygous Sey/+ mice have milder phenotypes. These mice display microphthalmia, frequently with cataracts, which manifest within a few weeks of age, retinal abnormalities and partial or complete absence of the iris. The morphogenesis of the optic nerve is also affected in Sey/+ mice. The cross sectional area and the myelinated fibre counts of optic nerves are decreased significantly in heterozygous mice, finding more severe in male than female mice; the mechanism is unclear.

Similar to the mouse, a Pax6−/− mutant rat model, rSey2 (rat Small eye), shows that homoygotes (rSey/rSey) do not develop lens and nasal placodes and are perinatal lethal, while heterozygotes (rSey/r+) have small eyes. Later in life, heterozygotes have impaired prepulse inhibition, altered social interaction and low performance in fear-conditioned memory tests, leading the authors to suggest an autism-like phenotype.

The pleiotropic role of PAX6 during development can be appreciated through the detailed investigation of several Pax6 mutant mouse models. Pax6 consists of three functional domains: the paired domain (PD), the homeodomain (HD) and the transactivating proline-serine-threonine domain. Pax6 mutations in different functional domains yield different phenotypes. For example, Haubst et al compared the Pax6(Noe) mutants (HD mutation) and Pax6(4Ne) mutants (PD mutation), and found out that while the former had only subtle effects on forebrain development, the latter had severe impairment of neurogenesis, cell proliferation and patterning in the developing forebrain. The molecular consequences of Pax6local and Pax6ocal mutants, which carry point mutations in two different subdomains within the PD domain, also differed greatly. While Pax6ocal mutants increased the number of mitoses in the developing cerebral cortex, Pax6ocal mutants showed the opposite. Moreover, neurogenesis was only affected in Pax6ocal, but not Pax6ocal mutants. With more than 400 unique human PAX6 variants reported to date (Leiden Open Variation Database (http://lsdb. hgu.mrc.ac.uk/home.php?select_db=PAX6)), and considering the diverse clinical phenotypes in human patients, the specific mutation needs to be considered to provide accurate diagnosis, counselling and management.

SOX2

SRY (sex determining region Y)-box 2 (SOX2) encodes a transcription factor essential for embryonic development of multiple organs, including brain and eyes. Heterozygous SOX2 mutations are the most common genetic cause for bilateral anophthalmia and severe microphthalmia. They account for 10%–20% of all patients with microphthalmia/anophthalmia. Among 235 individuals with congenital hypothalamic-pituitary disorders, Kelberman et al reported two patients (patient 7; p.G130A and patient 8; p.A191T) with bilateral ONH (case 2; p.N63fs101X) with unilateral ONH

and cataract, atypical coloboma and esotropia in the other eye. The patient had a thin corpus callosum. Ragge et al.\textsuperscript{46} reported two patients (case 6; p.L314fsX46 and case 7; p.G236fsX5) with bilateral anophthalmia, attenuated optic nerves without visible chiasm, global developmental delay and malformation of the hippocampus. Jayakody et al.\textsuperscript{47} reported a patient (patient 1; p.L97P) with bilateral microphthalmia, left sclerocornea and aphakia. MRI data showed right microphthalmos with a prosthesis in situ, a colobomatous left globe, and small optic nerves and chiasm.

Homozygous knockout of Sox2 causes embryonal lethality in mice, with the products of conception dying shortly after implantation. Heterozygous knockout mice appear normal, except for decreased male fertility.\textsuperscript{48} Although heterozygous knockout mice do not seem to recapitulate the human eye phenotypes, Sox2 hypomorphic/null compound heterozygous adult mice (expressing 40% of Sox2 compared with wild type) show hypoplasia of optic nerves and chiasmata, with eye phenotypes ranging from mild bilateral microphthalmia to severe anophthalmia,\textsuperscript{49} much like heterozygous patients. The authors argued that the striking similarity between heterozygous patients and compound heterozygous mouse models could be explained by species differences; alternatively, it has been suggested that humans with Sox2-related eye phenotypes may indeed be compound heterozygotes, carrying a null allele and a hypomorphic allele that brings the total functional level of SOX2 down to a range that results in phenotypic expression.\textsuperscript{50}

\section*{NR2F1}

Nuclear receptor subfamily 2 group F member 1 (NR2F1) encodes a conserved orphan nuclear receptor, which plays a critical role in cortical patterning, axon guidance, neurogenesis, and eye and optic nerve development.\textsuperscript{51} We and others identified heterozygous NR2F1 mutations in individuals manifesting global developmental delay/intellectual disability and ONH/optic atrophy (Bosch-Boonstra-Schaaf Optic Atrophy syndrome, BBSOAS, MIM 615722).\textsuperscript{39, 41, 42} The phenotypic spectrum of BBSOAS included hyptonia, seizures, autism, oromotor dysfunction, thinning of the corpus callosum and hearing defects.\textsuperscript{43} To date, pathogenic NR2F1 variants have been reported as missense, translation initiation variants, frameshifting indels and whole gene deletions. The missense mutations were enriched in the two functional domains of NR2F1: the DNA-binding domain (DBD) and the ligand-binding domain. Notably, patients with missense mutations in the DBD generally had more severe phenotypes compared with those carrying a heterozygous whole gene deletion. Given that NR2F1 binds to DNA in the form of dimers,\textsuperscript{44} a dominant negative effect may be the cause for this phenomenon. A genotype-phenotype correlation was proposed: patients with severe clinical phenotypes carry NR2F1 variants that tend to have almost completely blunted transcriptional activity, as assessed by in vitro luciferase assay.\textsuperscript{45}

Homozygous knockout Nr2f1\textsuperscript{−/−} mice die within the first 2 days after birth due to starvation and dehydration. Defects in the formation of the glosohypophysial nerve in Nr2f1\textsuperscript{−/−} pups have been proposed as the cause,\textsuperscript{45} and this observation may relate to the oromotor dysfunction seen in patients with BBSOAS. Abnormal development of the corpus callosum and the hippocampal commissure also is seen in embryonic Nr2f1\textsuperscript{−/−} brains.\textsuperscript{46} Eye-specific double knockout of Nr2f1 and Nr2f2, a paralogue of Nr2f1, leads to ocular colobomata, microphthalmia and abnormal optic cups. The expression of several regulatory genes critical for early optic vesicle development, such as Rx6 and Otx2, is altered in double knockout mice, resulting in abnormal differentiation of the progenitor cells at the optic vesicle.\textsuperscript{40} Although all the patients with BBSOAS identified so far carry heterozygous NR2F1 variants, a heterozygous knockout (Nr2f1\textsuperscript{+/-}) mouse model has not been reported.

\section*{OTX2}

Orthodenticle homebox 2 (OTX2) encodes a HD-containing transcription factor that plays an important role in forebrain and eye development.\textsuperscript{47} Heterozygous mutations in OTX2 account for 2%-8% of patients with microphthalmia/anophthalmia,\textsuperscript{48, 49} making them the second most common genetic cause of microphthalmia/anophthalmia (after SOX2). Using a candidate gene approach, Ragge et al first reported OTX2 variants in 11 affected individuals from eight families in a cohort diagnosed with ocular malformation spectrum defects. All of these eight probands had microphthalmia/anophthalmia. The optic nerves and chiasm were absent or reduced in four out of the six patients who had MRI, CT or ultrasound data available for review.\textsuperscript{50} Later studies showed that 35% of the patients with OTX2 mutations had ONH, while other eye defects such as coloboma and retinal dystrophies were less common.\textsuperscript{49} In addition to ocular abnormalities, the phenotypic spectrum of OTX2 mutations included structural and functional abnormalities of the pituitary, global developmental delay, autism, attention-deficit disorder, feeding difficulties, seizures, microcephaly and other structural brain anomalies, affecting the corpus callosum and hippocampus.\textsuperscript{49, 51} Incomplete penetrance and variable expressivity have been reported for OTX2 mutations. In the original study, three out of six families with loss-of-function mutations inherited their variants from a phenotypically normal parent (two parents were constitutive mutation carriers, and one was gonosomal mosaic). Variable expressivity has been documented extensively, including individuals sharing the same variant, even among siblings.\textsuperscript{52} Homozygous knockout mice (Ot2x\textsuperscript{−/−}) are embryonically lethal and display abnormal development of the forebrain, midbrain and rostral hindbrain.\textsuperscript{45} Heterozygous mice show variable phenotypes, including anencephaly, holoprosencephaly, microphthalmia/anophthalmia, micrognathia/agnathia, and short nose.\textsuperscript{53}

\section*{VAX1}

Ventral anterior homeobox 1 (VAX1) encodes a homeobox transcription factor, which plays an important role in the forebrain and visual system.\textsuperscript{54} Slavotinek et al.\textsuperscript{45} identified a homozygous missense VAX1 variant (p.R152S) in a screen of 70 individuals with microphthalmia/anophthalmia. The affected male patient was born to phenotypically normal, consanguineous parents, who were confirmed as heterozygous carriers of the variant. In addition to microphthalmia, other clinical features included ONH, global developmental delay, hippocampal malformations, agenesis of the pineal gland and corpus callosum, and cleft lip/palate. Homozygous knockout Vax1\textsuperscript{−/−} mice are perinatally lethal, and the observed phenotypes bear remarkable similarity to the human patient: optic nerve dysgenesis, coloboma and abnormalities in brain structures (corpus callosum, hippocampus and anterior commissure).\textsuperscript{55} Heterozygous knockout Vax1\textsuperscript{+/-} mice appear normal, except for subfertility.\textsuperscript{55}

\section*{ATOH7}

Atonal homologue BHLH transcription factor 7 (ATOH7) encodes a basic helix-loop-helix transcription factor, which is critical for retinal ganglion cell and optic nerve formation.\textsuperscript{56} Khan
et al reported two homozygous ATOH7 variants (one missense and the other a frameshift variant) in two consanguineous families with isolated microphthalmia. Two affected siblings from the family with frameshift mutations also displayed ONH, corneal opacity and retinal detachment. Co-segregation of this mutation with the clinical phenotype was confirmed in the family. The finding was supported by two genome-wide association studies, which identified SNP (rs3858145, $p=3.4 \times 10^{-10}$) and SNP (rs1900004, $p=2.67 \times 10^{-13}$) within 20 kb and 10 kb of ATOH7, respectively. However, pathogenic ATOH7 variants were not discovered in an investigation of 34 patients with ONH and 76 patients with microphthalmia/anophthalmia/coloboma. Homozygous knockout $Atoh7^{−/−}$ mice are viable and fertile, and appear normal externally. Although they tend to have normalized eyes, there is an 80%–95% reduction in the number of retinal ganglion cells, with very thin or absent optic nerves.

Chromatin remodelling

KANSL1 (17q21.31 microdeletion)

KAT8 regulatory NSL complex subunit 1 (KANSL1) encodes a nuclear protein that is a key component of a histone acetyltransferase complex. KANSL1 is one of the five known protein-coding genes in the 17q21.31 microdeletion syndrome locus (MIM 610443). It was later found that haploinsufficiency of KANSL1 was sufficient to cause the phenotypes of 17q21.31 microdeletion syndrome, also known as Koolen-de Vries syndrome (KdVS). KdVS is a multisystem disorder, characterised by developmental delay/intellectual disability, hypotonia and characteristic facial dysmorphism. Additional features include oily skin and facial cafe-au-lait spots, hypogonadism, skeletal abnormalities and ectodermal anomalies. Zollino et al reported another deletion patient (patient 28) with hypoplastic ocular globe, unilateral ONH and microphthalmia. Zollino et al also shared brain malformations, including hydrocephalus, cerebellar hypoplasia and cleft palate. In a forward genetic screen for axon guidance defects in mice, it was found that hypomorphic loss-of-function $Ispd^{−/−}$ (leucine to premature stop codon) leads to neonatal lethality, abnormal axon guidance in the hindbrain and abnormal fission of the funiculus of the spinal cord. However, eye-related phenotypes were not reported in that mouse study.

Cytoskeleton and scaffolding protein

TUBA8

Tubulin alpha 8 (TUBA8) encodes a member of the $\alpha$-tubulin protein family. $\alpha$-Tubulins and $\beta$-tubulins heterodimerise and then assemble to form microtubules. Abdollahi et al reported homozygous indel in an intron of TUBA8 in three affected members of a consanguineous Pakistani family. The same homozygous deletion was found in an affected child from a second Pakistani family. The 14 bp deletion lies 11 bp upstream of the exon 2 splice junction. The deletion was predicted to interfere with correct splicing, which was verified by the reverse transcription PCR of lymphoblastoid cell line RNA from the patient. All four affected children have ONH with polymicrogyria, seizures, thin or absent corpus callosum and brainstem abnormalities. Surprisingly, expression of $Tubα8$ is relatively low in developing mouse and human brains, even though the clinical phenotypes mainly present as brain malformations.

CASK

Calcium/calmodulin-dependent serine protein kinase (CASK) encodes a member of the membrane-associated guanylate kinase (MAGUK) protein family, which consists of scaffolding proteins associated with intercellular junctions. Heterozygous or hemizygous mutations in the X-linked CASK gene in patients lead to microcephaly with pontine and cerebellar hypoplasia (MICPCH, MIM 300749). The phenotypic spectrum of CASK mutations includes autistic traits, developmental delay/intellectual disability, axial hypotonia and/or peripheral hypertonia, movement and behavioural disorders, and seizures. Although ONH is relatively low in developing mouse and human brains, even though the clinical phenotypes mainly present as brain malformations. Currently, there is no mouse model for $Cask^{−/}$ mutations.

ISPD

Isoprenoid synthase domain-containing protein (ISPD) encodes a protein that is required for proper $\alpha$-dystroglycan modification. Similar to B3GALNT2, ISPD mutations were identified in patients diagnosed with congenital muscular dystrophy-dystroglycanopathy with brain and eye anomalies, in this case type A7 (MDDGA7, MIM 614643). Willer et al identified seven individuals, including a pair of siblings, carrying homozygous or compound heterozygous mutations in ISPD. Two of the seven patients had ONH. One of the affected siblings was diagnosed with bilateral ONH, and the other had bilateral microphthalmia (status of optic nerves not mentioned in the study). Roscioli et al identified two individuals with MDDGA7, one with a homozygous and the other with compound heterozygous mutations in ISPD. However, instead of being described with ONH, they were diagnosed with optic atrophy. The four individuals also shared brain malformations, including hydrocephalus, cerebellar hypoplasia and cleft palate. In a forward genetic screen for axon guidance defects in mice, it was found that hypomorphic loss-of-function $Ispd^{−/−}$ (leucine to premature stop codon) leads to neonatal lethality, abnormal axon guidance in the hindbrain and abnormal fission of the funiculus of the spinal cord. However, eye-related phenotypes were not reported in that mouse study.

α-Dystroglycan glycosylation

B3GALNT2

Beta-1,3-N-Acetylgalactosaminyltransferase 2 (B3GALNT2) encodes a glycosyltransferase that helps synthesize $\alpha$-dystroglycan, which is an integral component of the dystrophin glycoprotein complex. Defects in glycosylation reduce the binding ability of $\alpha$-dystroglycan to extracellular matrix ligands, causing a dystroglycanopathy. Stevens et al reported seven individuals with congenital muscular dystrophy-dystroglycanopathy, and a phenotype defined as ‘brain and eye anomalies type A11’ (MDDGA11, MIM 615181). These individuals carried either homozygous or compound heterozygous mutations in B3GALNT2. Two of the affected individuals had ONH. Currently, there is no murine model for $B3galnt2$ loss-of-function studies; however, knockdown of $b3galnt2$ in zebrafish showed retinal degeneration, impaired motility and brain abnormalities.
or malformation of the brain midline. The study suggested that Cask regulates oxidative metabolism in the brain, and the rate of glucose oxidation was reduced by 20% in the brain of Cask−/− mice compared with wild-type littermates.

RNA splicing
PUF60
Poly(U) binding splicing factor 60 (PUF60) encodes a ribonucleo-protein-binding protein, which is involved in pre-mRNA splicing and transcriptional regulation. Dauber et al. identified the first patient with a de novo heterozygous variant, p.H169Y in PUF60. El Chehadeh et al. reported another five patients with de novo heterozygous variants in PUF60. All six patients identified to date manifest the same facial gestalt as seen in individuals with 8q24.3 microdeletion syndrome, also known as Verheij syndrome (MIM 615583). Other shared clinical features include bilateral ONH (2/6), developmental delay (6/6), cardiac defects (5/6), short stature (5/6), joint laxity and/or dislocation (5/6), vertebral anomalies (3/6) and feeding difficulties (3/6). Currently, there is no mouse model for Puf60 mutations.

MAPK signalling pathway
BRAF
B-Raf proto-oncogene (BRAF) encodes a serine/threonine-protein kinase that plays a role in regulating the MAP kinase signalling pathway. Mutations in BRAF are one of the causes of cardio-facio-cutaneous (CFC) syndrome (MIM 115150). Armour and Allison reported 38 individuals with CFC, 32 of which had autosomal dominant variants in BRAF. The remaining six individuals carried either MEK1 or MEK2 variants. Among the patients with BRAF mutations, ONH/dysplasia was diagnosed in 9 out of the 20 individuals who had provided ophthalmological assessments for review. Meanwhile, two out of six individuals carrying MEK1 or MEK2 variants had such diagnoses. MEK1, MEK2 and BRAF are integral parts of the MAP kinase pathway. Although the signs of CFC overlap substantially with Noonan syndrome, it was estimated that only 2% (3/139) of patients with Noonan syndrome had ONH. As most BRAF mutations in CFC are predicted to be gain of function, multiple corresponding mouse models have been generated. and BRAF−/−;L337V mouse models, both carrying an allele expressing constitutively active Braf protein, recapitulate certain patient phenotypes, including small body size, facial dysmorphism, cardiomegaly and eye abnormalities (cataacts).

DISCUSSION
Molecular network of transcription factors in eye development
Eye morphogenesis in vertebrates is an intricate multistep process, including the formation of the eye pit, optic vesicle, optic cup, lens and neurogenesis in the neural retina (NR) (figure 1). Many key transcription factors participate in these sequential events to ensure the proper formation and maturation of the eye. While most knowledge described here is derived from murine studies, a high level of conservation exists for the sequence and function of these key transcription factors in eye development between human and murine models, so the described processes carry significance in humans as well. In mice, the evagination of optic pits leads to the formation of the early optic vesicle at E9.5. Then, the invagination of optic vesicle at E10.5 results in the formation of a dual-layered optic cup, which consists of three main domains: the NR, retinal pigment epithelium and optic stalk (OS). The OS later becomes the optic nerve when the axons of the retinal ganglion cells fill the cavity of the stalk and complete the closure of the choroid fissure (figure 1).

The boundary between OS and NR is established at the optic disc, which serves an entrance for the blood vessels to the eye and as an exit for the axons of retinal ganglion cells from the eye. Pax6, an NR marker, and Pax2, a ventral OS marker, antagonise each other to establish the sharp boundary (figure 1). Reciprocal expansion of Pax2 and Pax6 gene expressions is seen in the corresponding loss-of-function mutant mice. Disruption of this boundary causes defects in the optic nerve, OS, retina, lens and optic fissure closure. Vax1 and Vax2 are also involved in the boundary formation by inhibiting Pax6 expression, given that the expression of Pax6 and Pax2 is rapidly acquired and lost from the OS in Vax1 and Vax2 double knockouts at E10.86

Another example of boundary formation defects is reported in Nr2f1 and Nr2f2 double knockout mice. Increased expression of Pax6 in NR and decreased expression of Pax2 in ventral OS, accompanied by reduced expression of Vax1 in the OS, shift the NR-OS boundary proximally, eventually leading to abnormal differentiation of the OS. These data suggested that Nr2f1 and Nr2f2 are key regulators that balance the expression of Pax6 and Pax2 during the early development of the optic cup,
However, the eye phenotypes in the individuals with heterozygous PAX6 mutations are generally more severe than those with heterogeneous NR2F1 mutations. This could be explained by the functional redundancy between NR2F1 and NR2F2, given that eye-specific double knockout of Nr2f1 and Nr2f2 in mice leads to major eye abnormalities but does not do so in eye-specific single knockout of Nr2f1.30

Two transcription factors synergistically regulating lens development are Pax6 and Sox2, again indicating the intricate interaction between transcription factors during eye development.97,98 Pax6 and Sox2 form a co-DNA-binding complex, which activates cooperatively the lens-specific enhancer element DC5 in order to differentiate embryonic ectoderm into lens ectoderm. In contrast to the synergistic relationship, the same two transcription factors antagonise each other in the developing optic cup to specify the multipotent optic cup progenitors towards a neurogenic fate (Sox2) or a non-neurogenic fate (Pax6).99 This suggests that the interplay between transcription factors may be highly cell-type specific and developmental stage specific during eye development.

Adding to the complexity of eye development is the fact that the aforementioned transcription factors are also involved in the morphogenesis of the forebrain and other brain regions, such as the midline brain, hypothalamus and pituitary gland. This involvement may explain why ONH is more commonly a part of a syndrome involving other structural brain anomalies, rather than an isolated finding. Similarly, most mutant mouse models manifest more extensive systemic defects, in addition to isolated ONH. To date, multiple genes are implicated in ONH; however, most of them are associated with other eye anomalies and/or brain structural defects. Nevertheless, the possibility that one single gene mutation leads to isolated ONH should not be discounted.

CONCLUSION
With ONH being the second most common cause of congenital visual impairment,100 the investigation of the causes and risk factors of ONH is of great importance. Although previous studies had mostly attributed ONH to the prenatal environment, the identification of an increasing number of genetic causes of ONH suggests multiple aetiological mechanisms, including gene–environment interactions, as well as monogenic causes with high penetrance. The consideration of gene–environment interactions and potential genetic modifiers is based, in part, on the presence of variable expressivity of related phenotypes among individuals carrying the same genetic variants.

Eye morphogenesis in mammalian species is an intricate process. Many key transcription factors relevant for eye development also play roles in the morphogenesis of forebrain. This interplay causes more complex clinical phenotypes, many of which involve cognitive deficits and behavioural alterations. With the advancement and clinical availability of genome-wide sequencing technology, we anticipate that more genes will be implicated in the aetiology of ONH. In some cases, the modes of inheritance may go well beyond Mendelian genetics, for example, digenic or oligogenic inheritance. These steps will lead to an increased molecular diagnostic rate for individuals with ONH per se. Additional research will investigate whether the functional consequences associated with the respective disorders are all due to structural deficits from altered neurodevelopment, or whether some function(s) could be regained, with therapeutic intervention, even started later in life.

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A key finding of the study is that the NR2F1 gene is associated with the broad phenotype of Bosch-Boonstra-Schaaf optic atrophy syndrome: 20 new cases and potential genotype-phenotype correlations. Genet Med 2016;18:1143–50.


