Meis1 coordinates a network of genes implicated in eye development and microphthalmia

Séverine Marcos1,2, Monica González-Lázaro3, Leonardo Beccari1,2, Laura Carramolino3, Maria Jesús Martín-Bermejo1,2, Oana Amarie4, Daniel Mateos-San Martín2, Carlos Torroja5, Ozren Bogdanović6,7, Roisin Doohan3, Oliver Puk4, Martin Hrabě de Angelis4, Jochen Graw4, Jose Luis Gomez-Skarmeta6, Fernando Casares6, Miguel Torres3,* and Paola Bovolenta1,2,*

ABSTRACT
Microphthalmos is a rare congenital anomaly characterized by reduced eye size and visual deficits of variable degree. Sporadic and hereditary microphthalmos have been associated with heterozygous mutations in genes fundamental for eye development. Yet, many cases are idiopathic or await the identification of molecular causes. Here we show that haploinsufficiency of Meis1, which encodes a transcription factor with evolutionarily conserved expression in the embryonic trunk, brain and sensory organs, including the eye, causes microphthalmic traits and visual impairment in adult mice. By combining analysis of Meis1 loss-of-function and conditional Meis1 functional rescue with ChIP-seq and RNA-seq approaches we show that, in contrast to its preferential association with Hox-Pbx BSs in the trunk, Meis1 binds to Hox/Pbx-independent sites during optic cup development. In the eye primordium, Meis1 coordinates, in a dose-dependent manner, retinal proliferation and differentiation by regulating genes responsible for human microphthalmia and components of the Notch signaling pathway. In addition, Meis1 is required for eye patterning by controlling a set of eye territory-specific transcription factors, so that in Meis1−/− embryos boundaries among the different eye territories are shifted or blurred. We propose that Meis1 is at the core of a genetic network implicated in eye patterning/microphthalmia, and represents an additional candidate for syndromic cases of these ocular malformations.

KEY WORDS: Developmental disorders, Notch signaling, Patterning, TALE transcription factors, Microphthalmia, Mouse

INTRODUCTION
Eye formation initiates with the specification of the retinal field in the anterior neural plate followed by morphogenetic rearrangement of retinal progenitors to form the optic vesicles. Subsequent interaction of the optic neuroepithelium with the surrounding tissue generates the optic cup, which is concomitantly patterned along its three main axes: proximodistal, nasotemporal and dorsoventral. This results in the formation of the neural retina, retinal pigment epithelium (RPE), optic stalk and lens (Martínez-Morales et al., 2004), the proliferation and differentiation of which generate a mature eye (Esteve and Bovolenta, 2006). Disruption of any of these events leads to ocular malformations, including anophthalmia (complete absence of the ocular globe) or microphthalmia (significant reduction of the globe axial length), which, in turn, cause severe visual deficits that, for microphthalmia, account for up to 11% of infant blindness in developed countries (Bardakjian and Schneider, 2011).

Cases of anophthalmia and microphthalmia have been associated with homozygous and heterozygous mutations in genes at the core of forebrain regulatory networks (Beccari et al., 2013), such as the transcription factors (TFs) SOX2 (Fantes et al., 2003), OTX2 (Ragge et al., 2005), PAX6 (Glaser et al., 1994), VSX2 (CHX10) (Ferda Percin et al., 2000), RAX (Veronina et al., 2004), FOXE3 (Reis et al., 2010) and perhaps SIX6 (Gallardo et al., 2004); in key components of cell to cell communication, including SHH (Schimmelt et al., 2003) and BMP4 (Reis et al., 2011); or in genes involved in retinal progenitor proliferation and survival such as STRA6 (Pasutto et al., 2007; White et al., 2008), BCO2R (Ng et al., 2004), HCCS (Indrieri et al., 2013; Morleo et al., 2005) and SMOC1 (Abouzeid et al., 2011; Okada et al., 2011). Yet, only a minor proportion of patients receive an accurate molecular diagnosis of the pathogenesis of their ocular malformation (Bardakjian and Schneider, 2011; Williamson and FitzPatrick, 2014), indicating that additional causative genes need to be identified. Given that anophthalmia and microphthalmia frequently occur in association with other birth defects, most commonly involving anomalies of the limbs, face, ears and skeletal muscle system (Slavotínek, 2011), genes implicated in multiple aspects of embryonic development, such as Meis1, are good candidates to be explored.

Meis1, its Drosophila homolog homothorax (hth) and the related Meis2 and Meis3, belong to a subfamily of TALE (three amino acid loop extension) homeomain-containing TFs (Longobardi et al., 2014). Meis proteins form stable heteromorphic complexes with other transcriptional regulators, enhancing their affinity and specificity of binding to DNA sites in the target gene locus (Penkov et al., 2013; Slattery et al., 2011). For example, together with Pbx1, Meis1 plays a major role as a co-factor for the TFs of the Hox complex, which, in turn, have a pivotal and evolutionarily conserved role in orchestrating embryonic trunk development (Duboule, 2007; Mallo and Alonso, 2013). In accordance with this notion, loss of Meis1 function impairs the formation of Meis1-expressing trunk organs and systems, such as the limbs, heart, blood and vasculature (Azcoitia et al., 2005; Erickson et al., 2010; Hisa et al., 2004; Mercader et al., 1999, 2009; Zhang et al., 2002).

Members of the Meis subfamily are however also expressed in the brain and sensory organs (Schulte and Frank, 2014), which are Hox-
free embryonic regions (Duboule, 2007; Mallo and Alonso, 2013). In particular, Meis1 is expressed in the vertebrate forebrain and sensory organ primordia, including the eye, being essential for the specification of part of these structures. Indeed, genetic inactivation of Meis1 in mice causes lens reduction and abnormal retinal morphology (Hisa et al., 2004). Cardiovascular-related embryonic lethality of Meis1−/− embryos (Azcoitia et al., 2005; Hisa et al., 2004) and the virtual lack of information on the alternative and Hox-independent transcriptional mechanisms that Meis1 must adopt in the head region (Longobardi et al., 2014) have presented hurdles to understanding why and how these eye defects arise.

Here, we have begun to address these issues by taking advantage of Meis1 loss-of-function and conditional Meis1 functional rescue in mice, combined with ChIP-seq and RNA-seq approaches. Our results indicate that Meis1, by binding to ‘Meis-only’ binding sites in the DNA, regulates (directly and indirectly) the expression of genes involved in patterning, proliferation and differentiation of the neural retina, including components of the Notch signaling pathway. Meis1 is also at the core of a genetic network implicated in mammalian microphthalmia, and its haploinsufficiency suffices to cause microphthalmic traits in adult mice, suggesting that Meis1 itself represents an additional candidate for this ocular malformation.

RESULTS

Meis1 deficiency causes embryonic microphthalmia

Meis1 is uniformly expressed in the zebrafish and chick eye primordium and progressively retracts from the central retina following the wave of retinal cell differentiation (Bessa et al., 2008; Heine et al., 2008). In both species, Meis1 regulates the expression of cyclin D1 (Cend1), thereby promoting G1-S transition of retinal cells and thus the generation of sufficient numbers of retinal progenitors (Bessa et al., 2008; Heine et al., 2008). Accordingly, interference with Meis1 expression causes eye hypoplasia (Bessa et al., 2008; Heine et al., 2008).

We reproduced these observations in mice. Meis1 mRNA localized to the eye field (Fig. 1). Its expression (Fig. 1A-E) and that of its protein (Fig. 11-K) was thereafter maintained in the optic neuroepithelium and the overlying surface ectoderm throughout eye formation, according to the distribution detected with a lacZ reporter (Hisa et al., 2004). Meis1 expression was also maintained in retinal neurons as defined by its co-expression with the neuronal differentiation marker Tuj1 (Tubb3) (Fig. 1L,M). Although Meis2 has been reported to be transiently expressed in E9.5 optic vesicles (Heine et al., 2008), we could not detect Meis2 expression at any early stages of eye development (Fig. 1F-H). Thus, early mouse eye development seems to depend mostly on Meis1 function, in contrast to what has been observed in zebrafish and chick, where Meis2 is instead clearly detected (Bessa et al., 2008; Heine et al., 2008).

Complete inactivation of Meis1 caused lens vesicle reduction, as described using a different Meis1−/− mouse line (Hisa et al., 2004), but we did not observe the reported retinal duplication (Hisa et al., 2004). Instead, we noticed a significant reduction of the optic cup compared with wild-type (wt) littermates. This reduction was first apparent at E11 (Fig. 2) and became accentuated with development, especially in the ventral side, so that E13 Meis1−/− eyes were roughly half the size of those of wt (Fig. 2S). This was associated with a significant decrease in BrdU incorporation and Cend1 expression (Fig. 2A-C,T; supplementary material Fig. S1D-F), although there was no statistically significant difference in the mitotic index [calculated as the number of cells in M phase (phospho-histone H3+)/area] among wt and Meis1 null embryos in both the neural retina and the RPE (Fig. 2U).

Together, these observations indicate that the proposed Hth/Meis1-mediated control of retinal progenitor proliferation is conserved in mice and complete loss of Meis1 function drastically affects ocular development, causing microphthalmia.

Microphthalmia is associated with decreased neurogenesis and increased apoptosis

Previous studies in Drosophila and zebrafish retina have shown that Meis1/Hth expression is turned off in differentiating cells and its
forced maintenance prevents the acquisition of a differentiated neuronal fate (Bessa et al., 2002, 2008). This downregulation was not observed in the embryonic mouse retina, in which differentiated neurons are still Meis1 positive (Fig. 1M). We thus examined whether the reduced eye size of Meis1 null mouse embryos is also associated with abnormal neurogenesis.

We first compared the onset of Fgf signaling, which triggers retinal neurogenesis (Martinez-Morales et al., 2005), in E11.5 wt and mutant embryos. Fgf15 was strongly expressed in the wt central retina but was visibly reduced in both level and extent in Meis1−/− embryos (Fig. 2G-I). Furthermore, the number of Otx2+ retinal progenitors (supplementary material Fig. S1G,I) (Bovolenta et al., 1997) and that of Tuj1+ or islet 1/2 (Isl1/2)+ differentiating neurons (Esteve et al., 2011) was reduced in E12/E13 Meis1−/− retinas (Fig. 2J,L,M,O). In contrast to what has been reported in zebrafish and chick (Bessa et al., 2008; Heine et al., 2008), in Meis1 null embryos, but not in wt, the prospective neural retina at E12.5-E13.5 showed a significant number of TUNEL+ and cleaved caspase 3+ apoptotic cells (Fig. 2P-R,V). The majority of apoptotic cells were concentrated in the regions of ongoing neuronal differentiation (compare Fig. 2O with 2R), suggesting a link between the two events.

Haploinsufficiency of Meis1 causes microphthalmic traits in adult mice

In humans, microphthalmia is often caused by dominant heterozygous mutations, especially when mutations hit genes fundamental for eye development (Williamson and FitzPatrick, 2014). We thus investigated if loss of one Meis1 allele suffices to impair eye growth. Indeed, the size of the eye in Meis1+/− embryos...
was slightly reduced in all of the embryos analyzed (30/30) as compared with wt (Fig. 2A,B,D,E,G,H,S) and associated with an evident decrease in Cnnd1 expression (Fig. 2B). Furthermore, the domain of expression of markers implicated in neuronal differentiation, including Fgf15, Otx2, Isl1/2 and Tuj1, was smaller than that observed in wt littermates but not as reduced as that in Meis1−/− embryos (Fig. 2G-O; supplementary material Fig. S1G-I). As in homozygous mutants, the retinas of Meis1+/− embryos presented an increased number of apoptotic cells in the region of active neurogenesis (Fig. 2Q).

Altogether, these observations suggested that heterozygous embryos present a milder version of the ocular phenotype seen in Meis1 null mice. To confirm this and exclude the possibility that reduced Meis1 function might simply delay eye development, we examined whether the observed embryonic defects persisted into adulthood, as Meis1−/− mice, in contrast to homozygous mice, are viable and fertile.

Scheimpflug imaging revealed no anterior segment abnormality in adult Meis1+/− animals as compared with wt littermates (supplementary material Fig. S2). Likewise, optical coherence tomography (OCT) showed no defects in the number and distribution of the main blood vessels when adult wt and Meis1 heterozygous animals were compared (Fig. 3A,B). By contrast, non-invasive analysis of left and right eye morphometrics and histological analysis of the retina showed that in Meis1+/− mice the axial length of the optic globe and the thickness of the neural retina were significantly decreased (Fig. 3C-H). This reduced thickness seemed to affect, albeit slightly, all nuclear layers (Fig. 3E,F) and could result from the decrease in neurogenesis observed in the heterozygous embryos coupled to the increase in apoptosis. Notably, these morphological changes were associated with a significant loss of visual performance (Fig. 3I), as determined by the virtual drum vision test (Prusky et al., 2004).

Thus, haploinsufficiency of Meis1 causes morphological and functional defects characteristic of microphthalmia (Williamson and FitzPatrick, 2014). Microphthalmia is likely to be a direct consequence of Meis1 requirement in the retinal neuroepithelium since blood vessels and lens, which may both influence retinal development, formed normally.

**Microphthalmia is not a consequence of Meis1 function in the vascular system**

To further confirm the idea that the microphthalmia observed in Meis1 mutant embryos is independent from the abnormal development of the hematopoietic/vascular system characteristic of Meis1 null embryos (Azcoitia et al., 2005; Hisa et al., 2004), we analyzed a mouse line with a targeted rescue of Meis1 function in the hematopoietic and vascular system in a Meis1a+/− background [Meis1a+/−;Tie2Cre;R26Meis2a (Rosello-Diez et al., 2014)].

In contrast to the evident rescue of the hemorrhage that is usually present in Meis1 null embryos (Fig. 4A-C) (Rosello-Diez et al., 2014), the eye size of all of the analyzed Meis1a+/−;Tie2Cre;R26Meis2a embryos (13/13) was still reduced and comparable to that observed in Meis1a+/−;Tie2Cre littermates (Fig. 4A-C). Indeed, at E13 the area of the neural retina of Meis1a+/−;Tie2Cre;R26Meis2a and Meis1a+/−;Tie2Cre embryos was on average 47%
sites in eye development using Hox/Pbx-independent binding and 48.2% smaller, respectively, than that of the Meis1a+/+; Meis1a+/+;Tie2Cre;R26Meis2a control littermates. This reduction is very similar to that seen in Meis1−/− embryos (Fig. 2S).

Likewise, in both Meis1a−/−;Tie2Cre and Meis1a−/−;Tie2Cre;R26Meis2a E13.5 retinas, the number of Tuj1+ differentiating neurons was similarly reduced (Fig. 4D-F) and the expression of optic cup patterning markers altered. For example, and as observed in Meis1 null embryos (supplementary material Fig. S1J-L; and see below), the distribution of the TF Pax2, which is normally restricted to cells of the optic disc at E12/E13 (Morcillo et al., 2006) (supplementary material Fig. S1J; Fig. 4G), was instead expanded in the ventral and dorsal retina of both Meis1a−/−;Tie2Cre and Meis1a−/−;Tie2Cre;R26Meis2a embryos (Fig. 4H-I), comparatively to that observed in Meis1 mutant embryos (supplementary material Fig. S1K-L).

Meis1 interacts with a set of enhancers specifically involved in eye development using Hox/Pbx-independent binding sites

Altogether, these data indicate that a full dose of Meis1 is required for the progression of retina development. Reduced Meis1 levels prevent retinal progenitors from undertaking a normal proliferative and differentiation program, ultimately leading to the death of some cells. As previously noted (Heine et al., 2008), Ccnld1 downregulation by itself is unlikely to explain this severe phenotype because retinal differentiation is normal in Ccnld1−/− mice (Scicinski et al., 1995) and overexpression of Ccnld1 only partially rescues the effect of loss of Meis1 function (Heine et al., 2008). Thus, besides Ccnld1, Meis1 is likely to regulate additional neurogenic pathways. This regulation must take place via a Hox/Pbx-independent mechanism because Hox genes, which are well-known partners of Meis in the trunk, are not expressed in the head (Schulte and Frank, 2014). Furthermore, there is no indication that Pbx genes contribute to early eye formation, even though compound knockout mice have been generated and extensively studied (Capellini et al., 2011; Stankunas et al., 2008).

To address this question and identify the binding sites (BSs) of endogenous Meis1 protein in the developing eye, we performed ChIP-seq analysis using isolated E10.5 optic cups, shortly before the detection of overt Meis1−/− eye defects. We identified a total of 5361 Meis1 BSs in the genome and a collection of 3182 genes with a transcription start site (TSS) closest to any Meis1 BS (GEO GSE62786). As previously reported (Penkov et al., 2013), most Meis1 BSs were located in regions remote from their closest associated TSS (Fig. 5A).

To study the functional relevance of Meis1 BSs we performed further ChIP-seq analysis of the E10.5 optic cup to determine further modification marks that identify promoter (H3K4me3) and enhancer (H3K4me1) regions. Meis1 BSs associated very significantly with both H3K4me1 and H3K4me3 marks, indicating a preference for enhancer and promoter region binding (Fig. 5B). When comparing Meis preference for binding to H3K4me1 and H3K4me3 marks, as reported in other tissues (Penkov et al., 2013), we found that Meis1 preferentially binds to enhancer regions (Fig. 5B). Meis1 selects two main sequences in the embryonic trunk: the Pbx-Hox binding sequence (A/TGATNNAT), to which it binds indirectly, and a direct BS (TGACAG) (Penkov et al., 2013).

To determine binding preferences in the developing eye, we identified consensus sequences in the E10.5 eye Meis BS collection. We found only one consensus sequence showing a unimodal distribution, with the maximum mapping to the center of the Meis BS and therefore representing the Meis1-bound core sequence (m1 sequence, Fig. 5C). We identified three additional consensus sequences showing a bimodal distribution, with maxima mapping at a certain distance from the Meis BS center, which are likely to represent cooperating sequences not directly bound by Meis1 (m2-m3, Fig. 5C). The m1 consensus is a very close variant of the Meis1 direct binding sequence identified in the trunk (Penkov et al., 2013), whereas m2-m3 sequences are low-complexity or rather relaxed sequences that we could not correlate to previously described consensus binding motifs.

These results suggest that in the eye Meis1 selects BSs and sequences unrelated to the Hox-Pbx network. In support of this view, the prominent pattern of Meis binding to the HoxA cluster seen in the trunk is completely absent in the E10.5 eye (Fig. 5D). We then looked for previously described Meis-regulated enhancers in the developing eye. Within the Meis1 BS collection, we found the previously described Meis BS in the Pax6 lens ectoderm enhancer (Zhang et al., 2002) and an additional peak in the Pax6 third intron, but not the Pax6-associated Meis BS reported after embryonic trunk ChIP-seq (Penkov et al., 2013) or those found in a pancreatic enhancer (Zhang et al., 2006) (Fig. 5E). The eye-specific Meis1 BS coincided with H3K4me1 high/H3K4me3 low marks typical of enhancer regions (Fig. 5E).

Remarkably, despite the distance between Meis1 BSs and TSSs, the analysis of ‘biological process’ and ‘MGI phenotypes’ Gene Ontology (GO) classes for the Meis1 BS-associated genes identified eye development classes as the most overrepresented, with a predominance of ‘eye size’ and ‘eye morphology’ categories (Fig. 5F). Thus, the Meis1 binding profile reveals its functional
association with enhancers involved in eye development, in contrast to what was observed in the embryonic trunk following a similar analysis (Penkov et al., 2013) as used here for comparison. Besides the ‘eye development’ categories, the ‘Notch signaling’ class appeared enriched in Meis1 BS-associated genes (Fig. 5F) in GO analysis.

**Meis1 regulates the expression of Notch pathway genes and of selected genes involved in mammalian microphthalmia**

To correlate the Meis1 BS pattern with actual gene expression regulation, we compared E10.5 wt and Meis1−/− eye cup transcriptomes by RNA-seq, identifying 406 downregulated and 242 upregulated transcripts (supplementary material Tables S1 and S2). The expression of transcripts encoding the core factors of the Notch pathway was extensively downregulated in Meis1 mutants (Fig. 6A), indicating that this pathway is a major target of Meis1 regulation in the developing eye. To determine whether some of the genes encoding core components of the Notch pathway could be direct targets of Meis1, we examined the occurrence of Meis1 BSs in the enhancer-promoter units (EPUs) described in the ENCODE project (Shen et al., 2012). We found Meis BSs associated with the enhancer regions of Notch2, Jag1, Hes2 and Hes5, coincident with enhancer histone marks in the E10.5 eye (supplementary material Fig. S3). A clear downregulation of Hes5 mRNA, a major effector
Fig. 6. Meis1 regulates components of the Notch signaling pathway and genes involved in microphthalmia. (A) RNA-seq expression level changes in genes encoding core components of the Notch signaling pathway detected in E10.5 Meis1\(^{-/-}\) versus wt eyes. (B,C) Representations of changes in gene expression detected in Meis1\(^{-/-}\) for all genes (B), mouse microphthalmia genes and mouse orthologs of human microphthalmia genes (C). Genes are ordered according to their expression change. A red line indicates the mean of expression variations. Gray boxes in C indicate genes with a log₂ fold change >±0.5. Genes highlighted in red have a human ortholog associated with microphthalmia. The complete list of mouse orthologs of human genes analyzed in C is shown to the right. (A,C) p indicates the familywise error rate. (D) Vsx2, Otx2 and Sox2 genes showing their described promoter-enhancer interactions (PEI) according to Shen et al. (2012), the Meis1 ChIP-seq read profile from E10.5 eye (this study) and E11.5 trunk (Penkov et al., 2013), the P0 DNAse-seq profile [from The ENCODE Project Consortium (2012), GEO:GSM1014188] and the H3K4me1 and H3K4me3 ChIP-seq profiles (this study). Detected Meis1 BSs are shown by arrowheads below the read profiles. Boxes highlight the E10.5 eye Meis BS regions and their coincidence with histone modification marks and described enhancer-promoter interactions.
of Notch signaling, was further confirmed by comparative in situ hybridization (ISH) analysis in wt and Meis1 mutants (Fig. 2D-F). These results suggest that Meis1 controls Notch pathway activity at various levels.

In addition, the association of Meis1 BSs with genes involved in eye size regulation, together with the reduced eye size of Meis1 mutants, further suggested a relationship between Meis1 function and the direct or indirect regulation of microphthalmia genes. RNA-seq analysis that was focused on 121 mouse genes linked to microphthalmia confirmed this association (Fig. 6B,C). Interestingly, the human orthologs of the five most downregulated genes belonging to this class, Pitx3, Smoc1, Cryba1, Cryaa, and Foxe3, have been associated with human microphthalmia (Fig. 6C) and a specific survey of all the mouse orthologs of human microphthalmia genes showed a very significant trend to downregulation in Meis1 mutants (Fig. 6C). These results identify Meis1 as a major regulator of microphthalmia-associated genes.

To analyze possible direct targets within genes that change their expression levels, we determined the presence of Meis BSs in the EPUs of the 35 microphthalmia-associated genes that showed the strongest change in expression. We found that 11 out of these 35 genes contained one or more Meis BSs in their EPUs in coincidence with enhancer histone marks in E10.5 eyes (Fig. 6D; supplementary material Fig. S4; data not shown). Interestingly, 12 of the 35 genes showing altered expression and 8 of the 11 genes with Meis1 BSs in their EPUs encode TFs, including some of those more frequently associated with human microphthalmia (Otx2, Vsx2, Sox2; Fig. 6D).

These results suggest that Meis1 controls eye size at various levels but predominantly by orchestrating the regulation of microphthalmia-associated TFs.

**Meis1 is required to sharpen the boundaries between the different eye territories**

Because eye development gene classes were overrepresented in Meis1 ChIP-seq analysis (Fig. 5F), developmental processes other than neurogenesis were likely to be affected in Meis1 mutant eyes. To test this possibility we analyzed the distribution of well-established markers of eye patterning. Although most of these markers were detected, their distribution was generally shifted and with blurred boundaries: for example, the border between Pax2, a marker of the proximal eye (optic stalk), and Pax6, a marker of the distal eye, was distally shifted, with a clear increase in Pax2 expression in Meis1 mutants versus wt embryos (Fig. 7A-F); this is also in agreement with the enhanced expression of Shh in mutants (Fig. 6C), which is known to expand the optic stalk. Similarly, Otx2, an RPE marker (Martinez-Morales et al., 2004), was abnormally extended in the ventrodistal retina (Fig. 7G-I), in accordance with RNA-seq analysis and the presence of Meis BSs in its locus (Fig. 6C,D). The Otx1+ peripheral retina invaded the Vax2+ central retina (Fig. 7J-O), again in agreement with our RNA-seq and ChIP-seq analysis indicating that Meis1 might activate Vax2 (Fig. 6C,D). Patterning along the dorsoventral axis was also abnormal, with an expansion of the Tbx5+ dorsal region and a reduction of the Vax2+ ventral retina, whereas the expression of Foxd1, a temporal retinal marker, was considerably reduced (Fig. 7P-X). Notably, blurring of all boundaries was dose-dependent, as these defects were milder in Meis1+/- eyes (Fig. 7).

**DISCUSSION**

In mammals, Meis1 is crucial for the formation of the heart, vasculature and hematopoietic system (Axcoitia et al., 2005; Hisa et al., 2004). During the development of these structures, as well as that of the limbs, Meis1 acts as a co-factor for Hox proteins, often in cooperation with the related Pbx TFs (Penkov et al., 2013). Our study demonstrates that Meis1 is also crucial for the progressive...
formation of the eye, but, in this case, its function is mediated by Hox/Pbx-independent BSs on the DNA. In the absence of Meis1, the expression of the main patterning determinants of the optic cup is altered and the boundaries between the proxi-modistal, dorsoventral and nasotemporal domains of the cup are shifted or blurred. Retinal neurogenesis is also affected because Meis1, directly or indirectly, controls the expression of components of the neurogenic cascade mediated by the Notch receptor. Furthermore, Meis1 is required for the expression of a set of genes involved in mammalian microphthalmia. Accordingly, Meis1 haploinsufficient adult mice present morphological and functional defects characteristic of this congenital defect. Therefore, our data, together with previous studies showing that Meis1 controls lens development and Ccnd1-mediated retinal proliferation (Bessa et al., 2008; Heine et al., 2008; Zhang et al., 2002), indicate that Meis1 is a global regulator of eye development.

At least in mammals, this key function does not seem to be shared by the related Meis2 or Meis3. Meis3 is expressed in the eye only when the first retinal ganglion cells begin to differentiate (Gray et al., 2004). Both Meis2 and Meis1 contribute to lens specification by binding to the same BS present in a lens-specific enhancer of the Pax6 locus (Zhang et al., 2002), but only Meis1 is strongly and continuously expressed in the retinal neuroepithelium, according to our data and the distribution previously reported (Zhang et al., 2002). Meis2−/− mice have no evident eye alterations (M.T., unpublished observations), suggesting that the reported Meis2 expression in the optic vesicle (Heine et al., 2008) is either too transient to be consistently detected and/or dispensable in the gene regulatory network that controls early eye formation. This predominant role of Meis1 in the mammalian eye primordium differs from that reported in chick and fish, in which alteration of Meis2 levels also perturbs eye development (Conte et al., 2010; Heine et al., 2008). Furthermore, in contrast to its role in zebraﬁsh where it is limited to neurogenesis (Bessa et al., 2008), Meis1 is also crucial for patterning and neuronal differentiation in the mouse retina. This latter function is supported by the maintenance of Meis1 expression in differentiated neurons, which are very much reduced in number in Meis1−/− mouse embryos. A similar role has been observed in chick, in which interference with Meis function compromises the appearance of retinal differentiation markers (Heine et al., 2008), including Foxn4, a TF directly regulated by Meis1 and important for the generation of horizontal and amacrine neurons (Islam et al., 2013). As shown here, Meis2 rescues Meis1 deﬁciency in the vascular system, indicating that the two proteins are functionally similar and can show redundancy during eye development. Differential evolution of the regulatory elements controlling Meis1 and Meis2 expression, rather than Meis1/2 protein functional specialization, might thus underlie their different requirement in fish, avian and mammalian eye development.

Our expression and genomic analyses indicate that Meis1 must act upstream in the gene regulatory network controlling eye formation, as several of its targets are themselves TFs at the core of the network, such as Sox2, Otx2 and Pax6 (Beccari et al., 2013). Genetic inactivation of Meis1 does not prevent the formation of the eye primordium, although it has, however, a fuzzy pattern. This “fuzziness” affects its main tissues – optic stalk, neural retina and RPE – as well as its entire axes, indicating that Meis1 is crucial to consolidate boundaries between the different eye domains. Meis1 could, for example, render the activity of each of the tissue determinant genes [e.g. Otx2 for the RPE (Martinez-Morales et al., 2001)] more efﬁcient. There are various and not mutually exclusive mechanisms by which this could occur. In a view based around its cooperation with Hox/Pbx in the trunk (Duboule, 2007; Penkov et al., 2013), Meis1 could act as a co-factor with an as yet undeﬁned predominant partner, perhaps binding to the m2-m3 core sequence that we have identiﬁed. This interaction would make the putative factor more efﬁcient, allowing the correct expression of target genes. Alternatively, Meis1 could interact with a wide variety of TFs in the eye, including its own putative targets such as Sox2, Pax6 and Otx2, reinforcing their activity. The latter possibility is supported by the observation that the related Meis2 has been shown to interact at least with Otx2, Pax3, Pax6 and Pax7 (Agoston et al., 2014, 2012; Agoston and Schulte, 2009). Alternatively, and based on the predominant presence of a ‘Meis1-only’ targeted sequence (m1, Fig. 5) in the eye chromatin, we favor the hypothesis that Meis1 directly binds on enhancers of many determinant genes. Its binding would be necessary to achieve sufﬁcient levels of target expression, and indispensable for regulating the extent of each domain. This mechanism could be illustrated by possible direct regulation by Meis1 of Pax6 in the retina and the establishment of proximodistal patterning of the optic vesicle. Indeed, the boundary between the proximal and distal optic vesicle is known to depend on a cross-regulatory loop between Pax6 expressed distally and Pax2 expressed proximally (Schwarz et al., 2000). We have identiﬁed a Meis1 BS on a Pax6 enhancer that is different to that known to mediate lens development (Zhang et al., 2002). In the absence of Meis1, retinal Pax6 expression is strongly reduced, probably allowing Pax2 upregulation. This should result in a weak cross-repressive loop between the two TFs and thus in a shifted proximodistal boundary, which is indeed observed in Meis1 mutant embryos. This mechanism could be reinforced by a possible direct repression of Meis1, as we identiﬁed by ChIP-seq Meis BSs in the Pax6 locus. Similar considerations could apply for other TFs known to act in a cross-regulatory loop during boundary establishment, as with FoxG1 and FoxD1 in the speciﬁcation of the nasotemporal domains of the retina (Hatini et al., 1994; Huh et al., 1999). Notably, we identiﬁed by ChIP-seq Meis BSs also in the Foxd1 locus.

A similar potential direct regulation could also be relevant in the control of components of the Notch signaling pathway, including the Notch2 receptor and the Notch signaling effectors Hes2 and Hes5. For other members of the pathway, the decreased expression identiﬁed in our RNA-seq comparison might instead be indirect. Nevertheless, whether direct or not, the poor Notch pathway activation, in conjunction with decreased expression of Ccnd1 and other microphthalmia-associated genes, could explain the Meis1−/− microphthalmic phenotype. Indeed, Notch signaling controls the number of progenitors entering retinal differentiation: loss of Notch function forestalls retinal neurogenesis (Jadhav et al., 2006), whereas abnormal Notch receptor activation transiently increases retinal proliferation and differentiation (Esteve et al., 2011). Notably, Meis1 action on the Notch pathway and on microphthalmia-related genes could be linked since Sox1, Sox2 and Notch signaling have been shown to regulate each other’s activity in various contexts (Genethliou et al., 2009; Kan et al., 2004; Neves et al., 2011). Most notably, Sox2 regulates the Notch signaling pathway in retinal progenitor cells in a concentration-dependent manner, so that the levels of Sox2 directly correlate with the levels of Notch1 (Taranova et al., 2006), a correlation that we have also observed between Meis1 levels and Hes5 expression.

Our RNA-seq analysis reveals a strong association between Meis1 function and genes linked to microphthalmia. As expected from the use of complete E10.5 eye cups, we identiﬁed genes expressed only in the lens, such as the TF Foxe3 and the crystallins (Graw, 2009), or in the neural retina, including the TF Vzx2 and
phenotypic traits. The possibility that reduced MEIS1 levels could contribute to the MEIS1 have been linked to alterations in chromosome 2 (Waters et al., 1993; Weaver et al., 1999), representing an additional candidate for syndromic cases associated with this ocular malformation. In this respect, eye neurogenesis of the developing eye through the regulation of signaling pathways and patterning genes, indicating that the retinal neuroepithelium is more sensitive to the levels of MEIS1 expression, directly implicating MEIS1 in retina development.

In conclusion, our data support that MEIS1 has a crucial and previously unreported role in integrating patterning and neurogenesis of the developing eye through the regulation of signaling pathways and patterning genes. MEIS1 seems to be at the core of a genetic network implicated in human microphthalmia, itself representing an additional candidate for syndromic cases associated with this ocular malformation. In this respect, eye developmental defects, including bilateral microphthalmia, have been linked to alterations in chromosome 2 (Waters et al., 1993; Weaver et al., 1999), at a location that may include the extensive MEIS1 regulatory region (Royo et al., 2012), raising the possibility that reduced MEIS1 levels could contribute to the phenotypic traits.

MATERIALS AND METHODS

Animals

Meis1a heterozygous mice were generated as described (Azcoitia et al., 2005). Embryos were obtained from timed (vaginal plug as E0.5) mating of Meis1a−/− mice or outbred CD1 mice. Animals were treated according to institutional or national guidelines for the use of animals in scientific research.

BrdU incorporation

BrdU (10 mg/ml; Roche) was injected (50 µg/g body weight) into pregnant mice intraperitoneally. Embryos were sacrificed and collected 1 h later.

TUNEL

Staining was performed using the In Situ Cell Death Detection Kit (Roche) on cryosections following the manufacturer’s instructions.

In situ hybridization

E10.5-13.5 embryos were immersion fixed in 4% paraformaldehyde in PBS for 3 h. Tissue was processed for cryosectioning in the frontal or horizontal plane and ISH was performed as previously described (Causar et al., 2004) using the following digoxigenin-labeled mouse-specific antisense riboprobes were used: Fgf15, Cnd1, Hez5, Thx5, Vax2, Foxd1, Otx1, Otx2.

Immunohistochemistry

Cryosections were incubated with 0.1% Triton X-100 in PBS (PBST) and immunofluorescence was performed in PBST with 1% normal goat serum. For Otx2, Pax6 and Pax2 staining, sections were heated at 110°C for 2 min in 10 mM citrate buffer (pH 6) using a decloaking chamber (Biocare Medical). The following primary antibodies were used (at 1:1000 unless stated otherwise): rabbit anti-Meis1a/2a (Mecard et al., 2005), anti-Otx2 (Abcam, ab21990), anti-cleaved caspase 3 (Cell Signaling, 9661), anti-Pax2 (Invitrogen, 71-6000), anti-Pax6 (Covance, PRB278P), mouse anti-phospho-histone H3 (Millipore, 06-570), anti-BrdU [1:4000; DSHB, G3H4(AntiBrdUr)], -anti-Isil1/2 (1:500; DSHB, 39.4DS) and -anti-Tuj1 (ßIII tubulin, Babco, MMS-435P). Secondary antibodies were conjugated to Alexa 488 or Alexa 594 (1:1000; Molecular Probes). Counterstaining was with DAPI (1 µg/ml; Vector Labs).

RNA-seq

For RNA-seq library production, RNA of intact E10.5 optic cups (thus including the lens) from eight homozygous and wt embryos (out of 41 embryos from seven litters) was isolated using standard procedures, quantified (260 nm in a NanoDrop) and checked for integrity (Agilent Bioanalyzer). Total RNA was processed with the TruSeq RNA Sample Preparation v2 Kit (Illumina) to construct index-tagged cDNA libraries. The quality, quantity and the size distribution of the Illumina libraries were determined using the DNA-1000 Kit (Agilent Bioanalyzer). Prepared cDNA libraries were applied to an Illumina flow cell for cluster generation (TruSeq SR Cluster Kit V2 v.4, Illumina) and sequence-by-synthesis single reads of 75 bp using the TruSeq SBS Kit v5 (Illumina) were generated on the Genome Analyzer Ix (Illumina) following the standard RNA sequencing protocol. Sequencing adapter contaminations were removed from reads using cutadapt software (http://code.google.com/p/cutadapt/) and the resulting reads were mapped and quantified on the transcriptome (Ensembl gene build 70) using RSEM v1.2.3 (Li and Dewey, 2011). Only genes with at least five counts per million in at least one sample were considered for statistical analysis. Data were then normalized and differential expression tested using the Bioconductor package edgeR (Robinson et al., 2010). Genes were considered differentially expressed when they presented a fold change ≥40%. Data were analyzed using Gene set enrichment and Ingenuity pathway software (Biobase International). Mouse microphthalmia genes were obtained by searching the Jackson Laboratory Mouse Genome Informatics database for the term ‘microphthalmia’ in the field ‘mouse phenotypes and mouse models of human disease’ of the ‘genes and markers’ query. Data are deposited in the NCBI GEO database under accession number GSE62786.

ChIP-seq

ChIP assays to determine the histone methylation marks were performed using ~100 eyes from E10.5 mouse embryos. Chromatin was cross-linked with 1% formaldehyde for 15 min and fragmented to obtain DNA in the range 200-500 bp. DNA was divided in three pools of (10 µg) and precipitated with 2 µg anti-H3K4m1 (CS-037-100, Diagenode) or anti-H3K4m3 (pAB-033-050, Diagenode). Immunoprecipitated DNA was purified with QIAQuick columns (Qiagen). Data are deposited in the NCBI GEO database under accession number GSE62786. ChIP data for Meis1 were obtained from ~200 eyes of E10.5 CD1 embryos. Two pools of ~20 µg total chromatin were immunoprecipitated with 4 µg anti-Meis1 antibody (Mecard et al., 2005) and the immunoprecipitated DNA was purified and pooled together. ChIP-seq and bioinformatic processing were performed as described (Penkov et al., 2013). Chromatin was cross-linked with 1% formaldehyde for 15 min and fragmented to 300-500 bp. Data have been deposited in the NCBI GEO database under accession number GSE62786. Annotation of Meis1 BSs and identification of Meis1 BS-associated genes or overrepresentation in GO and phenotype-association databases was performed with the ‘genomic regions enrichment of annotations tool’ (GREAT) (McLean et al., 2010). For the identified peaks, ‘de novo motif discovery’ was run to identify consensus sequences enriched in the selected regions versus the whole genome using rGADEM (Li, 2009).

Morphometric and functional analysis of the eye

The visual acuity and eye morphology of Meis1a mutant mice were evaluated at 15 weeks of age by virtual optokinetic drum, Scheimpflug imaging, OCT and laser interference biometry (LIB). For LIB and OCT, the eyes were treated with 1% atropine to ensure pupil dilation and mice were further anesthetized with 137 mg ketamine and 6.6 mg xylazine per kg body weight. For all tests, previously published protocols were followed: virtual drum vision test (Prusky et al., 2004), Scheimpflug imaging (Puk et al., 2013a), OCT (Puk et al., 2013b) and LIB (Puk et al., 2006).

Quantification and statistical analysis

Area measurements and cell counting were performed with a Leica DM 5000M fluorescence microscope and a Leica DFC 500 camera. All
statistical analysis was performed using a minimum of 3 or 6 embryos or eyes per genotype, using ImageJ software (NIH). Differences between calculated averages were considered significant when P<0.05 by Student’s t-test. For each of the ISH probes or immunohistochemical markers used in this study, analysis was performed on a minimum of three embryos for each genotype. For each embryo, all sections from both eyes were photographed and compared using sections at the same axial level.

Acknowledgements
We thank J. R. Martinez-Morales (CBD) for critically reading the manuscript; V. García for mouse care; the CMBMO Genomics Facility for help with Chip-seq; and M. J. Gómez-Rodríguez, Manuel Gómez and F. Sánchez-Cabo (CNIC) for biochemical analyses. The CNIC Genomics Unit performed the RNA-seq procedures.

Competing interests
The authors declare no competing or financial interests.

Author contributions
P.B., M.T. and S.M. conceived the study; J.G. and M.H.D.A. conceived the phenotypic tests; S.M., M.G.-L., L.B., L.C.D., R.O., O.A. and M.J.M.-B. performed experiments; S.M., L.B., O.B., J.G., D.M.-S.M., C.T., J.L.G.-S., F.C., M.T. and P.B. analyzed the data; M.T. and P.B. wrote the paper. All authors approved the manuscript.

Funding
This work was supported by grants from the Spanish Ministry of Economy and Competitiveness (MINECO) [BFU2010-16031; BFU2013-43213-P] supported by FEDER Funds, the CIBERER, Instituto de Salud Carlos III (ISCIII) to P.B. and an Institutional Grant from the Fundación Ramón Areces; by MINECO [BFU2012-31086] and ISCIII [RD12/0019/0005] to M.T.; by Comunidad Autonoma de Madrid (CAM) [S2010/BMD-2315] to P.B. and M.T.; by MINECO [BFU2013-41322-P] and Andalusian Government [BIO-396] to J.L.G.-S.; and by MINECO [BFU2014-55738-REDT] to P.B., J.L.G.-S. and F.C. M.G.-L. was supported by a grant from the CONACyT. O.B. is supported by an Australian Research Council Discovery Early Career Researcher Award-DECRA [DE140101962]. The CNIC is supported by MINECO and the Pro-CNIC Foundation.

Supplementary material
Supplementary material available online at http://dev.biologists.orglookup/suppl doi:10.1242.dev.122176/-/DC1

References


