

Review Article

The Eyes Absent proteins in development and in developmental disorders

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The Eyes Absent (EYA) transactivator-phosphatase proteins are important contributors to cell-fate determination processes and to the development of multiple organs. The transcriptional regulatory activity as well as the protein tyrosine phosphatase activities of the EYA proteins can independently contribute to proliferation, differentiation, morphogenesis and tissue homeostasis in different contexts. Aberrant EYA levels or activity are associated with numerous syndromic and non-syndromic developmental disorders, as well as cancers. Commensurate with the multiplicity of biochemical activities carried out by the EYA proteins, they impact upon a range of cellular signaling pathways. Here, we provide a broad overview of the roles played by EYA proteins in development, and highlight the molecular signaling pathways known to be linked with EYA-associated organ development and developmental disorders.

Introduction

The Eyes Absent (EYA) proteins are part of the well-conserved retinal determination gene network (RDGN) that contributes to cell-fate determination processes in multiple tissues and species (reviewed in [1–4]). In addition to the EYA proteins, the RDGN consists of the master regulatory transcription factor PAX6 (eyeless *ey* and twin of eyeless *toy* in flies), the SIX family of homeodomain transcription factors (SIX1–6; *sine oculis* and *optix* in flies), and the transcription factor DACH (dachshund). Interactions between components of the RDGN are summarized in Figure 1. While the RDGN was first described in *Drosophila* eye development [5], surveys of the eukaryote genome suggest that the RDGN was employed in two different contexts early in evolution, eye development and oocyte development [6]. In vertebrates, the proteins coded by members of the RDGN are widely implicated in cell survival and differentiation during tissue specification. Here, we describe our current understanding of the roles played by EYA proteins during development and in tissue homeostasis. Particular emphasis is placed on linking the multiple biochemical activities of the EYA proteins with their developmental roles whenever possible. We will highlight how the EYA proteins interface with other signaling pathways involved in organ development, the emerging evidence that EYA3 contributes to photoperiodism, and mutations in the *Eya* genes associated with human disorders.

EYA protein architecture and its placement in the RDGN

Mammals have four *Eya* paralogs (*Eya1–4*) and their expression begins during embryonic development. *Eya* expression is much more restricted to specific adult tissues, with *Eya3* having the most wide-spread expression. The intrinsically cytoplasmic EYA proteins physically partner with the SIX proteins and are then translocated to the nucleus where they play an essential role in the regulation of gene expression driven by the RDGN (Figure 1b).

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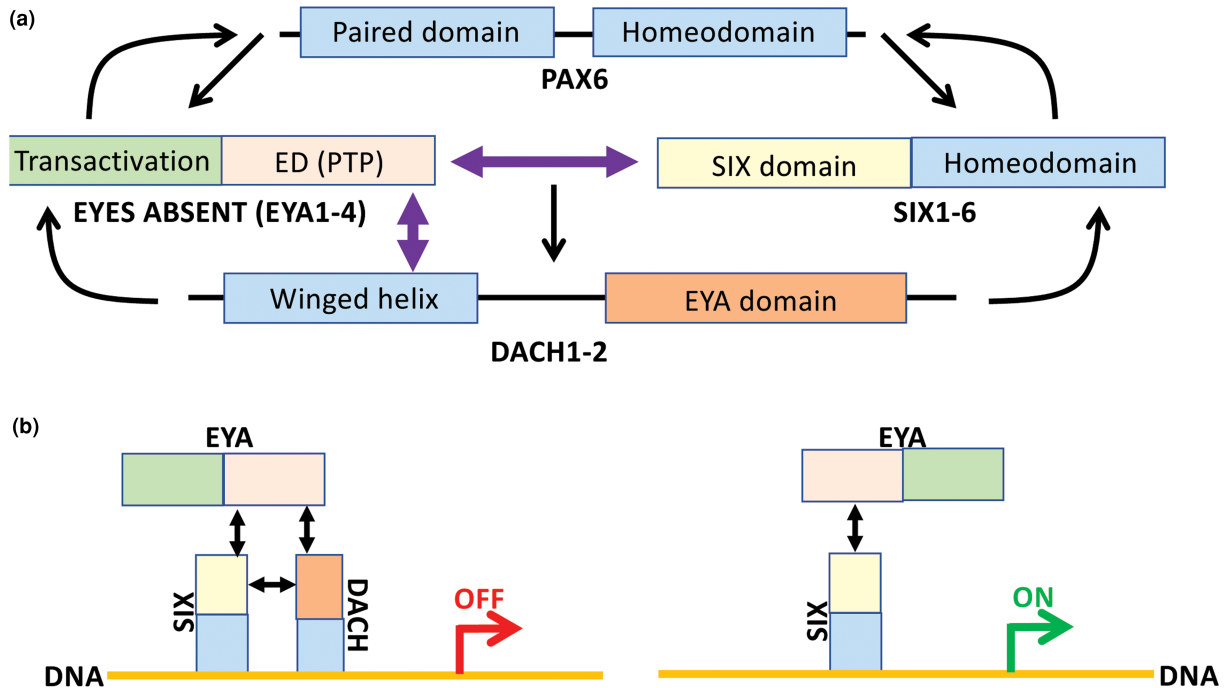


Figure 1. EYA proteins and the Retinal Determination Gene Network.

(a) A schematic of the proteins encoded by genes in the retinal determination gene network (RDGN), and the regulatory interactions (black arrows). PAX6, the master regulator, is a paired-homeodomain family transcription factor. The SIX proteins are also homeodomain DNA-binding proteins with an N-terminal domain (SIX domain) that interacts with the EYA proteins (indicated by the double-headed arrow). This interaction translocates the intrinsically cytoplasmic EYA proteins into the nucleus. The DACH proteins have a winged-helix DNA-binding domain that may be involved in DNA interaction [90]. The DACH C-terminal domain is involved in EYA interaction (double-headed arrow). The EYA proteins have a highly conserved C-terminal domain commonly referred to as the EYA domain (ED). This domain has protein tyrosine phosphatase activity (PTP). The N-terminal domain is poorly conserved and can activate transcription when bound to DNA as a complex with the SIX proteins. (b) Various models of transcriptional regulation mediated by the SIX, DACH and EYA proteins have been proposed. SIX proteins can bind DNA as well as the EYA proteins, together activating target genes through the N-terminal transactivation domain in EYA proteins that can recruit RNA pol II and co-activators such as CREB binding protein. Recruitment of DACH is generally associated with transcriptional repression. The domains within the EYA, SIX and DACH proteins are color-coded as in (a). Double-headed arrows indicate physical interactions.

All animal EYA proteins are characterized by a highly conserved C-terminal ~270 amino-acid domain referred to as the EYA domain (ED) (Figure 1a). Interaction with the SIX proteins occurs through the ED and there is strong evidence that ED has tyrosine phosphatase activity [7–9]. However, ED bears no structural or sequence similarity to the classical protein tyrosine phosphatases (PTP). This places the EYA proteins in the unique position of being PTPs that do not employ the nucleophilic Cysteine residue-mediated catalytic mechanism characteristic of the classical PTPs (recently reviewed in [3]). Few EYA-PTP substrates have yet been identified (recently reviewed in [3]). The best-characterized of these is the DNA damage repair-associated histone protein H2AX [10,11]. Dephosphorylation of the terminal C-tyrosine of H2AX promotes DNA damage repair and survival of cells. In addition, the tumor suppressor estrogen receptor-β and the cytoskeleton modulating protein WDR1 have also been identified as likely EYA-PTP substrates [12,13]. The PTP activity of the EYA proteins also promotes cell motility possibly via the Cdc42/Rac GTPases [14,15], but no EYA substrate has yet been identified in this context. The N-terminal domain of the EYA proteins has an independent transactivation function localized to a Pro/Ser/Thr-rich ~210 amino-acid segment in *Drosophila Eya* [16]. In addition, a threonine phosphatase activity (either intrinsic or via interaction with protein phosphatase 2A (PP2A)) is associated with the N-terminal domain [17–22].

This juxtaposition of distinct biochemical activities in a single polypeptide places the EYA protein in the unique position of participating directly in both the regulation of gene transcription and in signal transduction

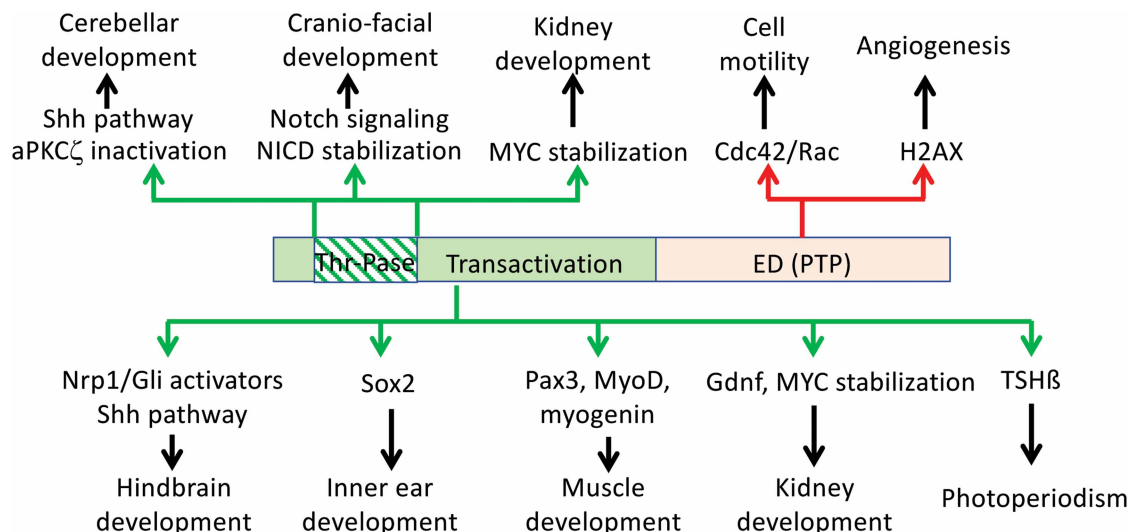


Figure 2. EYA biochemical activities, signaling pathways influenced and roles in development/physiology.

Schematic showing the interaction of the individual EYA biochemical activities with molecular signaling pathways as they impact upon the roles of the EYA proteins discussed here. The putative threonine phosphatase activity (either mediated by EYA itself or through interaction with PP2A) is indicated by the hatched green box.

processes. A schematic overview of molecular pathways impacted by EYA proteins as they participate in the processes described below is provided in [Figure 2](#).

EYA in eye development

Loss of the *eya* gene in *Drosophila* eye progenitor cells anterior to the furrow (*eya*² mutant flies) resulted in viable but completely eyeless flies due to apoptosis of eye progenitor cells [23]. The introduction of mouse *Eya2* in progenitor cells prior to furrow formation in the *eya*² mutant background was able to restore eye formation, speaking to a high degree of conservation of function for these EYA proteins through evolution [24]. Initial reports suggested that MAPK-catalyzed phosphorylation of Eya positively regulates fly eye development [25–27]. However, subsequent investigation revealed that MAPK-mediated Eya phosphorylation was dispensable for normal eye development or survival [28].

Whether the tyrosine phosphatase activity of *Drosophila* Eya contributes to eye development has been addressed multiple times with varying conclusions. The original studies using overexpression or mis-expression showed that phosphatase-dead forms of Eya were defective in the rescue of the *eya*-null eyeless phenotype [8,9]. However, when genomic transgenes mimicking endogenous spatial and temporal levels of Eya were used in rescue experiments, phosphatase-dead Eya complemented the *eya* null alleles [29]. When such dose-controlled rescue experiments were conducted in genetically sensitized backgrounds (heterozygosity for other RDGN components *sine oculis* or *dachshund*), the phosphatase-dead form of Eya was not able to support normal retinal development [30]. Hence the current thinking is that *Drosophila* Eya is not essential on its own, but rather contributes to the ‘robustness’ of RDGN output in fly eye development [30].

It is not straightforward to extrapolate from fly eye development to the more complicated process of vertebrate eye development. In flies, development initiates at a single imaginal disc epithelium. In contrast, in vertebrates, the optic vesicle evaginates from the forebrain and forms the optic stalk, the retina and the retinal pigment epithelium, while the lens and cornea derive from the surface ectoderm. *Eya1* is seen earliest in the ectoderm-derived lens placode, *Eya2* in the retina, and *Eya3* in the optic vesicle. While no gross eye phenotype has yet been reported upon knockout of any *Eya* gene in mice, there is one report of congenital cataracts and anterior segment anomalies in humans with an *Eya1* mutation [31]. *Eya1*^{-/-} mice die at birth with severe cranio-facial and skeletal defects. They also lack thymus, parathyroid glands, ears and kidneys [32]. Except for open eyelids, there appear to be no eye development defects. *Eya2*^{-/-} and *Eya3*^{-/-} mice have no obvious phenotype and are viable and fertile [33,34]. No eye phenotype has been recorded in double *Eya1*^{-/-}/*Eya2*^{-/-}

mice [33]. The only reported ocular effect upon loss of an EYA protein is a mild delay in the development of the post-natal mouse retinal vasculature upon endothelial-specific deletion of *Eya3* [35].

In this context, it is relevant that the loss of other components of the RDGN have variable effects on vertebrate eye development. *Six3*-null mice lack all forebrain structures including eyes [36]. Loss of *Dach1*, which is expressed in the developing retina, results in no eye phenotype [37]. *Pax6*^{-/-} mice die at birth with a complete disruption of eye development [38], and heterozygous *Pax6* mutation in humans results in small eyes [38]. Dosage effects of the *Pax6* gene on eye formation have been demonstrated through the use of the CRISPR/Cas system to generate a mosaic mixture of mutant and wild-type mice [39]. Notably, lens development from the surface ectoderm requires higher *Pax6* gene dosage than retinal development from the optic vesicle [39]. These observations suggest that the roles of the RDGN proteins in eye development are more complex than can be deciphered from simple loss-of-function experiments, and are likely to be influenced by genetic background, somatic mosaicism and perhaps environmental factors.

EYA in ear development

EYA1 contributes to multiple stages of inner ear development. The inner ear has six sensory organs and each one has sensory hair cells as well as non-sensory supporting cells. *Eya1* and the transcription factor *Sox2* are co-expressed in the otocyst where pro-sensory epithelia are formed and play a role in specifying the sensory cell lineage [40]. EYA1 along with SIX1 and the BRG1-associated SW1/SNF chromatin remodeling complex (BRG1-BAF) induce *Sox2*, and thereby promote the specification of a pro-neurosensory-restricted progenitor cell fate from an ectodermal cell [41]. The model proposed by these studies is that EYA1 bridges SIX1 and the BRG1-BAF complex, thus inducing the formation of a compact structure that enables binding to distant *cis*-regulatory elements, and hence *Sox2* induction [41]. Together, EYA1 and SOX2 are required for the expression of sensory markers including *Jag1*, *Lfng*, *Bmp4*, and *Fgfs*, and for cell cycle progression of these pro-sensory progenitors. Once the progenitors become committed to a hair cell fate, *Sox2* expression is no longer detected. However, *Eya1* continues to be expressed in differentiating hair cells along with *Atoh1*. Consistent with this, *Eya1*-null mice completely lack inner ear sensory organs. There is evidence that dose-dependent EYA1 activity is necessary for the development of different parts of the ear [40], mirroring the variation in inner ear malformation seen in patients with *Eya1* mutation-associated developmental disorders (described below). According to an *Eya2*^{lacZ} knock-in reporter study *Eya2* is also expressed in differentiating hair cells in the sensory epithelia of the inner ear and *Eya2*^{-/-} mice have a mild hearing deficit [41]. These new studies once again point to the likelihood that *Eya* genes can act synergistically during development, as well the possibility that they can compensate for each other and complicate loss-of-function studies. No studies have yet specifically queried the involvement of the C-terminal PTP activity of the EYA proteins in ear development.

EYA in muscle development

EYA proteins are implicated in various stages of trunk myogenesis. As in the case of the ear, the different *Eyas* are expressed at different timepoints during muscle development, and they work in conjunction with at least three SIX proteins. During early myocyte specification and myogenesis, *Eya1* and *Eya2* are expressed in the developing limb buds. *In vitro* reporter assays show that the N termini of these EYA proteins are sufficient to drive transactivation [42]. While some studies conclude that there is no requirement for EYA1 or SIX1 in early myogenesis [43] and that *Eya1* knockout mice show no muscle phenotype [44], others report that *Eya1* knockout mice have delayed myogenesis between e11 and e13, and that *Eya1*^{-/-}/*Eya2*^{-/-} mice have severe muscular abnormalities [33]. EYA1 also plays an important role in post-natal muscle development where it can switch a slow-twitch muscle to a fast-twitch phenotype by replacing the myosin I and IIA heavy chain isoforms to the fast-acting IIB and IIX isoforms [45]. *Eya3* knockout mice are also reported to have weaker muscle strength [34].

RDGN member SIX1 also plays a critical role in muscle development; *Six1* mutant mice have impaired myogenesis and extensive muscle defects in the forelimb, hindlimb and diaphragm [46]. There is a complete absence of all hypaxial muscles and a severe reduction in epaxial muscle in *Six1*^{-/-}/*Eya1*^{-/-} mice [44]. The EYA1-SIX1 complex activates SIX1 target genes involved in myogenesis including *Pax3*, *MyoD* and *Myogenin* [33]. Indeed, ectopic expression of *Eya1* and *Six1* (along with *Esrrb* (Estrogen related receptor-beta) and *Pax3*) is sufficient to induce myogenic stem cells with differentiation capacity *in vitro* and *in vivo* [47]. In flies, *eya* and *so* induce *tinman* expression (ortholog of mammalian NKX2-5), which in turn activates the JAK/STAT pathway to initiate myocyte differentiation [48]. In *Caenorhabditis elegans*, myogenic vs non-myogenic fate is determined by the SIX-EYA complex downstream of WNT signaling [49].

No specific examination of whether the tyrosine phosphatase function of the EYA proteins contributes to muscle development has been reported, and the implication in all of the studies cited above is that EYA acts as an activator of transcription in complex with the SIX proteins.

EYA in kidney development

Eya1^{+/-} mice have renal abnormalities while *Eya1*^{-/-} mice completely lack kidneys [32]. Ureteric bud outgrowth and consequently metanephric induction are compromised in the absence of EYA1. Downstream of *Eya1*, *Gdnf* expression is down-regulated in *Eya1*-null mice. *Eya1* is one of two genes (the other is *Osr1*) that are required for the initial formation of the metanephric mesenchyme which condenses to form a precursor cell population. These precursors can either differentiate (epithelialization to form the renal vesicle, the precursor of the nephron), or self-renew to maintain a progenitor pool at the tip of the ureteric bud (cap mesenchyme). A balance between self-renewal and differentiation is crucial to appropriate kidney development. *Eya1* (and *Six2*) are expressed in the cap mesenchyme throughout nephrogenesis representing an essential multipotent cell population [50].

Nuclear EYA1 in nephron progenitors stabilizes MYC, which in turn promotes the proliferation of undifferentiated cells. This occurs through dephosphorylation of Thr58 on MYC, thus preventing MYC degradation and increasing MYC half-life. EYA1-mediated MYC stabilization induces nephron progenitor cell proliferation [50]. Threonine phosphatase activity in the N-terminal domain of the EYA proteins had been previously shown to play a role in the innate immune response [18]. While no structural or sequence similarity with known phosphatase families could be found in the poorly conserved N-terminal domain of the EYAs, threonine phosphatase activity was confirmed by several follow-up studies [17,19]. However, a recent report has raised the possibility that the threonine phosphatase activity ascribed to the EYA proteins is actually mediated through an interaction with the PP2A B55 α subunit [21]. But in glioblastoma stem cells EYA1 directly interacts with MYC, and the EYA1-MYC axis regulates GSC proliferation, migration and self-renewal [51]. Regardless of the mechanism through which it occurs (either directly mediated by EYA or via PP2A), links between EYA proteins and MYC stabilization continue to emerge in contexts beyond kidney development (Figure 2).

EYA proteins in other developmental contexts

Knockout studies show that the development of several neural-crest derived cranial structures are EYA1-dependent. *Eya1*^{-/-} embryos have defective pharyngeal arches and lack proximal arch structures contributing to a broad spectrum of defects in cranio-facial morphogenesis [52]. Interestingly, this is another developmental context in which a putative EYA1 threonine phosphatase activity is implicated: threonine dephosphorylation of the Notch intracellular domain (NICD) is believed to stabilize the NICD and thus enhance Notch signaling, a crucial contributor to cranio-facial development (Figure 2).

EYA1 is also required for the morphogenesis of organs derived from the third pharyngeal pouch (thymus, parathyroid, thyroid). *Eya1*^{-/-} mice display thyroid hypoplasia and the thymus and parathyroid fail to form [53]. *Eya1*^{-/-} mutants also have a spectrum of abnormalities in cardiovascular development, the most common being aortic arch defects [54]. This is exacerbated in *Six1*^{-/-}/*Eya1*^{-/-} double mutants (cardiac outflow tract and aortic arch defects), partially due to a reduction in fibroblast growth factor 8 (Fgf8) levels [54].

EYA1, along with SIX1, contributes to hindbrain development through its ability to promote *Nrp1* transcription and favor Gli activators over Gli repressors following sonic hedgehog (Shh) stimulation [55]. In keeping with this role, *Eya1* is expressed in Shh-subtype medulloblastomas and promotes tumor growth [55]. A Shh-Eya1 axis is also involved in promoting symmetric cell divisions during cerebellar development [22]. This is believed to occur through dephosphorylation of Thr410 and thus inactivation of the atypical protein kinase aPKC ζ [22], once again implicating an EYA-linked threonine phosphatase activity in development.

A recent report shows that *Eya1* is expressed in the bitter taste receptor cells of the oral epithelium and in the differentiating taste bud cells in circumvallate and fungiform papillae and the soft palate [56]. The signaling pathway(s) through which EYA contributes to the generation and differentiation of taste buds (specifically bitter cells) remains to be established.

EYA in photoperiodism

An intriguing association between EYA3 and photoperiodism is emerging largely through studies on large seasonal animals and birds. Photoperiodism is a phenomenon through which functional and behavioral responses accommodate changes in the length of dark and light cycles, thus allowing plants and animals to adjust to

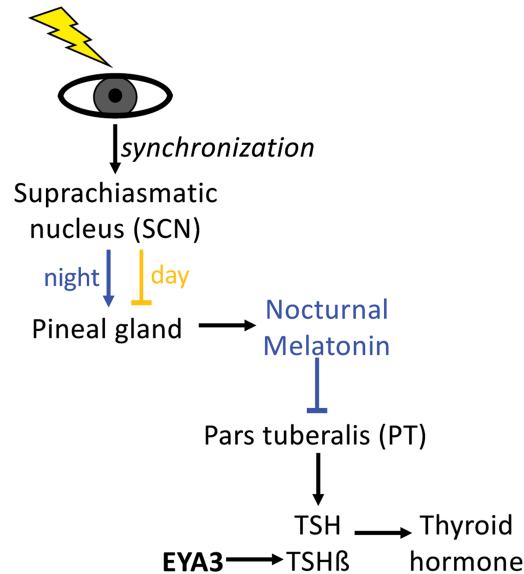


Figure 3. EYA3 in photoperiodism.

A simplified schematic showing how light signaling through the eye is transmitted through the SCN and inhibits melatonin release by the pineal gland. Hence melatonin is exclusively secreted at night. TSH levels in the thyrotrophic cells of the PT display melatonin-dependent photoperiodic changes; high TSH under long photoperiod, and low levels under short photoperiod. EYA3 promotes transcription of the TSH β subunit and thus acts as an ‘on-switch’ for TSH, making EYA3 a central player in photoperiodic time measurement [91]. EYA3 is induced 12.5 h after the onset of melatonin expression. As a result, EYA3 levels rise at first light in the summer and during the final hours of darkness in the winter.

seasonal variation. In animals, photoperiodism impacts phenomena such as growth, metabolism, migration, reproductive behavior, and hibernation. In mammals, light-sensitive retinal ganglion cells (RGCs) transmit light information to the suprachiasmatic nucleus (SCN) in the hypothalamus (Figure 3). This signal is then transmitted via light-sensitive neurons to the pineal gland, where nocturnal melatonin is synthesized. The length of the melatonin signal is consequently proportional to the length of the dark period, or night, and is read by the pars tuberalis (PT) in the pituitary gland [57]. Long days (summer) induce thyroid stimulating hormone (TSH; a heterodimer of α and β subunits) in the PT. TSH in turn promotes thyroid hormone production and activity in the basal hypothalamus, thus interfacing with the regulation of crucial season-guided physiology such as reproduction.

An EYA3-SIX1-TEF complex up-regulates TSH β transcription in the PT [58]. EYA3 expression in the PT is rhythmic, peaking transiently 12.5 h after the onset of darkness or melatonin expression. As a result, in winter EYA3 peaks late in the night while in summer EYA3 peaks at dawn. *Eya3* expression is thus central to the PT coincidence timing mechanism. Furthermore, through a positive feedback loop EYA3 promotes its own transcription and amplifies the EYA3-dependent coincidence-timer. As a consequence, EYA3 is a key player in the ability to switch between the winter and summer phenotypes that follow from gradual changes in day length in the Spring and Fall [59].

The tyrosine phosphatase-dead form of EYA3 was able to potentiate TEF/SIX1-mediated TSH β transcription to levels comparable to the wild-type protein [58], suggesting that the tyrosine phosphatase activity is dispensable for EYA3’s role in photoperiodism. Collectively, the currently available evidence supports a role for EYA3’s trans-activation activity in measuring night length and tuning the circadian clock with seasonal changes [60].

Developmental disorders associated with EYA mutations

The importance of EYA proteins (and the RDGN network) during crucial stages of embryonic development is reflected in the numerous developmental disorders associated with *Eya* mutations. These are typically manifest as defects in eye, ear, neck, cranio-facial, and heart development (summarized in Table 1). Below we describe the developmental defects frequently associated with *Eya* mutations and, when available, links between the biochemical activities of the EYA proteins and these disease states.

Table 1. A summary of *Eya* mutations associated with developmental disorders

Disease/affected organ(S)	GENE	Mutations	References
Branchio-oto-renal Syndrome 1 (BOR)/disrupted development of tissues in neck, malformation of ears and kidneys	<i>EYA1</i>	Deletions, insertions, mis-sense mutations	[61,64–66,69,70]
Branchio-oto-syndrome 1 (BOS)/disrupted development of tissues in neck, malformation of ears		Insertions, deletions	[66]
Oto-facio-cervical Syndrome (OFC)/facial dysmorphism, ear anomalies, branchial cysts or fistulae, anomalies of the vertebrae and should girdle, mild intellectual disability	<i>EYA1</i>	Deletions, splice site mutations	[63,67]
Anterior segment anomalies, congenital cataracts/defects of the cornea, lens, iris and aqueous humor	<i>EYA1</i>	Mutations, substitutions	[31]
Cardio-facial Syndrome/asymmetric crying face and heart defect	<i>EYA1</i>	Deletions, frame-shifts	[73]
Late-onset deafness (non-syndromic)	<i>EYA4</i>	Truncations, mutations	[77,78]
Dilated cardiomyopathy with sensorineural hearing loss/progressive defect in cardiac muscle, defects affecting inner ear and auditory nerve	<i>EYA4</i>	Deletions	[75,80]
Oculo-auriculo-vertebral Spectrum (Goldenhar Syndrome)/deformity of external ear and small ipsilateral half of face, vertebral anomalies	<i>EYA3</i>	Mis-sense mutation	[81]

Eya1 is one of the three known causative genes for BOR (Branchio-oto-renal syndrome also known as Melnick–Fraser syndrome; the other two genes being RDGN members *SIX1* and *SIX5* [61,62]). BOR is an autosomal dominant disorder characterized by malformations of the neck, ears and kidney. These include (to varying degrees) branchial fistulae or cysts, hearing loss as a result of inner, middle and outer-ear malformations, and kidney abnormalities ranging from hypoplasia to agenesis. Features of BOR partially overlap with otofaciocervical syndrome (OFC), a rare developmental defect characterized by distinctive facial features (triangular face, broad forehead, narrow nose and mandible, high arched palate), prominent ears, long neck, branchial fistulae or cysts, sloping shoulders and clavicles, hearing impairment and mild intellectual defects. *Eya1* mutations are also associated with OFC [63]. Furthermore, *Eya1* mutations are sometimes seen in patients with congenital cataracts and ocular segment anomalies, sometimes associated with BOR [31]. Deletions, mis-sense mutations as well as complex rearrangements of the *Eya1* gene are reported in BOR and OFC patients [61,64–70]. Most of the mutations are unique to individual families and no apparent genotype–phenotype correlation has yet emerged. Several experimental studies tried to link individual mis-sense mutations to biochemical activities, variably reporting impaired tyrosine phosphatase activity as well as impaired interaction with the SIX proteins [71,72].

Eya1 mutations have been reported in patients with congenital cardiac abnormalities [73,74], and mutation of *Eya4* is associated with dilated cardiomyopathy [75]. Genetic studies using compound deletions in mice show that *EYA1* and *SIX1* play a role in cardiovascular development, and it is proposed that a *Tbx1-Six1/Eya1-Fgf8* regulatory cascade underlies a common mechanism important for the morphogenesis of both the heart and the face [54]. This data has led to the speculation that the pathogenesis of BOR and cardio-facial syndrome could be linked to *Eya1* and *Six1* mutations via a common molecular program [54].

Eya4 mutations are reported in several families with non-syndromic autosomal dominant post-lingual progressive hearing loss (late-onset deafness) [76–79]. Most of these mutations result in truncated *EYA4* protein lacking most, or all, of the conserved ED (tyrosine phosphatase) domain. There is some evidence that while loss of just the tyrosine phosphatase domain causes non-syndromic sensorineural hearing loss, disruption of both the ED and the N-terminal domains is associated with syndromic (dilated cardiomyopathy with sensorineural hearing loss) disease [75,78]. One clinically actionable extension of these studies on the pleiotropic effects of *Eya4* gene variants is described in a recent study where a ‘genotype-first’ approach was used to identify as-yet undiagnosed cardiac conduction disorders in adults presenting with hearing loss [80].

A recurrent mutation in *Eya3* (resulting in an Asn358Ser substitution) causing oculo-auriculo-vertebral spectrum has recently been reported [81]. This mutation appeared to increase the half-life of *EYA3* but have no impact on tyrosine phosphatase activity. This report notwithstanding, in general *Eya2* and *Eya3* mutations are

rarely been linked with developmental disorders. This could be a consequence of redundancy, since while both genes are broadly expressed during development, they are most often co-expressed with other *Eya* genes.

Conclusions

Many decades after *Drosophila* EYA was first described, insights into the roles of EYAs in normal development, physiology and disease continue to emerge. Not described here, but of emerging clinical importance, is the therapeutic potential of targeting the EYA PTP activity for diseases ranging from cancer [82–84] to pulmonary arterial hypertension [85] and proliferative retinopathies [35]. Much remains to be clarified regarding EYA protein function and regulation. The question of whether the N-terminal domain and C-terminal domain activities of the EYA proteins impact on each other is still a matter of some debate. The fact that interaction with the SIX proteins is mediated by the ED domain, while transactivation potential exists in the N-terminal domain suggests that, at least for the transactivation activity in the context of the RDGN, the two domains are functionally linked. It is curious that the PTP activity of the EYA proteins has not yet been linked to any major developmental role, other than contributing to post-natal vascular development in the murine retina [35]. This is particularly notable since the EYA-PTP activity promotes DNA damage repair [10] and cell motility [14,15], two processes important in development: embryonic development involves rapid cell proliferation inevitably accompanied by DNA damage, and cell motility plays a crucial role in morphogenesis. It is likely that subtle developmental defects attributable to the PTP activity will be uncovered upon more careful examination in the future.

How did the EYA proteins come to have so many biochemical activities in a single polypeptide? It is interesting to speculate about where these activities originated. Notably, plants have an EYA protein that is comprised solely of the ED domain [7], and no significant amino-acid sequence homology exists between the EYA N-terminal domain and any other known protein sequence [4]. It has been suggested that some animal EYA proteins with an ED-like domain have very weak, or no, tyrosine phosphatase activity [86]. But this has not been experimentally queried. Could the EYA proteins we see in vertebrates have emerged from an ancestral ED domain-containing protein that may, or may not, have had tyrosine phosphatase activity? Does the N-terminal domain have intrinsic threonine phosphatase activity? Evolutionary biochemists suggest that all enzymes are promiscuous (have an average of 10 promiscuous activities [87–89]). Perhaps the putative threonine phosphatase activity of the EYA proteins is one such instance of evolution in progress? In this review, we have attempted to match the observed biochemical activities of the EYA proteins with their developmental roles, as understood from our vantage point at one moment in the evolutionary journey of the EYA proteins.

Perspectives

- EYA transactivator-phosphatase proteins play crucial roles in embryonic development and in tissue homeostasis. Mutations or mis-expression of EYA are linked to human genetic disorders and cancers, offering opportunities for the development of therapeutics and genetic diagnoses.
- The vast majority of the studies thus far implicate the EYA transactivation function in cell-fate determination. However, a growing body of evidence suggests that the tyrosine phosphatase activity (and the putative threonine phosphatase activity) could contribute to disease states. These observations are now being exploited in efforts to devise EYA-targeted therapeutics.
- Beyond the further examination of the myriad signaling pathways impacted by EYA-mediated transactivation and dephosphorylation events, examination of the molecular evolution of this unusual protein is of great interest. Such studies could be important contributors to our understanding of how phosphorylation-based signaling mechanisms evolved in general.

Competing Interests

The authors declare that there are no competing interests associated with the manuscript.

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Author Contributions

US helped write, edit, and generate figures, K.R. helped write and edit, R.S.H. wrote this article and generated figures.

Abbreviations

BOR, branchio-oto-renal; EYA, Eyes Absent; NICD, Notch intracellular domain; OFC, otofaciocervical syndrome; PP2A, protein phosphatase 2A; PTP, protein tyrosine phosphatases; RDGN, retinal determination gene network; TSH, thyroid stimulating hormone.

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