Regulation of the SOX3 Gene Expression by Retinoid Receptors

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Summary

Sox3/SOX3 gene is considered to be one of the earliest neural markers in vertebrates. Despite the mounting evidence that Sox3/SOX3 is one of the key players in the development of the nervous system, limited data are available regarding the transcriptional regulation of its expression. This review is focused on the retinoic acid induced regulation of SOX3 gene expression, with particular emphasis on the involvement of retinoid receptors. Experiments with human embryonal carcinoma cells identified two response elements involved in retinoic acid/retinoid X receptor-dependent activation of the SOX3 gene expression: distal atypical retinoic acid-response element, consisting of two unique G-rich boxes separated by 49 bp, and proximal element comprising DR-3-like motif, composed of two imperfect hexameric half-sites. Importantly, the retinoic acid-induced SOX3 gene expression could be significantly down-regulated by a synthetic antagonist of retinoid receptors. This cell model provides a solid base for further studies on mechanism(s) underlying regulation of expression of SOX3 gene, which could improve the understanding of molecular signals that induce neurogenesis in the stem/progenitor cells both during development and in adulthood.

Key words

SOX3 • Retinoic acid • Retinoid receptors • Embryonal carcinoma cells • Neuronal differentiation

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Sox3/SOX3 gene

The Sox/SOX gene family encodes transcription factors that act as key regulators of diverse developmental processes, such as early embryogenesis, gastrulation, neural induction, formation of various organs and tissues, specification and differentiation of many cell types (Lefebvre et al. 2007, Pevny and Lovell-Badge 1997, Wegner 1999). It is known that SOX transcription factors carry a DNA-binding HMG domain and perform their functions in complex interplay with other transcription factors in a manner highly dependent on cell type and promoter context (Kamachi et al. 2000). They show both classical and architectural modes of action (Pevny and Lovell-Badge 1997), either activating or repressing specific target genes (Wilson and Koopman 2002). Based on protein sequence comparisons, Sox/SOX transcription factors are divided into 10 distinct groups designated A-J (Bowles et al. 2000).

SOX3 together with SOX1 and SOX2 belongs to the SOXB1 subgroup of transcriptional activators (Uchikawa et al. 1999), which are pan-neurally expressed and have redundant roles in maintaining the broad developmental potential and identity of neural stem cells (Bylund et al. 2003, Pevny and Placzek 2005). In addition to regulating progression of neurogenesis, this group of activators is also operative in post-mitotic neurons (Ekonomou et al. 2005, Ferri et al. 2004, Rizzoti et al. 2004).

Sox3/SOX3 gene is an X-linked member of the family and the closest relative of sex-determining region Y gene (SRY) (Stevanovic et al. 1993). It is considered to be one of the earliest neural markers in vertebrates,
playing a role in specifying neuronal fate (Brunelli et al. 2003). This gene is also implicated in the genetic cascades that direct gonadal development, brain formation, and cognitive function (Pevny and Lovell-Badge 1997, Stevanovic et al. 1993, Wegner 1999, Weiss et al. 2003). The Sox3/SOX3 gene is highly expressed in the ventral diencephalon and its deletion is thought to result in either cell death or defects in neuronal activity (Rizzoti et al. 2004). Dysfunction of the SOX3 protein disturbs the cellular processes required for cognitive and pituitary developments, leading to mental retardation and growth hormone deficiency in humans (Laumonnier et al. 2002, Stankiewicz et al. 2005, Woods et al. 2005).

Despite the mounting evidence that Sox3/SOX3 is one of the key players in the development of the nervous system, limited data are available regarding the transcriptional regulation of its expression. Using mouse transgenic reporter assays, Brunelli et al. (2003) identified cis-regulatory regions of the mSox3 gene that direct its tissue-specific expression. It has been shown that genomic region comprising 3 kb upstream and 3 kb downstream of the mSox3 open reading frame, is sufficient to mimic most aspects of the gene’s endogenous expression pattern, from the onset of neurogenesis up to midgestation stages (Brunelli et al. 2003). The study in Xenopus laevis embryos by Rogers et al. (2008) indicated that the 1.5 kb upstream regulatory region contains most of the information necessary to recapitulate the spatial and temporal expression of xSox3 gene. Fine dissection of xSox3 promoter has revealed the presence of two enhancer regions necessary for full xSox3 expression, as well as one repression module that restricts the expression of this gene to neuroectoderm (Rogers et al. 2008).

Previously we generated data regarding transcriptional regulation of the human SOX3 gene using embryonal carcinoma (EC) cell line NT2/D1, as a model system. Initially, we determined the SOX3 transcription start point (tsp), promoter region that confers basal promoter activity, as well as positive regulatory elements necessary for optimal promoter activity (Kovacevic Grujicic et al. 2005). Also, we found that ubiquitous transcription factors Sp1 (specificity protein 1), USF1 (upstream stimulatory factor 1), NF-Y (nuclear factor Y), MAZ (myc-associated zinc finger protein) and PBX1/MEIS1 (pre-B-cell leukaemia homeobox 1/myeloid ecotropic viral integration site 1 homologue) act as positive regulators of SOX3 gene expression (Krstic et al. 2007, Mojsin and Stevanovic 2010, Kovacevic Grujicic et al. 2005, Kovacevic Grujicic et al. 2008, Stevanovic 2009). Furthermore, our previous work indicated that retinoic acid (RA) induction of NT2/D1 cells is accompanied by up-regulation of SOX3 gene expression (Mojsin et al. 2006, Stevanovic 2003). This review is focused on the RA-induced regulation of SOX3 gene expression, with particular emphasis on the involvement of retinoid receptors in this process.

**NT2/D1 cell line as a model system for neural differentiation**

EC cells are stem cells derived from teratocarcinomas, which arise from transformed germ cells, and are generally considered to be the malignant counterparts of human embryonic stem (ES) cells (Andrews 2002). To date, the most widely characterized EC cell line is NT2/D1. These cells are derived by cloning the NTERA-2 cells established from a nude mouse xenograft of the TERA-2 cell line, which was originally derived from a metastasis of a human testicular teratocarcinoma (Andrews 1984). NT2/D1 cells resemble early ES cells in morphology, antigen expression patterns, biochemistry, developmental potential, and gene regulation (Andrews 1984). Upon culture in RA, NT2/D1 cells differentiate into well developed, morphologic, and immunophenotypic central nervous system-like neurons, with associated loss of cell growth and tumorigenicity (Andrews 1984, Kurie et al. 1993, Spinella et al. 1999). These cells have properties similar to those of progenitor cells in the central nervous system (CNS), providing an excellent in vitro model system for studying human genes that promote and regulate neural differentiation (Spinella et al. 2003).

**The role of RA in neurodevelopment**

Retinoid signaling contributes to development of the CNS (Maden 2002). In lower vertebrates, it is required for generating the adequate numbers of primary neurons, and for their correct positioning (Sharpe and Goldstone 2000). In the embryonic vertebrate CNS, RA has a role in patterning both the anteroposterior and dorsoventral axes (Cunningham et al. 1994). Its main sites of action are the hindbrain and anterior spinal cord (Glover et al. 2006). RA also regulates interneuron and motor neuron development along the dorsoventral axis (Sockanathan and Jessell 1998).

Moreover, important regulatory role of RA within the adult CNS has been described (Christie et al. 2002).
2008). Namely, it was shown that specific areas of the brain, known to undergo active remodeling of neural connections throughout adulthood, synthesize RA (the basal ganglia, olfactory bulbs, hippocampus and auditory afferents) (Dev et al. 1993). Importantly, the high levels of RA and associated proteins in the hippocampus, the dentate gyrus in particular, strongly implied the involvement of these molecules in region-specific neurogenesis (Jacobs et al. 2006). It was revealed that RA contributed significantly to neuronal differentiation within the dentate gyrus, being involved at a very early stage throughout this process (Jacobs et al. 2006).

Deregulation of RA signaling has been suggested to be an underlying cause of several neurological disorders, such as Alzheimer’s and Parkinson’s diseases (Christie et al. 2008). Accordingly, understanding the mechanisms of RA action in the developing and adult CNS is an important issue, and recently gained additional significance as a therapeutic strategy.

**RA signaling**

Retinoic acid is naturally occurring, main vitamin A derivative that plays a critical role in the development and homeostasis of all vertebrate tissues, including cell differentiation, proliferation, metabolism and apoptosis (Altucci and Gronemeyer 2001, Ross et al. 2000). The retinoid signal is primarily mediated by two families of nuclear retinoid receptors: RA receptors (RARs; NR1B) and retinoid X receptors (RXRs; NR2B), which work as ligand activated transcription factors in a spatio-temporal specific manner (Kastner et al. 1997). There are three different RAR and RXR isotypes (α, β and γ) that are encoded by separate genes at distinct chromosomal loci (Chambron 1996). Members of these two retinoid receptor families form stable heterodimers that, in response to RA binding, modulate the transcription of target genes via cis-acting RA response elements (REs), RAREs (Mangelsdorf and Evans 1995). The majority of classical RAREs, specifically recognized by RXR/RAR heterodimers, consist of a direct repeat (DR) of two hexameric half-sites with the consensus sequence 5’-PuG(G/T)TCA-3’, most commonly separated by two or five ‘spacer’ nucleotides (DR-2 or DR-5, respectively) (Bastien and Rochette-Egly 2004, Laudet and Gronemeyer 2002).

In addition, the biological activity of RA is extended by the fact that RXR acts as a homodimer (IJpenberg et al. 2004), or as an obligate heterodimeric partner for a various array of other members of the intracellular receptor superfamily, such as thyroid hormone receptors (TRs), vitamin D receptors (VDRs), peroxisome proliferator-activated receptor (PPAR), farnesoid X-activated receptor (FXR), liver-X receptor (LXR) and other (Laudet and Gronemeyer 2002, Lefebvre et al. 2010). These various receptors strongly interact with RXR, and their transcriptional activities are exerted mainly by the resulting heterodimers. RXR thus functions as a “master regulator” of multiple signaling pathways that are essential for mammalian physiology and development (Germain et al. 2006). RXR homodimers bind to REs in which the half-sites are separated by 1 bp (DR-1), and RXR containing heterodimers exhibit distinct preferences for a certain spacer length that could be one to five nucleotides (DR-1 to DR-5, respectively) (Laudet and Gronemeyer 2002). Therefore, configuration of these REs, i.e. the arrangement and the spacing between the half-sites, is an important determinant that confers the selectivity and binding specificity of RXR homo/heterodimers (Glass 1994, Laudet and Gronemeyer 2002).

Hundreds of genes have now been shown to be regulated by RA during the processes of neuronal differentiation and neurite outgrowth (Maden 2001). However, only for a minority of them it has been unquestionably shown that are direct targets of the classical RAR–RXR–RARE pathway (Balmer and Blomhoff 2002, Blomhoff and Blomhoff 2006). In many cases, the gene regulation appears to be indirect, reflecting the actions of intermediate transcription factors, non-classical associations of receptors with other proteins, or even more distant mechanisms (Blomhoff and Blomhoff 2006).

Many RA-regulated genes have been discovered in human EC cells. However, precise understanding of the particular gene regulation by retinoids in these cells is yet to be accomplished (Soprano et al. 2007). Therefore, the study of the human SOX3 gene expression, for which we have shown that is a direct RA downstream target in NT2/D1 EC model system, is valuable for future investigation of molecular events underlying EC cells neuronal differentiation following RA treatment.

**Localization of RA responsive regions and involvement of retinoid receptors in the regulation of SOX3 gene expression**

Initially, we showed that SOX3 gene is expressed in NT2/D1 cells and that early phases of differentiation and
neural induction, which take place within 48 h of RA exposure, involve up-regulation of this gene expression at both mRNA and protein levels (Mojsin et al. 2006, Stevanovic 2003). This is also in correlation with the literature data based on microarray analysis (Freemantle et al. 2002). Since the molecular mechanism(s) underlying regulation of SOX3 gene by RA are still unknown, our first goal was to search for regions within SOX3 promoter that mediate RA-induced transcription.

Using enhancer-dependent reporter plasmid approach, we showed that regulatory elements responsible for both, basal and RA-induced transcripational activation of SOX3 gene are localized within the 400 bp of its 5'-flanking region (Mojsin et al. 2006). To explore whether the SOX3 induction is mediated by retinoid receptors, overexpression studies with RXRα were employed. The RXRα has been chosen as the representative of retinoi d receptors, to serve as a tool in the study of SOX3 gene responsiveness to RA. Overexpression of RXRα resulted in up-regulation of SOX3 gene expression in response to RA (Mojsin et al. 2006). These results confirmed that RA effect on SOX3 gene expression is mediated by retinoid receptors.

Localization of RA/RXR response elements

A more systematic search for regulatory regions that are able to mediate responsiveness to RA was performed by deletion mapping of the SOX3 400 bp 5'-flanking region (Mojsin et al. 2006, Nikcevic et al. 2008). Two response elements involved in RA/RXR-dependent activation of the SOX3 gene expression were identified (Mojsin et al. 2006, Nikcevic et al. 2008), designated as distal and proximal REs (Fig. 1).

The distal RA/RXR response element is pinned down to two regulatory elements (Mojsin et al. 2006). Only in the presence of both elements, full RA/RXR inducibility is achieved, suggesting they act synergistically. By DNase I footprinting and gel shift analyses, RXR binding motifs were determined, revealing that these regulatory elements comprise two unique G-rich boxes separated by 49 bp (Mojsin et al. 2006). Since these motifs did not show any homology to known nuclear receptor REs commonly present in RA-responsive genes, we have proposed it should be considered as a novel, atypical RA/RXR response element (Mojsin et al. 2006) (Fig. 1). Interestingly,
literature data indicate that RAREs can be increasingly diverse in the core consensus motifs, with unusual spacing or symmetry attributes (Balmer and Blomhoff 2005). For example, activation of the Burkitt lymphoma receptor 1 gene (blr1) by RA seems to depend on RARE (17 bp in length), that contains two, arbitrarily named, GT box elements (Wang and Yen 2004). Also, composite response unit that encompasses two degenerate, GC-rich sequences, separated by 30 nucleotides, mediates RA induction of the human retinol-binding protein gene (RBP) (Panariello et al. 1996).

Further deletion analysis pointed to the presence of an additional, proximal SOX3 regulatory region responsive to RA that contains an RA/RXR responsive region, as determined by overexpression of RXRα in NT2/D1 (Nikcevic et al. 2006, Nikcevic et al. 2008). By competition and scanning gel-shift analyses, this region was narrowed down to a 31 bp fragment that directly interacts with recombinant RXRα. Furthermore, by gel-shift mutation analysis of 31 bp fragment, we identified the sequence 5'-GGGTCCcccGGTGTG-3' as an RXR binding site (Nikcevic et al. 2008). It represents a DR-3-like motif, composed of two hexameric half-sites, separated by 3 bp (Fig. 1).

In addition, functional significance of the DR-3-like element was indicated by mutational analyses, which showed that disruption/mutation of this element caused significant reduction of RA/RXR transactivation of the SOX3 promoter (Nikcevic et al. 2008). Moreover, the crucial evidence for functional relevance of this regulatory region came from results showing that 31 bp oligonucleotide, encompassing the DR-3-like element, is capable of independently mediating the RA/RXR effect in a heterologous promoter context (Nikcevic et al. 2008).

### Involvement of retinoid receptors in the regulation of SOX3 gene expression

Testing the binding ability of the described DR-3-like motif revealed that both recombinant and RXRα from nuclear extracts of RA-treated NT2/D1 cells interact with this motif in a sequence-specific manner. In addition, we have analyzed the potential binding of RARs and VDRs to the DR-3-like SOX3 RE. The involvement of nuclear receptor VDR was analyzed because the identified DR-3 binding site resembled the configuration of RE characteristic for vitamin D receptors (Aranda and Pascual 2001). However, our experiments suggested that neither RARs nor VDRs participate in complex formation as RXRs heterodimeric partners (Nikcevic et al. 2008). This finding emphasized the need to continue study of the SOX3 gene responsiveness to RA in natural settings, and for that purpose, we have employed synthetic retinoids.

Specifically, advances in the understanding of nuclear receptors at both structural and functional level enabled the design of ligands, selective receptor modulators that have specific agonist or antagonist features (Altucci et al. 2007, de Lera et al. 2007). In order to assess the involvement of each class of retinoid receptors in RA-induced SOX3 up-regulation on the endogenous level, we treated NT2/D1 cells with RXRs and RARs pan-antagonists (LG101208 and LG100815, respectively) in the presence of RA (Nikcevic et al. 2008). The results of western blot analysis showed that the RA induction of SOX3 protein expression was reduced in the presence of RXR antagonist, whereas the treatment with RAR antagonist did not markedly alter the RA effect on SOX3 expression (Nikcevic et al. 2008). This data pointed to RXRs, but not RARs, as mediators of the RA effect on the endogenous SOX3 up-regulation in NT2/D1 cells. It is important to underline that by using this approach, we showed for the first time, that RA-induced SOX3 gene expression could be significantly down-regulated by the synthetic antagonist of RXR.

The observed RA effect on SOX3 gene expression that relies on RXR and not on RAR, might indicate integration of RA and another signaling pathway(s) through defined RXR binding site(s) within the SOX3 promoter. In that view, potential RXR partner(s), whose activity might be ligand dependent, would be particularly interesting implying another signaling that together with RA pathway could be responsible for the fine-tuning of SOX3 gene regulation.

We also studied potential involvement of RXR homodimers in mediating the RA effect on the up-regulation of SOX3 gene expression in NT2/D1 cells. For that purpose, we used a potent and efficacious activator of RXR homodimers (LG100268). Results of western blot analysis showed that RXR homodimers are not responsible for mediating the RA effect on endogenous SOX3 gene expression (Savic et al. 2009).

Additional experiments, focusing on defining the RXR partners, are necessary for the precise characterization of this RA–RXR–SOX3 signaling and its wider biological significance.
The involvement of other transcription factors in the up-regulation of SOX3 gene expression by RA

Our work pointed to multiple CCAAT box control elements within the SOX3 promoter that could be recognized as modulators of RA-induced activation of SOX3 gene expression (Krstic et al. 2007). Also, we recently showed that the TALE (three-amino-acid loop extension) transcription factors PBX1 and MEIS1 participate in regulating RA-dependent up-regulation of SOX3 gene expression. It appears that PBX1/MEIS1 directly interact with the binding site within SOX3 basal promoter region, which is conserved in all analyzed mammalian orthologues, and that these transcription factors are responsible, at least in part, for SOX3 responsiveness to RA (Mojsin and Stevanovic 2010).

It is also interesting that NF-Y and TR/RXR nuclear receptors functionally interact to confer triiodothyronine (T3)-stimulated transactivation of the hepatic S14 gene (Jump et al. 1997). Furthermore, it was reported that PBX1/MEIS1 heterodimers interact with TR/RXR complex to enhance T3 regulation of malic enzyme transcription in hepatocytes (Wang et al. 2001). In accordance with these data, it is reasonable to speculate that accurate expression of the SOX3 gene during specific stages of development depends on differential usage and/or interplay of the described multiple RAREs, PBX1/MEIS1 and NF-Y binding sites within the promoter of this gene (Fig. 1). Accordingly, further studies are needed to identify the coordinated action of nuclear receptors, NF-Y, PBX1/MEIS1, and other, not yet identified transcription factor(s), in the up-regulation of SOX3 gene expression during early stages of RA-induced neural differentiation of NT2/D1 cells.

Significance and future directions

Recently, considerable attention has been focused on understanding the molecular basis of pluripotency and the earliest differentiation processes. The knowledge gained through these studies would pave the path to grow and manipulate pluripotent ES cells efficiently, reproducibly and in a manner appropriate for clinical applications (Johnson et al. 2008). NT2/D1 cells are considered as an important alternative to stem cells, having properties similar to those of progenitor cells in the CNS. Therefore, elucidating mechanism(s) underlying regulation of expression of SOX3 gene in this human EC cells model system will improve the understanding of molecular signals that induce neurogenesis in the stem/progenitor cells both during development and in adulthood. The presented line of study should also accelerate the evaluation of SOX genes as potential targets for modulation of proliferation and differentiation of neural progenitors.

Because the neuronal loss is a common feature of many neurological disorders, including stroke, Parkinson’s and Alzheimer’s diseases, and traumatic brain injury, it is worthy highlighting the following. First, after exposure to RA, NT2 cells were used for transplantation as cell therapy for brain injury, ischemia, and neurodegenerative diseases in animal models as well as in two clinical trials of human stroke patients (Newman et al. 2005). Second, it was postulated that RA-dependent molecular cascade could play a central role in the intrinsic regenerative capacity of the CNS (Malaspina and Michael-Titus 2008). However, despite the recent progress, the replacement of lost cells, either by cell transplantation or by the manipulation of patient’s progenitor cells in situ, is still far from the routine therapeutic practice. In that respect, it is essential to dissect each step of adult neurogenesis in order to enable selection of those mechanisms that could be targets for potential pharmaceutical approaches and future clinical applications. We believe that elucidating mechanism(s) underlying regulation of expression of human SOX3 gene in NT2/D1 cells could represent valuable contribution to this field.

Conflict of Interest

There is no conflict of interest.

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