Sry: the master switch in mammalian sex determination

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Summary

SRY, the mammalian Y-chromosomal testis-determining gene, induces male sex determination. Recent studies in mice reveal that the major role of SRY is to achieve sufficient expression of the related gene *Sox9,* in order to induce Sertoli cell differentiation, which in turn drives testis formation. Here, we discuss the cascade of events triggered by SRY and the mechanisms that reinforce the differentiation of the testes in males while actively inhibiting ovarian development.

Key words: *Sry*, Sex determination, *Sox9*, Testis, Sertoli cell

Introduction

The development of two sexes is observed in most animals and is essential for their survival and evolution. Disorders of sex development (DSDs; see Glossary, Box 1) are among the most common genetic diseases in humans and are often associated with genital ambiguity (Kronenberg and Williams, 2007). Because of its clinical and biological importance, identifying the mechanism of sex determination – the developmental decision to generate either testes or ovaries – continues to attract the attention of a broad range of researchers, including developmental biologists, biomedical scientists, evolutionary biologists and ecologists.

In mammals, two major breakthroughs have shaped our current understanding of sex determination. First, in 1959, two human DSDs, Turner syndrome (XO females) and Klinefelter syndrome (XXY males) were identified and reported (Ford et al., 1959; Jacobs and Strong, 1959), and these studies established that the Y chromosome carries a gene that determines maleness. It would take another 30 years before the second breakthrough was made: the discovery of *SRY* (sex-determining region on the chromosome Y, denoted *Sry* in species other than humans). The human *SRY* gene was identified by searching for conserved sequences among translocated Y chromosomal DNA from four XX male patients (Sinclair et al., 1990). The presence of a similar gene, *Sry*, on the mouse Y chromosome was consistent with this gene having a sex-determining function (Gubbay et al., 1990). The role of *Sry* as the switch gene for mammalian sex determination was confirmed in experiments in which XX mice were converted to males by the introduction of *Sry* (Koopman et al., 1991).

Sry and the molecular mechanisms of sex determination have continued to be studied intensely over the past 20 years. Unlike other developmental systems that are well conserved through evolution, sex determination is highly variable in the animal kingdom, and the genetic mechanisms involved in common laboratory model organisms, such as flies, nematode worms, chickens and frogs, bear little, if any, resemblance to those used in mammals. Indeed, *Sry* is found only in mammals, though not in all mammalian orders – monotremes (see Glossary, Box 1), for example, lack *Sry*. Most of our current understanding of *Sry* and

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Box 1. Glossary

Cell-autonomous. Occurring within a cell, not involving signalling between cells.

Chromatin immunoprecipitation (ChIP). A method used to identify the transcriptional targets of a given transaction factor by precipitating the transcription factor while it is bound to DNA, then characterizing the bound DNA.

Coelomic epithelium. Layer of cells lining the body cavity of an embryo.

Disorder of sex development (DSD). Any one of a spectrum of conditions where the development of internal or external sexual organs differs from 'typical' male or female, or is not as expected given the sex chromosomes present.

Eutherian mammals. A subclass of mammals that have a placenta.

Genital ridges. Pair of thickened rows of coelomic epithelial cells either side of the midline in the trunk of an embryo that are the precursors of the gonads.

Granulosa cells. The 'nurse' cells in ovarian follicles that nurture germ cells.

High-mobility group. A specific family of transcription factors that have structurally related DNA-binding domains ~80 amino acids long.

Leydig cells. Cells in the interstitium of testes that produce androgens.

Mesonephros. Embryonic structure attached to each genital ridge, from which the male or female internal sexual ducts arise.

Monotremes. A subclass of mammals, represented by platypus, that lay eggs instead of giving birth to live young.

Nuclear localization signal. A short sequence of amino acids that allows proteins such as transcription factors to move from the cell cytoplasm into the cell nucleus.

Ovotestis. A gonad containing both ovarian and testicular tissue.

Paracrine signalling. Short-range chemical communication between cells.

Pre-Sertoli cells. Cells in an XY genital ridge that have activated *Sry* and *Sox9* expression, but have not yet assembled into testis cord structures.

Sertoli cells. Testicular cells that form testis cords and interact with and nurture germ cells.

Testis cord. The precursors of the adult spermatogenic tubules, composed of germ cells enclosed by a layer of Sertoli cells.

Theca cells. Cells in the outermost layer of the ovarian follicle that produce androgen as a source for neighbouring granulosa cells to convert to estrogens.

WT1(+KTS)/WT1(–KTS). Isoforms of the Wilms tumour suppressor protein (WT1) that have three amino acids (lysine, threonine, serine: KTS) inserted or excluded, respectively.

ZZ/ZW sex determining system. A system in which males have two identical sex chromosomes and females have two different sex chromosomes, in contrast to the situation with an XX/XY sex-determining system.
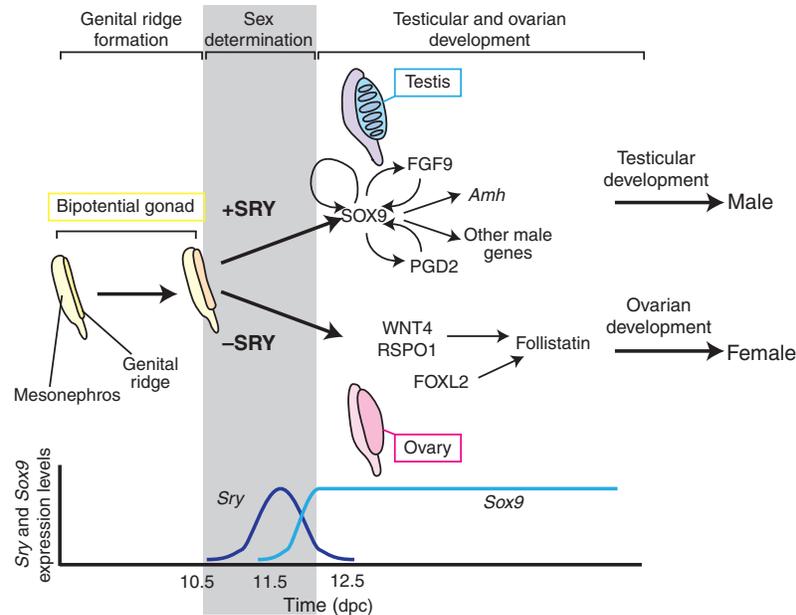
Fig. 1. Overview of sex determination in mice. Chronological flow of early mouse sex differentiation; the grey area indicates the period of sex determination. During mouse embryogenesis, bi-potential gonads (yellow) arise from the genital ridges by 10.5 dpc. In somatic cells of XY genital ridges, *Sry* expression (shown in dark blue beneath the schematic) starts at 10.5 dpc, reaches a peak at 11.5 dpc and then wanes by 12.5 dpc. A few hours later, *Sox9* expression (shown in light blue beneath the schematic) is upregulated to induce differentiation of Sertoli cells. *Sox9* expression peaks at 11.5-12.5 dpc, continues to be expressed postnatally and is supported by several positive-feedback loops (including FGF9, prostaglandin D2 and SOX9 itself), and SOX9 subsequently activates many male-specific genes, including *Amh*. At 12.5 dpc, testis cords have formed, and morphological differences between testis (blue) and ovary (pink) are evident. In the absence of SRY, genes such as *Wnt4, Rspo1* and *Foxl2* are expressed in a female-specific manner and induce ovarian development, as characterized by the expression of follistatin and many other ovary-specific genes. Abbreviations: *Amh*, anti-Müllerian hormone; dpc, days post coitum; FGF9, fibroblast growth factor 9; FOXL2, forkhead box L2; PGD2, prostaglandin D2; RSPO1, R-spondin 1; SOX9, SRY box containing gene 9; SRY, sex-determining region on the chromosome Y; WNT4, wingless-type MMTV integration site family, member 4.

mammalian sex determination has come from studies in mice. In this primer, we summarize the results of these studies and discuss the insights they have provided into the molecular and cellular biology of mammalian testis development.

An overview of the mammalian sex determination pathway

The most detailed studies of mammalian sexual determination have been carried out using mice as a model (Fig. 1). In mice, the gonadal primordia, which are called the genital ridges (see Glossary, Box 1) arise at 10.0 days post coitum (dpc). At this stage, there are no morphological or functional differences between male and female genital ridges, and both structures contain precursor cells that have the ability to differentiate into Sertoli cells (which support germ cells in the testis, see Glossary, Box 1) or granulosa cells (which have a cognate role in the ovary, see Glossary, Box 1).

Sex-specific gonadal development is triggered by *Sry* expression in somatic gonadal cells of XY genital ridges at 10.0-10.5 dpc (Fig. 2A). SRY activity upregulates *Sox9* (SRY box containing gene 9) transcription in Sertoli cell precursors, which in turn upregulates other genes involved in the differentiation of Sertoli cells. Logically, SRY activity must also directly or indirectly suppress the female sex-determining pathway, which would otherwise continue to be active, as it is in XX genital ridges. Differentiating Sertoli cells then assemble into testis cords (tubular structures that contain the germ cells; see Glossary, Box 1) (Fig. 2). The Sertoli cells then stimulate the sex-specific development of germ cells, androgen-

producing Leydig cells (see Glossary, Box 1), testis vascular cells and other interstitial (i.e. non-cord) cell types. The formation of testes is the hallmark of male sex determination.

By contrast, in the absence of *Sry* in XX gonads, genes such as *Wnt4* (wingless-type MMTV integration site family, member 4) and *Foxl2* (forkhead box L2) start to be expressed in a female-specific manner at 11.5-12.5 dpc, and upregulate other downstream female genes, such as follistatin. The female-specific programme of gene expression leads to the differentiation of granulosa cells and theca cells (see Glossary, Box 1), the production of oocytes, and the formation of ovarian follicles (Fig. 1). These events also occur in XY gonads that lack SRY function, supporting the key role for SRY in both activating the testis-determining pathway and suppressing the ovarian-determining pathway.

SRY structure and function

SRY is the founding member of the SOX (SRY-related HMG box) family of transcription factors. The SOX family is found throughout the animal kingdom, and comprises 20 members in mice and humans. SOX proteins have diverse roles in embryogenesis and in the development of many organs, typically acting as cell differentiation switches (reviewed by Bowles et al., 2000). SRY, like other SOX transcription factors, is characterized by a high mobility group (HMG; see Glossary, Box 1) DNA-binding domain (Fig. 3A). This domain binds to the sequence (A/T)ACAA(T/A) in the minor groove of DNA, inducing a 60-85° bend (Harley and Goodfellow, 1994) (Fig. 3B). Biochemical analysis of mutant human SRY protein from XY females has revealed that both DNA-binding and

A SRY

11.0 dpc   11.5 dpc

B SOX9

12.0 dpc   13.5 dpc
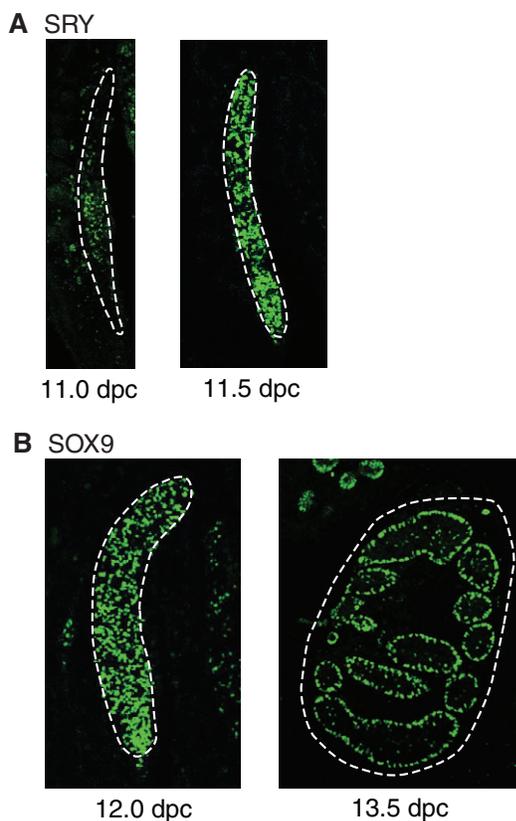
Fig. 2. Chronological sequence of SRY and SOX9 expression during sex determination and early testis development in mice. (**A**) At 11.0 dpc, SRY (sex-determining region on the chromosome Y) protein is expressed initially in a group of somatic cells (green) in the centre of the genital ridge (indicated by a broken line). The domain of SRY-expressing cells then expands to occupy the entire length of the genital ridge; these cells are referred to as supporting cell precursors. (**B**) By 12.0 dpc, SOX9 (SRY box containing gene 9) expression is activated in these same cells, now referred to as pre-Sertoli cells. The SOX9-expressing cells assemble into testis cords by 12.5 dpc and are referred to as Sertoli cells. SOX9 continues to be expressed in Sertoli cells at 13.5 dpc and beyond. Proteins were visualized by immunofluorescence using antibodies to SRY and SOX9. Images are courtesy of Dr Dagmar Wilhelm (The University of Queensland, Brisbane, Australia).

-bending are essential for SRY function. Furthermore, most human XY females have mutations in the HMG domain, reflecting the importance of this domain for the function of SRY (reviewed by Harley and Goodfellow, 1994).

In contrast to the HMG domain, the remaining parts of SRY are poorly conserved between species, and no additional conserved functional domains have been identified (Fig. 3A). For example, in mice, only two amino acids make up the N-terminal region that usually comprises 30-60 amino acids in other species (Gubbay et al., 1990). In the C-terminal region of mouse SRY, a long glutamine (Q)-rich domain is present that is not found in other mammalian species but that might act as a transcriptional activation domain (Dubin and Ostrer, 1994). *Sry* transgene constructs that lack this domain fail to cause male development (Bowles et al., 1999), although it is not known whether this failure reflects a reduced stability of the truncated protein. XX transgenic mice that express human or goat *SRY* develop as males (Lovell-Badge et al.,

2002; Pannetier et al., 2006), suggesting that the non-HMG-domain regions of SRY either are conserved in function but not in sequence, or have no function. In support of the former possibility, the human SRY protein has to be of full length to show normal DNA-binding ability in vitro (Sanchez-Moreno et al., 2008).

SRY protein also carries two nuclear localization signals (NLSs; see Glossary, Box 1) and target sites for acetylation and phosphorylation (Fig. 3A). The NLSs lie at each end of the HMG domain and are conserved between mouce and human (Sudbeck and Scherer, 1997); these bind calmodulin (a calcium-binding protein) and importin β (a nuclear import protein), respectively (Harley et al., 1996; Forwood et al., 2001; Sim et al., 2005) (Fig. 3A). Mutations in either NLS can cause human XY sex reversal, indicating that they are not functionally redundant (Battiloro et al., 1997; Veitia et al., 1997; Harley et al., 2003; Sim et al., 2005). Human SRY is acetylated at a single lysine residue that is well-conserved between species (Fig. 3A); acetylation enhances the nuclear localization of SRY by facilitating its interaction with importin β (Thevenet et al., 2004). Furthermore, human SRY is phosphorylated by cAMP-dependent protein kinase (PKA) on serine residues (S31-S33) located in the N-terminal part of the protein. This PKA-dependent phosphorylation of SRY increases its DNA-binding ability and its subsequent transcriptional activity, and is conserved across primates (Desclozeaux et al., 1998). Other possible phosphorylation residues (serine or threonine) are conserved in the N-terminal domain of SRY in all eutherian mammals (see Glossary, Box 1), except rodents, but the precise function of these residues has not been elucidated.

A number of proteins, including KRABO (kruppel-associated box domain only) (Oh et al., 2005; Peng et al., 2009), WT1 (Wilms tumour 1) (Matsuzawa-Watanabe et al., 2003), SIP1 (SRY-interacting protein 1) (Poulat et al., 1997) and PARP1 [Poly (ADP-ribose) polymerase] (Li et al., 2006) have been shown to interact with mouse and human SRY (Fig. 3A). However, most studies of these protein-protein interactions to date have been based on in vitro systems, and so their physiological significance is as yet unclear.

In summary, our understanding of the molecular mode of action of SRY remains rudimentary. Available evidence points to it having a role as a transcription factor that enters the nucleus, binds to DNA and then upregulates the expression of *Sox9* (see below), but detailed structure-function relationships and how SRY functions in different mammalian species, despite its high sequence divergence, remain to be determined.

Sry expression and its regulation

Most data on of the regulation of *Sry* have been obtained from studies in mice, a species in which the expression of *Sry* in gonads is tightly regulated in both space and time. In the mouse embryo, *Sry* expression starts at 10.5 dpc in somatic cells of XY genital ridges, reaches a peak at 11.5 dpc and wanes by 12.5 dpc (Koopman et al., 1990; Hacker et al., 1995; Jeske et al., 1995; Bullejos and Koopman, 2001; Wilhelm et al., 2005) (Fig. 1, Fig. 2A). Its expression is associated with the differentiation of Sertoli cells in the testis but, clearly, continued *Sry* expression in mice is not needed to maintain the Sertoli cell phenotype.

In all other species studied, *Sry* expression in the gonads is maintained rather than transient, for reasons that are not clear. Furthermore, in some species, such as humans and wallabies, *Sry* expression is not limited to the gonads, and is instead expressed in many tissues during foetal development (Clepet et al., 1993; Harry et al., 1995). In these species, the function of SRY beyond its role in testis development has not been determined.
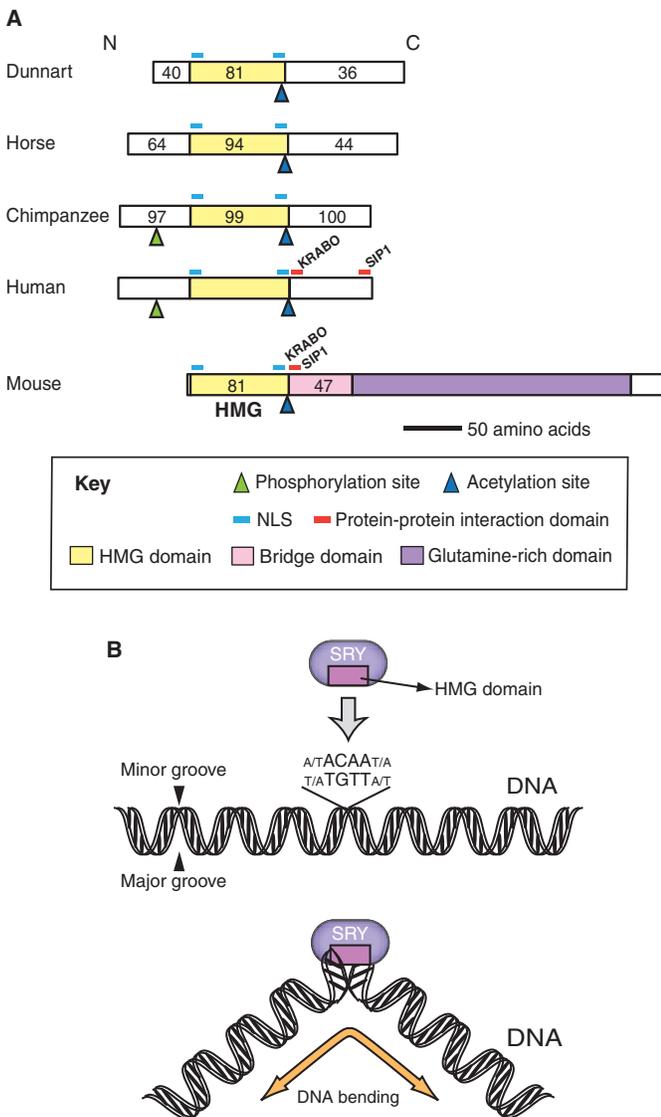
Fig. 3. SRY protein structure and function. (A) A comparison of SRY
(sex-determining region on the chromosome Y) protein structure
among five mammalian species: dunnart (*Sminthopsis macroura,* a
marsupial), horse (*Equus caballus*), chimpanzee (*Pan trglodytes*), human
(*Homo sapiens*) and mouse (*Mus musculus*). The HMG (high-mobility
group) domain is shown in yellow. Numbers indicate the percentage of
amino acids identical to human SRY. The locations of post-translational
modification sites [nuclear localization signals (NLSs), phosphorylation
sites, acetylation sites] and protein-protein interaction domains are
indicated. Mouse SRY has a unique glutamine-rich domain, shown in
purple. Between the HMG and glutamine-rich domains, mouse SRY has
a 'bridge' domain of unknown function, indicated in pink. Kruppel-
associated box domain only and SRY-interacting protein 1 interacting
sites are indicated (KRABO and Slp1). (B) SRY protein binding to DNA.
The double-helix structure of DNA contains two different grooves,
major and minor. The HMG domain of SRY binds to the sequence motif
(A/T)ACAA(T/A) in the minor groove of DNA, bending double-stranded
DNA at 60-85°.

One of the unique characteristics of mouse *Sry* expression is its
peculiar spatio-temporal wave-like pattern: *Sry* expression is
initiated in the centre of the genital ridge before extending to the
whole length of the gonad over a period of several hours (Fig. 2A)
(Bullejos and Koopman, 2001; Wilhelm et al., 2005). Thus, not all

parts of the genital ridge are exposed to *Sry* transcripts, or protein,
at the same time. The transient and dynamic expression of *Sry* in
mice has highlighted the concept that *Sry* functions within a critical
window of time in individual somatic cells of the developing
gonad. This concept was suggested after observations of the
phenomenon known as B6-YDOM sex reversal, which arises when
specific variants of the Y chromosome from the mouse species *Mus
domesticus* (YDOM) are crossed onto the genetic background of
the C57BL/6J (B6) inbred mouse strain. Repeated crossing to B6
mice leads to a variety of phenotypes, ranging from delayed
testicular development to the development of ovotestes (see
Glossary, Box 1) or ovaries (Eicher et al., 1982). Curiously, when
ovotestes develop, they tend to have a testicular structure in the
centre, flanked by ovarian regions (Eicher et al., 1982). Detailed in
situ hybridization studies have demonstrated that a delay in
initiating the expression of *Sry* underlies B6-YDOM sex reversal:
the peak level of *Sry* expression in XY B6 Ypos gonads is delayed
by up to 10 hours (Bullejos and Koopman, 2005). Thus, a critical
window of time during which *Sry* can direct Sertoli cell
development appears to close while the *Sry* expression wave is still
confined to the central region of these XY gonads (Fig. 4A).

The existence of a narrow and crucial time window for the
expression and function of *Sry* has been confirmed in transgenic
mice that carry a *SRY* gene driven by the heat shock protein 70.3
(*Hsp70.3*) promoter, which allows for the experimental induction
of *Sry* at various time points. In this system, a 6-hour delay of *Sry*
induction results in a failure to initiate the testis development
pathway (Hiramatsu et al., 2009). The limits of this window may
be dictated by the need to pre-empt the pathway of ovarian
granulosa cell development that occurs in the absence of *Sry*, or by
the availability of partner proteins required for SRY protein to
activate *Sox9*.

In contrast to the timing of *Sry* expression, the initiation of
which is particularly important, the duration of *Sry* expression
appears to be immaterial, as it varies between species. For example,
in humans and goats, *Sry* gene expression persists well beyond sex
determination and is observed even after birth (Hanley et al., 2000;
Pannetier et al., 2006). Taken together, the crucial factor that
determines the ability of SRY to induce Sertoli cell differentiation
appears to be whether or not it is able to exceed a required
threshold level of expression in any precursor cell within a given
window of opportunity (Fig. 4A).

In addition to the threshold of *Sry* expression being required for
Sertoli cell differentiation, there is another threshold to consider:
the number of Sertoli cells required for proper testicular
development. In experiments in which chimaeras were generated
by combining XX and XY early mouse embryos, gonads
containing various proportions of XY cells were produced. When
35-40% of somatic cells were XY, testes were formed, but when
fewer than 10% were XY, ovaries were formed (Burgoyne et al.,
1988) (Fig. 4B). Intermediate proportions of XY cells resulted in
ovotestes.

A further observation to arise from these studies was that most,
but not all, Sertoli cells in XX↔XY chimaeras were XY (Palmer
and Burgoyne, 1991). These findings suggested that SRY
expression normally drives Sertoli cell differentiation; however, it
was also clear that SRY expression might not be an absolute
requirement, and that XX cells could be recruited to the Sertoli cell
population, perhaps by paracrine signalling (see Glossary, Box 1).
More recently, studies of normal mouse testicular development
using SOX9 and SRY antibodies have revealed the existence of
pre-Sertoli cells (see Glossary, Box 1) that express SOX9 without
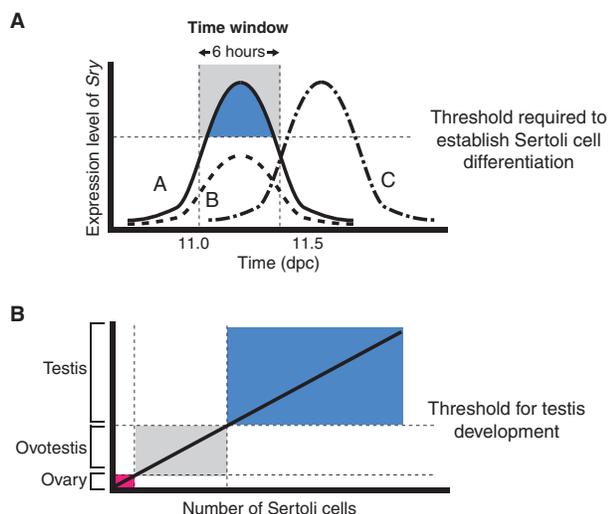
Fig. 4. Two thresholds important for mouse sex determination.
(**A**) *Sry* expression levels must exceed a certain threshold (blue) within a narrow time window (grey) in individual somatic gonadal cells of developing mouse gonads in order to induce Sertoli cell differentiation (curve A). If the level of *Sry* expression does not reach the threshold, as in WT1(+KTS)-null mice (curve B), or is delayed and misses the critical window, as in YDOM sex reversal (curve C), somatic gonadal cells fail to differentiate into Sertoli cells. (**B**) The number of supporting cell precursor cells that differentiate as pre-Sertoli cells must also reach a certain threshold level in order to induce testis formation (blue). In XX-XY mouse chimaera experiments (Burgoyne et al., 1988; Palmer and Burgoyne, 1991; Patek et al., 1991), in which the proportions of XY and XX cells making up an embryo varies, the gonad fails to form a testis if the number of Sertoli cells is below a threshold, resulting in the development of an ovotestis (grey) or an ovary (red). Abbreviation: *Sry*, sex-determining region on the chromosome Y.

having first expressed SRY (Wilhelm et al., 2005). Moreover, in in vitro cultures that contain a mix of XX genital ridge cells that constitutively express a fluorescent marker and XY wild-type genital ridge cells, it has been shown that when the XY cells are in contact with the XX cells, the XX cells are induced to express *Sox9*, confirming the existence of a paracrine recruitment mechanism (Wilhelm et al., 2005). This phenomenon can be

artificially induced by prostaglandin D2 (PGD2), and inhibited by a chemical blocker of the PGD2 receptor, implicating PGD2 in this paracrine recruitment mechanism (Wilhelm et al., 2005). Accordingly, *Pgds* (prostaglandin D synthase)-knockout mice show decreased *Sox9* expression in male gonads (Moniot et al., 2009). This mechanism is likely to provide a backup system to ensure and to reinforce male pathway activation by SRY.

In spite of the importance of its correct temporal and spatial expression, the regulation of *Sry* is still poorly understood. Regions that flank *Sry* are remarkably poorly conserved between mammalian species, hampering efforts to find potentially important regulatory elements. Although sequence analysis has revealed four intervals of relatively high DNA sequence conservation upstream of *SRY* among human, bovine, pig and goat genomes (Ross et al., 2008), the physiological significance of these sequences has not been determined. Transgenic mouse assays (in which critical regulatory regions are pinpointed by sequential deletion analysis) have so far not been useful for identifying a gonadal enhancer of *Sry*.

Despite these complications, several proteins have been implicated in regulating *Sry* expression (Table 1). Analyses of gene knockout mouse models have shown that the absence of these proteins leads to reduced levels of *Sry* expression, and results in XY sex reversal. In most cases, it is not clear whether the loss of these factors reduces the level of *Sry* expressed per cell or the overall number of cells that express *Sry*. How loss of their function leads to reduced *Sry* is also unclear for most of these proteins. For example, FOG2 (friend of GATA2; now known as ZFPM1 – Mouse Genome Informatics) is known to be involved in the repression rather than in the activation of several GATA-dependent target genes, such as anti-Müllerian hormone (*Amh*) and inhibin α (Robert et al., 2002). CBX2 (chromobox homologue 2), MAP3K4 (mitogen-activated protein kinase kinase kinase 4) and insulin receptors are not transcription factors, and so how they might influence *Sry* regulation remains to be determined. A recent bioinformatics study identified a region of mouse chromosome 1 between 33 and 49 cM that controls the expression of *Sry*, but none of the above genes is located within this region (Munger et al., 2009).

Among the molecules described above, much attention has focused on WT1 as a potential regulator of *Sry*. When WT1(+KTS) (see Glossary, Box 1) is reduced in humans, XY sex reversal occurs, accompanying a condition known as Frasier syndrome (Barbaux et al., 1997). Studies in mice show that

Table 1. Genes implicated in regulating *Sry* expression

Gene	Type of protein	Loss-of-function phenotype		References
		Human	Mice	
Wt1 (+KTS)	Transcription factor/RNA-binding protein	Frasier syndrome (XY sex reversal, glomerulo-nephropathy)	XY sex reversal, dysplastic kidney	Barbaux et al., 1997 Hammes et al., 2001
Cbx2	Transcriptional co-factor	XY sex reversal	XY sex reversal, skeletal defects	Katoh-Fukui et al., 1998 Biason-Lauber et al., 2009
Gata4/Fog2	Transcription factor/co-factor (co-repressor)	*	XY sex reversal, foetal lethal	Tevosian et al., 2002
Map3k4	Kinase (enzyme)	*	XY sex reversal, spina bifida	Bogani et al., 2009
Ir, Irr, Igf1r†	Membrane receptors	*	XY sex reversal, neonatal death	Nef et al., 2003

*No mutations in human sexual reversal patients identified.
†Loss-of-function phenotype observed in triple knockout mice.
Cbx2, chromobox homolog 2 (also known as *m33*); *Fog2*, friend of GATA2; *Gata4*; Gata binding protein 4; *Igf1r*, insulin-like growth factor 1 receptor; *Ir*, insulin receptor; *Irr*, insulin receptor-related receptor; *Map3k4*; mitogen-activated protein kinase kinase kinase 4; *Wt1*(+KTS), Wilms tumour 1 gene, encoding an isoform that includes a three-amino acid motif (lysine-threonine-serine).

WT1(+KTS) plays a cell-autonomous (see Glossary, Box 1) role in regulating *Sry* expression in individual cells of the Sertoli cell lineage in vivo (Bradford et al., 2009b), but it is not clear whether *Sry* is a direct or indirect transcriptional target of WT1. In in vitro systems, WT1(+KTS) activates the promoter of mouse but not of human *Sry* (Shimamura et al., 1997; Hossain and Saunders, 2001; Miyamoto et al., 2008); moreover, WT1(+KTS) preferentially binds to unspliced pre-mRNAs, promoting gene expression by mRNA processing (Morrison et al., 2008). Thus, the mechanism of *Sry* regulation by WT1(+KTS) is unclear and requires further study.

In summary, the precise regulation of both the levels and onset of *Sry* expression is important for Sertoli cell differentiation and hence for testis development. The mechanistic details of how this regulation is achieved, however, remain unknown.

Mechanism of SRY action

After the discovery of *Sry*, attention turned to the issue of whether it might directly upregulate the male sex-determining pathway, or repress a repressor of that pathway (see Box 2). Much of this work focused on the relationship between *Sry* and *Sox9*, another important and early-acting gene that is expressed in Sertoli cells. In particular, studies have aimed to address whether SRY might regulate *Sox9* expression directly or indirectly, and whether *Sox9* might be just one of many targets of SRY.

Sox9: a major SRY target

Sox9, which encodes another member of the SOX transcription factor family, is expressed in several developing vertebrate organ systems, including the skeleton, heart, kidneys and brain (Wright et al., 1995). In XY mouse gonads, *Sox9* expression is upregulated in pre-Sertoli cells immediately after the onset of *Sry* gene expression, and mimics the wave-like pattern of *Sry* expression (Kent et al., 1996; Morais da Silva et al., 1996; Sekido et al., 2004; Bullejos and Koopman, 2005; Wilhelm et al., 2005). However, unlike *Sry* in mice, *Sox9* expression persists in the gonad beyond 12.5 dpc (Fig. 2B) (Kent et al., 1996; Morais da Silva et al., 1996), suggesting that it is able to sustain its own expression once initiated (Fig. 1), and that its continued expression might be linked to the maintenance of the Sertoli cell phenotype (DiNapoli and Capel, 2008).

The importance of *SOX9* for sex determination was revealed when heterozygous human *SOX9* mutations were found to be associated with a skeletal deformity syndrome: campomelic dysplasia (CD) (Foster et al., 1994; Wagner et al., 1994). In 75% of XY individuals with CD, partial or complete male-to-female sex reversal occurs, indicating that *SOX9* is necessary for testis determination in humans (Mansour et al., 1995). In addition, a duplication of *SOX9* had previously been identified in a mosaic XX sex-reversed individual (Huang et al., 1999). These observations indicated that *SOX9* is sufficient and necessary for testis determination, a conclusion confirmed by the sex reversal phenotype of XY *Sox9*-null (Chaboissier et al., 2004; Barrionuevo et al., 2006) and XX *Sox9*-overexpressing mice (Bishop et al., 2000; Vidal et al., 2001). Consistent with the role of SOX9 as a testis-determining factor, several genes that have a crucial role in testicular development, such as *Amh* and *Pgds*, have been identified as direct targets of SOX9 (De Santa Barbara et al., 1998; Wilhelm et al., 2007).

Unlike *Sry*, *Sox9* is conserved among non-mammalian vertebrate species. In addition, *Sox9* is linked with sexual dimorphism and with gonadal development in species such as the chicken, which has a ZZ/ZW sex-determining system (see Glossary, Box 1) (Schmid et al., 1989), and red-eared slider turtles and alligators,

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**Box 2. The quest to find the molecular function of SRY**

Despite being long suspected, it took over a decade to prove that SRY (sex-determining region on the chromosome Y) regulates *Sox9* (SRY box containing gene 9) directly. Why did it take so long? *Sry* has some peculiar features that make it particularly difficult to work with. The non-HMG domain sequence of mouse *Sry* gene does not have obvious functional domains and is poorly conserved between species. As a result, it was not known whether SRY acts as a transcriptional activator or a repressor, or even as an architectural factor that acts by changing DNA structure. The fact that SRY binds to a short (seven-base) target sequence that occurs frequently in the genome made it difficult to identify potential target genes bioinformatically. Furthermore, a lack of suitable cell lines and antibodies hampered molecular approaches. Useful and specific antibodies to SRY now exist, although cell lines remain a problem, as cells typically lose SRY expression after a few passages in culture.

Nor has it been easy to work backwards from *Sox9* to find out what regulates its expression, or whether SRY is involved. Translocations and deletions affecting *Sox9* function indicate that regulatory elements exist 1 Mb or more upstream of this gene in mice and humans (Bishop et al., 2000; Pfeifer et al., 1999). Painstaking deletion analysis in transgenic *Sox9* reporter mice finally revealed the gonadal-specific enhancer of *Sox9*, called testis-specific enhancer of *Sox9* core (TESCO), on which SRY acts directly (Sekido and Lovell-Badge, 2008). Even now it is not clear whether TESCO is the only element important for *Sox9* regulation during sex determination.

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which have a temperature-dependent sex-determining system (Spotila et al., 1998; Western et al., 1999). Therefore, the role of SOX9 in sex determination is considered to be ancestral and pivotal among vertebrates. Furthermore, because the phenotype of *Sox9* overexpression in mouse XX gonads recapitulates that of *Sry* overexpression, *Sox9* is thought to be the only gene that is required downstream of *Sry* to activate the remainder of the testis-determining programme.

How does SRY upregulate *Sox9* expression? A recent analysis using transgenic reporter assays and in vivo chromatin immunoprecipitation (ChIP, see Glossary, Box 1) assays identified a gonad-specific enhancer of mouse *Sox9*, called TESCO (for testis-specific enhancer of *Sox9* core) (Sekido and Lovell-Badge, 2008). TESCO is a 1.4 kb sequence that is located 11-13 kb upstream of the *Sox9* transcription start site and is highly conserved in rat, dog and human genomes. SRY and SF1 (steroidogenic factor 1), an orphan nuclear receptor that regulates many genes involved in the differentiation of gonadal and adrenal cells, were found to cooperatively upregulate mouse *Sox9* by directly binding to TESCO (Sekido and Lovell-Badge, 2008) (Fig. 5), providing the first evidence that SRY acts as a transcriptional activator in vivo.

The discovery of TESCO also clarified another significant mechanism of *Sox9* regulation: an auto-regulatory positive-feedback loop (Fig. 5). SOX9 itself binds to TESCO with SF1 to stimulate its continued expression (Sekido and Lovell-Badge, 2008). This positive feedback loop is important not only to maintain *Sox9* expression after *Sry* subsides in mice, but also to ensure that the SRY signal is captured and amplified in each developing Sertoli cell. A positive-feedback loop is also observed between fibroblast growth factor 9 (FGF9) and SOX9 (Kim et al., 2006). *Fgf9* has not been proven to be a target of SOX9, but is known to be necessary for the maintenance of *Sox9* expression.
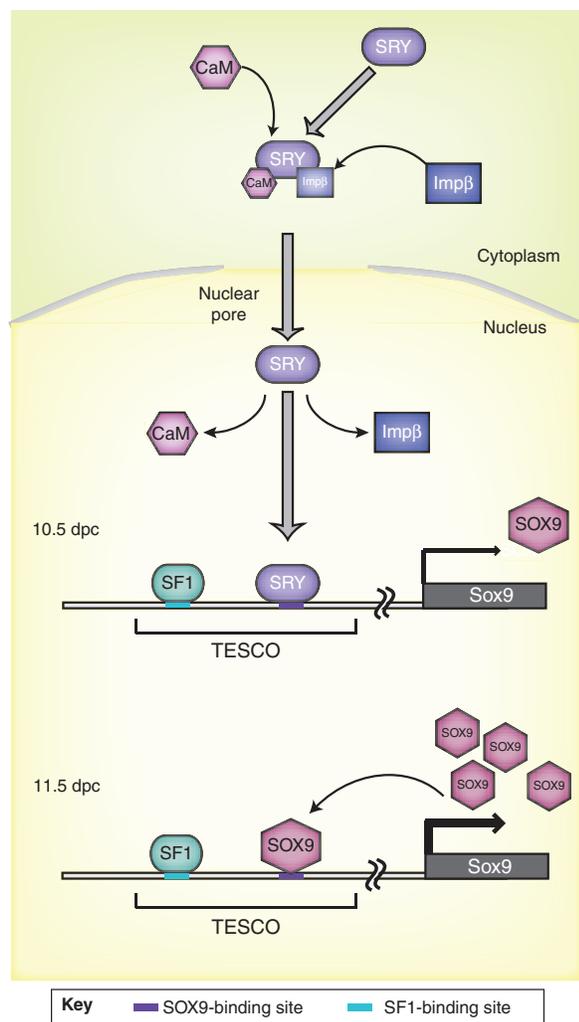
Fig. 5. Cellular mechanism of SRY function. A schematic of the cellular mechanisms of SRY action. In the cytoplasm, SRY is bound by calmodulin (CaM) and importin β (Impβ), which recognize the N- and C-terminal nuclear localization signals (NLSs) on SRY, respectively, and recruit it to enter the nucleus. At 10.5 dpc, SRY and steroidogenic factor 1 (SF1) bind directly to specific sites ('TESCO', testis-specific enhancer of *Sox9* core) that lie within the gonadal specific enhancer of *Sox9* (indicated by the coloured regions on the DNA) and upregulate *Sox9* expression cooperatively. At 11.5 dpc, after initiation of *Sox9* expression, an auto-regulation system operates in which SOX9 also binds directly to TESCO with SF1 to prolong and amplify *Sox9* expression. Abbreviations: SOX9, SRY box containing gene 9; SRY, sex-determining region on the chromosome Y.

Fgf9-null mice or mice lacking FGFR2, the main receptor for FGF9, show XY sex reversal (Colvin et al., 2001; Kim et al., 2007), attesting to the importance of FGF9 in the testis-determining pathway. Furthermore, a centre-to-pole diffusion of FGF9 appears to be essential for proper testicular development in the polar extremities of male mouse gonads, because polar fragments of mouse foetal XY genital ridges cultured separately from central fragments did not maintain *Sox9* expression or form testis cords (Hiramatsu et al., 2010).

Thus, at least three mechanisms are used to ensure the continued expression of *Sox9* and to recruit gonadal somatic cells to the *Sox9*-positive Sertoli cell population: cell-autonomous *Sox9*

Box 3. *Sry* and sex-specific brain function
In mice, *Sry* (sex-determining region on the chromosome Y) is not only expressed in developing gonads, but also in the brain. It is tempting to hypothesise that SRY has some direct role in brain sex determination. So far, a few genes encoding proteins such as monoamine oxidase A (MAO-A) and tyrosine hydroxylase (TH), have been identified as potential targets of SRY in the brain (Milsted et al., 2004; Dewing et al., 2006; Wu et al., 2009). However, the physiological significance of these pathways and the regulatory mechanisms of *Sry* in the brain have yet to be elucidated. Because so little is known about sex-specific brain differentiation, and because the topic itself is fraught with controversy, it is a challenging task to prove that SRY has a direct role.

autoregulation, PGD2-mediated signalling and FGF9-mediated signalling from Sertoli cells. These regulatory loops induce the activation of other downstream male pathway events, such as *Amh* expression, cell proliferation in the coelomic epithelium (see Glossary, Box 1), cell migration from the mesonephros (see Glossary, Box 1) and testis-specific glycogenesis (Martineau et al., 1997; Capel et al., 1999; Schmahl et al., 2000; Schepers et al., 2003; Matoba et al., 2005; Matoba et al., 2008).

Additional SRY targets in gonads
Other than *Sox9*, few SRY target molecules in gonads have been reported. A recent in vivo ChIP study showed that the cerebellin 4 precursor gene (*Cbln4*) is a direct target of mouse SRY (Bradford et al., 2009a). *Cbln4* encodes a transmembrane protein and is expressed in a male-specific manner. However, the function of *Cbln4* product in testicular development is not known.

Human and mouse SRY have also been found to interact with β-catenin and to repress β-catenin-mediated TCF-dependent gene activation (Bernard et al., 2008; Tamashiro et al., 2008; Lau and Li, 2009). β-Catenin is the downstream effector molecule of WNT4/R-sponsin 1 (RSPO1) signalling and appears to be essential for initiating the development of the female gonad (Maatouk et al., 2008). It is attractive to speculate that, in order to activate the male pathway efficiently, SRY suppresses the function of the key female molecule β-catenin. However, evidence that SRY affects β-catenin function is based solely on in vitro data and its physiological significance in vivo has not yet been demonstrated.

In summary, the only clear direct target of SRY during testis determination is *Sox9*, and so understanding the role of SRY in engaging the testis-determining pathway becomes an issue of studying the molecular roles of SOX9. Interestingly, in mice, *Sry* is also expressed in the brain, where other potential targets of its protein have been identified (see Box 3); these targets are brain specific and so are not relevant to gonadal development.

Conclusion
Despite its dramatic biological role, *Sry* is a fragile and partly debilitated gene. The structure and regulatory sequences of *Sry* may have been degraded because of its location on the rapidly degrading Y chromosome (see Box 4). To respond to the weak *Sry* expression signal and to establish the male pathway efficiently, *Sox9*, apparently the only meaningful target of SRY, has acquired support mechanisms for its own regulation, in the form of cell-autonomous and intercellular signalling-based positive-feedback loops. Thus, SRY provides the trigger for male sex determination,

Box 4. Y-chromosome evolution and *Sry*

Sry (sex-determining region on the chromosome Y) determines the sexual fate of the organism, but also the fate of the Y chromosome itself. Gene-mapping analysis suggests that the X and Y chromosomes evolved from a pair of identical chromosomes (Graves, 2006) that began to differentiate when one copy of *Sox3* (SRY box containing gene 3) acquired a new function in male sex determination. The chromosome carrying this new gene, *Sry*, became the Y chromosome. The ancestral *Sox3*, the role of which is largely restricted to brain development, resides on what has become the X chromosome.

Having established a new Y chromosome, subsequent selection favoured restricted recombination with the new X, so that Y genes would stay on the Y chromosome. Because recombination is part of the mechanism used by cells to proofread and repair genes, genes in the non-recombining region of the Y chromosome tend to become lost and/or degraded. As a result, the human Y chromosome has shrunk to ~60 Mb and contains only 50 functional genes, whereas the human X chromosome is ~165 Mb and carries ~1000 genes (Graves, 2002; Graves, 2006; Wallis et al., 2008). Erosion of the Y chromosome is reflected in the accumulation of *Sry* mutations, explaining the high level of sequence divergence between mammalian species and perhaps accounting for its relatively low expression levels in mice. Not surprisingly, the use of *Sry* as a testis-determining trigger seems to have been lost altogether in some species, such as the mole voles *Ellobius lutescens* and *E. tancrei*, and the Japanese spinous country rats *Tokudaia osimensis osimensis* and *T. osimensis* (Just et al., 1995; Sutou et al., 2001). The sex chromosomes in these species are XO or XX; no Y chromosome or any trace of *Sry* are present, suggesting the existence of a completely new sex-determining system.

but it is actually SOX9, and not SRY, that is the key element that orchestrates and stabilizes Sertoli cell differentiation to lock in the testis-determining program. At the same time, SOX9 provides a means of blocking the pathway of gene activity that leads to the differentiation of ovarian cells, but the mechanism by which it does so remains unclear.

Intensive studies spanning more than 20 years since the discovery of *Sry* have identified several genes important for sex determination and gonadal development, and yet 30-40% of human XY DSD cases still remain undiagnosed. Given the importance of correct *Sry* regulation, as demonstrated in experimental studies, it may be that regulatory mutations in the unidentified enhancer sequences of *SRY* may be an important contributing factor to human DSDs. Further study is required to test this possibility. Other fundamental questions about this gene and its protein still remain unanswered: what are precise molecular mechanisms of *Sry* regulation; what are the functions of the non HMG-domain regions of the protein; and what is the physiological significance of its protein interactions? Recent technical advances, including bioinformatic analysis and the generation of genetically modified mice, will help to answer the remaining questions surrounding the process of mammalian sex determination, and may provide valuable information for the diagnosis and management of human DSDs.

References

Barbaux, S., Niaudet, P., Gubler, M. C., Grunfeld, J. P., Jaubert, F., Kuttenn, F., Fekete, C. N., Souleyreau-Therville, N., Thibaud, E., Fellous, M. et al. (1997). Donor splice-site mutations in WT1 are responsible for Frasier syndrome. *Nat. Genet.* **17**, 467-470.

Barrionuevo, F., Bagheri-Fam, S., Klattig, J., Kist, R., Taketo, M. M., Englert, C. and Scherer, G. (2006). Homozygous inactivation of Sox9 causes complete XY sex reversal in mice. *Biol. Reprod.* **74**, 195-201.

Battiloro, E., Angeletti, B., Tozzi, M. C., Bruni, L., Tondini, S., Vignetti, P., Verna, R. and D'Ambrosio, E. (1997). A novel double nucleotide substitution in the HMG box of the SRY gene associated with Swyer syndrome. *Hum. Genet.* **100**, 585-587.

Bernard, P., Sim, H., Knower, K., Vilain, E. and Harley, V. (2008). Human SRY inhibits beta-catenin-mediated transcription. *Int. J. Biochem. Cell Biol.* **40**, 2889-2900.

Biason-Lauber, A., Konrad, D., Meyer, M., DeBeaufort, C. and Schoenle, E. J. (2009). Ovaries and female phenotype in a girl with 46,XY karyotype and mutations in the CBX2 gene. *Am. J. Hum. Genet.* **84**, 658-663.

Bishop, C. E., Whitworth, D. J., Qin, Y., Agoulnik, A. I., Agoulnik, I. U., Harrison, W. R., Behringer, R. R. and Overbeek, P. A. (2000). A transgenic insertion upstream of sox9 is associated with dominant XX sex reversal in the mouse. *Nat. Genet.* **26**, 490-494.

Bogani, D., Siggers, P., Brixey, R., Warr, N., Beddow, S., Edwards, J., Williams, D., Wilhelm, D., Koopman, P., Flavell, R. A. et al. (2009). Loss of mitogen-activated protein kinase kinase kinase 4 (MAP3K4) reveals a requirement for MAPK signalling in mouse sex determination. *PLoS Biol.* **7**, e1000196.

Bowles, J., Cooper, L., Berkman, J. and Koopman, P. (1999). Sry requires a CAG repeat domain for male sex determination in Mus musculus. *Nat. Genet.* **22**, 405-408.

Bowles, J., Schepers, G. and Koopman, P. (2000). Phylogeny of the SOX family of developmental transcription factors based on sequence and structural indicators. *Dev. Biol.* **227**, 239-255.

Bradford, S. T., Hiramatsu, R., Maddugoda, M. P., Bernard, P., Chaboissier, M. C., Sinclair, A., Schedl, A., Harley, V., Kanai, Y., Koopman, P. et al. (2009a). The cerebellin 4 precursor gene is a direct target of SRY and SOX9 in mice. *Biol. Reprod.* **80**, 1178-1188.

Bradford, S. T., Wilhelm, D., Bandiera, R., Vidal, V., Schedl, A. and Koopman, P. (2009b). A cell-autonomous role for WT1 in regulating Sry in vivo. *Hum. Mol. Genet.* **18**, 3429-3438.

Bullejos, M. and Koopman, P. (2001). Spatially dynamic expression of Sry in mouse genital ridges. *Dev. Dyn.* **221**, 201-205.

Bullejos, M. and Koopman, P. (2005). Delayed Sry and Sox9 expression in developing mouse gonads underlies B6-Y(DOM) sex reversal. *Dev. Biol.* **278**, 473-481.

Burgoyne, P. S., Buehr, M. and McLaren, A. (1988). XY follicle cells in ovaries of XX–XY female mouse chimaeras. *Development* **104**, 683-688.

Capel, B., Albrecht, K. H., Washburn, L. L. and Eicher, E. M. (1999). Migration of mesonephric cells into the mammalian gonad depends on Sry. *Mech. Dev.* **84**, 127-131.

Chaboissier, M. C., Kobayashi, A., Vidal, V. I., Lutzkendorf, S., van de Kant, H. J., Wegner, M., de Rooij, D. G., Behringer, R. R. and Schedl, A. (2004). Functional analysis of Sox8 and Sox9 during sex determination in the mouse. *Development* **131**, 1891-1901.

Clepet, C., Schafer, A. J., Sinclair, A. H., Palmer, M. S., Lovell-Badge, R. and Goodfellow, P. N. (1993). The human SRY transcript. *Hum. Mol. Genet.* **2**, 2007-2012.

Colvin, J. S., Green, R. P., Schmahl, J., Capel, B. and Ornitz, D. M. (2001). Male-to-female sex reversal in mice lacking fibroblast growth factor 9. *Cell* **104**, 875-889.

De Santa Barbara, P., Bonneaud, N., Boizet, B., Desclozeaux, M., Moniot, B., Sudbeck, P., Scherer, G., Poulat, F. and Berta, P. (1998). Direct interaction of SRY-related protein SOX9 and steroidogenic factor 1 regulates transcription of the human anti-Mullerian hormone gene. *Mol. Cell. Biol.* **18**, 6653-6665.

Desclozeaux, M., Poulat, F., de Santa Barbara, P., Capony, J. P., Turowski, P., Jay, P., Mejean, C., Moniot, B., Boizet, B. and Berta, P. (1998). Phosphorylation of an N-terminal motif enhances DNA-binding activity of the human SRY protein. *J. Biol. Chem.* **273**, 7988-7995.

Dewing, P., Chiang, C. W., Sinchak, K., Sim, H., Fernagut, P. O., Kelly, S., Chesselet, M. F., Micevych, P. E., Albrecht, K. H., Harley, V. R. et al. (2006). Direct regulation of adult brain function by the male-specific factor SRY. *Curr. Biol.* **16**, 415-420.

DiNapoli, L. and Capel, B. (2008). SRY and the standoff in sex determination. *Mol. Endocrinol.* **22**, 1-9.

Dubin, R. A. and Ostrer, H. (1994). Sry is a transcriptional activator. *Mol. Endocrinol.* **8**, 1182-1192.

Eicher, E. M., Washburn, L. L., Whitney, J. B., 3rd and Morrow, K. E. (1982). Mus poschiavinus Y chromosome in the C57BL/6J murine genome causes sex reversal. *Science* **217**, 535-537.

DEVELOPMENT

Ford, C. E., Jones, K. W., Polani, P. E., De Almeida, J. C. and Briggs, J. H.
(1959). A sex-chromosome anomaly in a case of gonadal dysgenesis (Turner's
syndrome). *Lancet* **1**, 711-713.

Forwood, J. K., Harley, V. and Jans, D. A. (2001). The C-terminal nuclear
localization signal of the sex-determining region Y (SRY) high mobility group
domain mediates nuclear import through importin beta 1. *J. Biol. Chem.* **276**,
46575-46582.

Foster, J. W., Dominguez-Steglich, M. A., Guioli, S., Kwok, C., Weller, P. A.,
Stevanovic, M., Weissenbach, J., Mansour, S., Young, I. D., Goodfellow, P.
N. et al. (1994). Campomelic dysplasia and autosomal sex reversal caused by
mutations in an SRY-related gene. *Nature* **372**, 525-530.

Graves, J. A. (2002). Evolution of the testis-determining gene-the rise and fall of
SRY. *Novartis Found. Symp.* **244**, 86-97; discussion 97-101, 203-206, 253-257.

Graves, J. A. (2006). Sex chromosome specialization and degeneration in
mammals. *Cell* **124**, 901-914.

Gubbay, J., Collignon, J., Koopman, P., Capel, B., Economou, A.,
Munsterberg, A., Vivian, N., Goodfellow, P. and Lovell-Badge, R. (1990). A
gene mapping to the sex-determining region of the mouse Y chromosome is a
member of a novel family of embryonically expressed genes. *Nature* **346**, 245-
250.

Hacker, A., Capel, B., Goodfellow, P. and Lovell-Badge, R. (1995). Expression
of Sry, the mouse sex determining gene. *Development* **121**, 1603-1614.

Hammes, A., Guo, J. K., Lutsch, G., Leheste, J. R., Landrock, D., Ziegler, U.,
Gubler, M. C. and Schedl, A. (2001). Two splice variants of the Wilms' tumor 1
gene have distinct functions during sex determination and nephron formation.
Cell **106**, 319-329.

Hanley, N. A., Hagan, D. M., Clement-Jones, M., Ball, S. G., Strachan, T.,
Salas-Cortes, L., McElreavey, K., Lindsay, S., Robson, S., Bullen, P. et al.
(2000). SRY, SOX9, and DAX1 expression patterns during human sex
determination and gonadal development. *Mech. Dev.* **91**, 403-407.

Harley, V. R. and Goodfellow, P. N. (1994). The biochemical role of SRY in sex
determination. *Mol. Reprod. Dev.* **39**, 184-193.

Harley, V. R., Lovell-Badge, R., Goodfellow, P. N. and Hextall, P. J. (1996). The
HMG box of SRY is a calmodulin binding domain. *FEBS Lett.* **391**, 24-28.

Harley, V. R., Layfield, S., Mitchell, C. L., Forwood, J. K., John, A. P., Briggs, L.
J., McDowall, S. G. and Jans, D. A. (2003). Defective importin beta
recognition and nuclear import of the sex-determining factor SRY are associated
with XY sex-reversing mutations. *Proc. Natl. Acad. Sci. USA* **100**, 7045-7050.

Hiramatsu, R., Matoba, S., Kanai-Azuma, M., Tsunekawa, N., Katoh-Fukui,
Y., Kurohmaru, M., Morohashi, K., Wilhelm, D., Koopman, P. and Kanai, Y.
(2009). A critical time window of Sry action in gonadal sex determination in
mice. *Development* **136**, 129-138.

Hiramatsu, R., Harikae, K., Tsunekawa, N., Kurohmaru, M., Matsuo, I. and
Kanai, Y. (2010). FGF signaling directs a center-to-pole expansion of
tubulogenesis in mouse testis differentiation. *Development* **137**, 303-312.

Hossain, A. and Saunders, G. F. (2001). The human sex-determining gene SRY is
a direct target of WT1. *J. Biol. Chem.* **276**, 16817-16823.

Huang, B., Wang, S., Ning, Y., Lamb, A. N. and Bartley, J. (1999). Autosomal XX
sex reversal caused by duplication of SOX9. *Am. J. Med. Genet.* **87**, 349-353.

Jacobs, P. A. and Strong, J. A. (1959). A case of human intersexuality having a
possible XXY sex-determining mechanism. *Nature* **183**, 302-303.

Jeske, Y. W., Bowles, J., Greenfield, A. and Koopman, P. (1995). Expression of
a linear Sry transcript in the mouse genital ridge. *Nat. Genet.* **10**, 480-482.

Just, W., Rau, W., Vogel, W., Akhverdian, M., Fredga, K., Graves, J. A. and
Lyapunova, E. (1995). Absence of Sry in species of the vole Ellobius. *Nat.
Genet.* **11**, 117-118.

Katoh-Fukui, Y., Tsuchiya, R., Shiroishi, T., Nakahara, Y., Hashimoto, N.,
Noguchi, K. and Higashinakagawa, T. (1998). Male-to-female sex reversal in
M33 mutant mice. *Nature* **393**, 688-692.

Kent, J., Wheatley, S. C., Andrews, J. E., Sinclair, A. H. and Koopman, P.
(1996). A male-specific role for SOX9 in vertebrate sex determination.
Development **122**, 2813-2822.

Kim, Y., Kobayashi, A., Sekido, R., DiNapoli, L., Brennan, J., Chaboissier, M.
C., Poulat, F., Behringer, R. R., Lovell-Badge, R. and Capel, B. (2006). Fgf9
and Wnt4 act as antagonistic signals to regulate mammalian sex determination.
PLoS Biol. **4**, e187.

Kim, Y., Bingham, N., Sekido, R., Parker, K. L., Lovell-Badge, R. and Capel, B.
(2007). Fibroblast growth factor receptor 2 regulates proliferation and Sertoli
differentiation during male sex determination. *Proc. Natl. Acad. Sci. USA* **104**,
16558-16563.

Koopman, P., Munsterberg, A., Capel, B., Vivian, N. and Lovell-Badge, R.
(1990). Expression of a candidate sex-determining gene during mouse testis
differentiation. *Nature* **348**, 450-452.

Koopman, P., Gubbay, J., Vivian, N., Goodfellow, P. and Lovell-Badge, R.
(1991). Male development of chromosomally female mice transgenic for Sry.
Nature **351**, 117-121.

Kronenberg, H. and Williams, R. H. (2007). *Williams Textbook of Endocrinology*,
11th edn. Saunders/ Elsevier.

Lau, Y. F. and Li, Y. (2009). The human and mouse sex-determining SRY genes
repress the Rspo1/beta-catenin signaling. *J. Genet. Genomics* **36**, 193-202.

Li, Y., Oh, H. J. and Lau, Y. F. (2006). The poly(ADP-ribose) polymerase 1 interacts
with Sry and modulates its biological functions. *Mol. Cell. Endocrinol.* **257-258**,
35-46.

Lovell-Badge, R., Canning, C. and Sekido, R. (2002). Sex-determining genes in
mice: building pathways. *Novartis Found. Symp.* **244**, 4-18; discussion 18-22,
35-42, 253-257.

Maatouk, D. M., DiNapoli, L., Alvers, A., Parker, K. L., Taketo, M. M. and
Capel, B. (2008). Stabilization of beta-catenin in XY gonads causes male-to-
female sex-reversal. *Hum. Mol. Genet.* **17**, 2949-2955.

Mansour, S., Hall, C. M., Pembrey, M. E. and Young, I. D. (1995). A clinical and
genetic study of campomelic dysplasia. *J. Med. Genet.* **32**, 415-420.

Martineau, J., Nordqvist, K., Tilmann, C., Lovell-Badge, R. and Capel, B.
(1997). Male-specific cell migration into the developing gonad. *Curr. Biol.* **7**,
958-968.

Matoba, S., Kanai, Y., Kidokoro, T., Kanai-Azuma, M., Kawakami, H.,
Hayashi, Y. and Kurohmaru, M. (2005). A novel Sry-downstream cellular
event which preserves the readily available energy source of glycogen in mouse
sex differentiation. *J. Cell Sci.* **118**, 1449-1459.

Matoba, S., Hiramatsu, R., Kanai-Azuma, M., Tsunekawa, N., Harikae, K.,
Kawakami, H., Kurohmaru, M. and Kanai, Y. (2008). Establishment of testis-
specific SOX9 activation requires high-glucose metabolism in mouse sex
differentiation. *Dev. Biol.* **324**, 76-87.

Matsuzawa-Watanabe, Y., Inoue, J. and Semba, K. (2003). Transcriptional
activity of testis-determining factor SRY is modulated by the Wilms' tumor 1
gene product, WT1. *Oncogene* **22**, 7900-7904.

Milsted, A., Serova, L., Sabban, E. L., Dunphy, G., Turner, M. E. and Ely, D. L.
(2004). Regulation of tyrosine hydroxylase gene transcription by Sry. *Neurosci.
Lett.* **369**, 203-207.

Miyamoto, Y., Taniguchi, H., Hamel, F., Silversides, D. W. and Viger, R. S.
(2008). A GATA4/WT1 cooperation regulates transcription of genes required for
mammalian sex determination and differentiation. *BMC Mol. Biol.* **9**, 44.

Moniot, B., Declosmenil, F., Barrionuevo, F., Scherer, G., Aritake, K., Malki,
S., Marzi, L., Cohen-Solal, A., Georg, I., Klattig, J. et al. (2009). The PGD2
pathway, independently of FGF9, amplifies SOX9 activity in Sertoli cells during
male sexual differentiation. *Development* **136**, 1813-1821.

Morais da Silva, S., Hacker, A., Harley, V., Goodfellow, P., Swain, A. and
Lovell-Badge, R. (1996). Sox9 expression during gonadal development implies
a conserved role for the gene in testis differentiation in mammals and birds. *Nat.
Genet.* **14**, 62-68.

Morrison, A. A., Viney, R. L. and Ladomery, M. R. (2008). The post-
transcriptional roles of WT1, a multifunctional zinc-finger protein. *Biochim.
Biophys. Acta* **1785**, 55-62.

Munger, S. C., Aylor, D. L., Syed, H. A., Magwene, P. M., Threadgill, D. W.
and Capel, B. (2009). Elucidation of the transcription network governing
mammalian sex determination by exploiting strain-specific susceptibility to sex
reversal. *Genes Dev.* **23**, 2521-2536.

Nef, S., Verma-Kurvari, S., Merenmies, J., Vassalli, J. D., Efstratiadis, A.,
Accili, D. and Parada, L. F. (2003). Testis determination requires insulin receptor
family function in mice. *Nature* **426**, 291-295.

Oh, H. J., Li, Y. and Lau, Y. F. (2005). Sry associates with the heterochromatin
protein 1 complex by interacting with a KRAB domain protein. *Biol. Reprod.* **72**,
407-415.

Palmer, S. J. and Burgoyne, P. S. (1991). In situ analysis of fetal, prepuberal and
adult XX–XY chimaeric mouse testes: Sertoli cells are predominantly, but not
exclusively, XY. *Development* **112**, 265-268.

Pannetier, M., Tilly, G., Kocer, A., Hudrisier, M., Renault, L., Chesnais, N.,
Costa, J., Le Provost, F., Vaiman, D., Vilotte, J. L. et al. (2006). Goat SRY
induces testis development in XX transgenic mice. *FEBS Lett.* **580**, 3715-3720.

Patek, C. E., Kerr, J. B., Gosden, R. G., Jones, K. W., Hardy, K., Muggleton-
Harris, A. L., Handyside, A. H., Whittingham, D. G. and Hooper, M. L.
(1991). Sex chimaerism, fertility and sex determination in the mouse.
Development **113**, 311-325.

Peng, H., Ivanov, A. V., Oh, H. J., Lau, Y. F. and Rauscher, F. J., 3rd (2009).
Epigenetic gene silencing by the SRY protein is mediated by a KRAB-O protein
that recruits the KAP1 co-repressor machinery. *J. Biol. Chem.* **284**, 35670-35680.

Pfeifer, D., Kist, R., Dewar, K., Devon, K., Lander, E. S., Birren, B.,
Korniszewski, L., Back, E. and Scherer, G. (1999). Campomelic dysplasia
translocation breakpoints are scattered over 1 Mb proximal to SOX9: evidence
for an extended control region. *Am. J. Hum. Genet.* **65**, 111-124.

Poulat, F., de Santa Barbara, P., Desclozeaux, M., Soullier, S., Moniot, B.,
Bonneaud, N., Boizet, B. and Berta, P. (1997). The human testis determining
factor SRY binds a nuclear factor containing PDZ protein interaction domains. *J.
Biol. Chem.* **272**, 7167-7172.

Robert, N. M., Tremblay, J. J. and Viger, R. S. (2002). Friend of GATA (FOG)-1
and FOG-2 differentially repress the GATA-dependent activity of multiple
gonadal promoters. *Endocrinology* **143**, 3963-3973.

Ross, D. G., Bowles, J., Koopman, P. and Lehnert, S. (2008). New insights into
SRY regulation through identification of 5' conserved sequences. *BMC Mol. Biol.*
9, 85.

DEVELOPMENT

Sanchez-Moreno, I., Coral-Vazquez, R., Mendez, J. P. and Canto, P. (2008). Full-length SRY protein is essential for DNA binding. *Mol. Hum. Reprod.* **14**, 325-330.

Schepers, G., Wilson, M., Wilhelm, D. and Koopman, P. (2003). SOX8 is expressed during testis differentiation in mice and synergizes with SF1 to activate the Amh promoter in vitro. *J. Biol. Chem.* **278**, 28101-28108.

Schmahl, J., Eicher, E. M., Washburn, L. L. and Capel, B. (2000). Sry induces cell proliferation in the mouse gonad. *Development* **127**, 65-73.

Schmid, M., Enderle, E., Schindler, D. and Schempp, W. (1989). Chromosome banding and DNA replication patterns in bird karyotypes. *Cytogenet. Cell Genet.* **52**, 139-146.

Sekido, R. and Lovell-Badge, R. (2008). Sex determination involves synergistic action of SRY and SF1 on a specific Sox9 enhancer. *Nature* **453**, 930-934.

Sekido, R., Bar, I., Narvaez, V., Penny, G. and Lovell-Badge, R. (2004). SOX9 is up-regulated by the transient expression of SRY specifically in Sertoli cell precursors. *Dev. Biol.* **274**, 271-279.

Shimamura, R., Fraizer, G. C., Trapman, J., Lau, Yf, C. and Saunders, G. F. (1997). The Wilms' tumor gene WT1 can regulate genes involved in sex determination and differentiation: SRY, Mullerian-inhibiting substance, and the androgen receptor. *Clin. Cancer Res.* **3**, 2571-2580.

Sim, H., Rimmer, K., Kelly, S., Ludbrook, L. M., Clayton, A. H. and Harley, V. R. (2005). Defective calmodulin-mediated nuclear transport of the sex-determining region of the Y chromosome (SRY) in XY sex reversal. *Mol. Endocrinol.* **19**, 1884-1892.

Sinclair, A. H., Berta, P., Palmer, M. S., Hawkins, J. R., Griffiths, B. L., Smith, M. J., Foster, J. W., Frischauf, A. M., Lovell-Badge, R. and Goodfellow, P. N. (1990). A gene from the human sex-determining region encodes a protein with homology to a conserved DNA-binding motif. *Nature* **346**, 240-244.

Spotila, L. D., Spotila, J. R. and Hall, S. E. (1998). Sequence and expression analysis of WT1 and Sox9 in the red-eared slider turtle, Trachemys scripta. *J. Exp. Zool.* **281**, 417-427.

Sudbeck, P. and Scherer, G. (1997). Two independent nuclear localization signals are present in the DNA-binding high-mobility group domains of SRY and SOX9. *J. Biol. Chem.* **272**, 27848-27852.

Sutou, S., Mitsui, Y. and Tsuchiya, K. (2001). Sex determination without the Y chromosome in two Japanese rodents Tokudaia osimensis osimensis and Tokudaia osimensis spp. *Mamm. Genome* **12**, 17-21.

Tamashiro, D. A., Alarcon, V. B. and Marikawa, Y. (2008). Ectopic expression of mouse Sry interferes with Wnt/beta-catenin signaling in mouse embryonal carcinoma cell lines. *Biochim. Biophys. Acta* **1780**, 1395-1402.

Tevosian, S. G., Albrecht, K. H., Crispino, J. D., Fujiwara, Y., Eicher, E. M. and Orkin, S. H. (2002). Gonadal differentiation, sex determination and normal Sry expression in mice require direct interaction between transcription partners GATA4 and FOG2. *Development* **129**, 4627-4634.

Thevenet, L., Mejean, C., Moniot, B., Bonneaud, N., Galeotti, N., Aldrian-Herrada, G., Poulat, F., Berta, P., Benkirane, M. and Boizet-Bonhoure, B. (2004). Regulation of human SRY subcellular distribution by its acetylation/deacetylation. *EMBO J.* **23**, 3336-3345.

Veitia, R., Ion, A., Barbaux, S., Jobling, M. A., Souleyreau, N., Ennis, K., Ostrer, H., Tosi, M., Meo, T., Chibani, J. et al. (1997). Mutations and sequence variants in the testis-determining region of the Y chromosome in individuals with a 46,XY female phenotype. *Hum. Genet.* **99**, 648-652.

Vidal, V. P., Chaboissier, M. C., de Rooij, D. G. and Schedl, A. (2001). Sox9 induces testis development in XX transgenic mice. *Nat. Genet.* **28**, 216-217.

Wagner, T., Wirth, J., Meyer, J., Zabel, B., Held, M., Zimmer, J., Pasantes, J., Bricarelli, F. D., Keutel, J., Hustert, E. et al. (1994). Autosomal sex reversal and campomelic dysplasia are caused by mutations in and around the SRY-related gene SOX9. *Cell* **79**, 1111-1120.

Wallis, M. C., Waters, P. D. and Graves, J. A. (2008). Sex determination in mammals-before and after the evolution of SRY. *Cell. Mol. Life Sci.* **65**, 3182-3195.

Western, P. S., Harry, J. L., Graves, J. A. and Sinclair, A. H. (1999). Temperature-dependent sex determination in the American alligator: AMH precedes SOX9 expression. *Dev. Dyn.* **216**, 411-419.

Wilhelm, D., Martinson, F., Bradford, S., Wilson, M. J., Combes, A. N., Beverdam, A., Bowles, J., Mizusaki, H. and Koopman, P. (2005). Sertoli cell differentiation is induced both cell-autonomously and through prostaglandin signaling during mammalian sex determination. *Dev. Biol.* **287**, 111-124.

Wilhelm, D., Hiramatsu, R., Mizusaki, H., Widjaja, L., Combes, A. N., Kanai, Y. and Koopman, P. (2007). SOX9 regulates prostaglandin D synthase gene transcription in vivo to ensure testis development. *J. Biol. Chem.* **282**, 10553-10560.

Wright, E., Hargrave, M. R., Christiansen, J., Cooper, L., Kun, J., Evans, T., Gangadharan, U., Greenfield, A. and Koopman, P. (1995). The Sry-related gene Sox9 is expressed during chondrogenesis in mouse embryos. *Nat. Genet.* **9**, 15-20.

Wu, J. B., Chen, K., Li, Y., Lau, Y. F. and Shih, J. C. (2009). Regulation of monoamine oxidase A by the SRY gene on the Y chromosome. *FASEB J.* **23**, 4029-4038.