Targeted disruption of the murine junD gene results in multiple defects in male reproductive function

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SUMMARY

JunD is one of three mammalian Jun proteins that contribute to the AP-1 transcription factor complex. Distinct regulation and functions have been proposed for each Jun member, but less is known about the biological functions of each of these proteins in vivo. To investigate the role of JunD, we have inactivated the murine gene by replacement with a bacterial β-gal reporter gene. Embryonic JunD expression was initially detected in the developing heart and cardiovascular system. Subsequent broadening phases of JunD expression were observed during embryonic development and expression in the adult was widespread in many tissues and cell lineages. Mutant animals lack JunD mRNA and protein and showed no evidence of upregulation of c-Jun and JunB mRNA levels. In contrast to the other two Jun members, homozygous JunD−/− mutant animals were viable and appeared healthy. However, homozygous JunD−/− animals showed a reduced postnatal growth. Furthermore, JunD−/− males exhibited multiple age-dependent defects in reproduction, hormone imbalance and impaired spermatogenesis with abnormalities in head and flagellum sperm structures. No defects in fertility were observed in JunD−/− female animals. These results provide evidence for redundant functions for members of the Jun family during development and specific functions for JunD in male reproductive function.

Key words: AP-1, Growth, Infertility, Spermatogenesis, Mouse, junD

INTRODUCTION

JunD is a member of the mammalian Jun family of proto-oncogenes, which includes c-jun and junB (Angel et al., 1988; Bohmann et al., 1987; Hirai et al., 1989; Ryder et al., 1989). Each Jun protein can form either homodimers or heterodimers with members of the related Fos family (c-Fos, FosB, Fra-1 and Fra-2) or with the ATF family (ATF2, ATF3 and ATF4) to create the AP-1 transcription factor (Angel and Karin, 1991; Hai et al., 1989). Jun/Jun and Jun/Fos dimers bind to the TPA responsive element (TRE) TGACTCA present in many gene promoters, whereas Jun/ATF dimers bind preferentially to the cAMP responsive element (CRE) TGACGTCA (Angel and Karin, 1991).

The Jun and Fos factors are basic-leucine zipper (bZIP) proteins characterised by a basic DNA-binding domain joined to a C-terminal leucine zipper dimerisation domain (Kouzarides and Ziff, 1988; Landschulz et al., 1988; Sassone-Corsi et al., 1988). The three Jun proteins are similar in their interaction with Fos members and in DNA-binding affinity (Nakabeppu et al., 1988). The N-terminal transactivation domain is less conserved and may account for the different transactivation characteristics of the Jun proteins. For example, the c-Jun protein contains a binding site for the Jun N-terminal Kinase (JNK) and phosphorylation of adjacent serine residues enhances its transactivation potential (Smeal et al., 1991). JunD contains the N-terminal serine residues, but lacks a functional JNK docking site (Kallunki et al., 1996) and is a weaker transcriptional activator. In contrast to the other two Jun members, homozygous JunD−/− mutant animals were viable and appeared healthy. However, homozygous JunD−/− animals showed a reduced postnatal growth. Furthermore, JunD−/− males exhibited multiple age-dependent defects in reproduction, hormone imbalance and impaired spermatogenesis with abnormalities in head and flagellum sperm structures. No defects in fertility were observed in JunD−/− female animals. These results provide evidence for redundant functions for members of the Jun family during development and specific functions for JunD in male reproductive function.

Further differences in the biological functions of the Jun proteins may result from differential expression. High junD mRNA levels were observed in a range of tissues (Hirai et al., 1989; Ryder et al., 1989), whereas the other two jun genes have a restricted expression pattern (Wilkinson et al., 1989). Indeed, in situ analysis suggested that the distribution of different jun genes are non-overlapping in many organs. Tissue-specific expression of c-Jun and JunB during embryogenesis and organogenesis suggested distinct developmental roles
(Wilkinson et al., 1989). Differences have also been recorded in specific adult tissues. For example, the expression of the Jun proteins is restricted to distinct differentiation stages in the skin (Rutberg et al., 1996) and in testes (Alcivar et al., 1991; Cohen et al., 1993). When these patterns are viewed in parallel with the differential expression patterns of the fos genes, a complex picture of potential tissue-specific AP-1 dimers emerges. Discerning the function of specific dimers in different cellular contexts presents a challenge to understanding the complexity of AP-1 function in vivo.

Studies examining AP-1 function in vitro have implied distinct functions for individual AP-1 dimers in different cellular contexts, including cell proliferation, cell death and differentiation (Angel and Karin, 1991). For example, c-Jun has been specifically implicated in the control of cell death (Bossy-Wetzel et al., 1997; Ham et al., 1995) and ras-induced transformation (Johnson et al., 1996; Mchta et al., 1997). Opposing roles for c-Jun and JunD have been proposed based on differences in cell cycle regulation, mitogenic stimulation and oncogenic transformation. (Kovary and Bravo, 1991; Lallemand et al., 1997; Pfarr et al., 1994). Furthermore, JunD was shown to interact with menin, the product of the MEF2 tumor suppressor gene, supporting a role for JunD in growth inhibition (Agarwal et al., 1999). Hence, differential regulation of the Jun proteins may coordinate distinct responses to extracellular stimuli.

Several groups have used gene targeting to investigate the functions of individual AP-1 components in vivo. Disruption of the c-jun and junB genes resulted in embryonic lethality, indicating essential, nonoverlapping roles during mammalian development. Mice lacking c-Jun die at E12.5 and have a defect in hepatogenesis, whereas mice lacking JunB die earlier with defects in the extraembryonic tissues (Hilberg et al., 1993; Johnson et al., 1993; Schorpp-Kistner et al., 1999). Hence, differential regulation of the Jun proteins may coordinate distinct responses to extracellular stimuli.

Here we report the generation of a null allele for the murine junD gene by replacement with a lacZ cassette. These animals enabled us to characterise the expression pattern of junD during development and the phenotype of mice lacking JunD (JunD−/− mice). In contrast to the other two murine jun genes, mutation of the junD locus produced homozygous JunD−/− mice which are viable. Homozygous mice exhibited a postnatal growth retardation. Furthermore, male JunD−/− mice exhibit significantly reduced fertility, characterised by defects in mating behaviour and a specific block in spermogenesis. These results emphasise the complexity of unravelling specific physiological functions for individual AP-1 dimers.

MATERIAL AND METHODS

Construction of JunD targeting vector

A library of mouse 129/Sv genomic DNA was screened with a JunD cDNA probe (Hirai et al., 1989). One phage was isolated that included the 5′ flanking sequence, the entire coding region and 1.9 kb of 3′ sequence. Two different genomic fragments, an EcoRI-NorI fragment of 6.2 kb from the 5′ flanking region and a SphI-EcoRI fragment of 2.4 kb from the 3′ region, were used to construct a replacement vector in which the complete junD coding region was replaced by a NLS-lacZ reporter gene and a PGK-neoR cassette. Briefly, a JunD promoter fragment (~140 to +120) was amplified by PCR and cloned into the pucBM20 vector (Bohringer). A BamHI-HindIII NLS-lacZ cassette was inserted at the HindIII site downstream of the promoter. A NorI-SalI fragment encompassing the 260 bp of the promoter followed by the lacZ gene was excised and cloned upstream of the PGK-neoR cassette of a modified pPNT plasmid containing the 2.4 kb lacZ gene (Fig. 1A). The 6.2 kb 5′ genomic fragment was cloned into a Bluescript plasmid (Stratagene) and a 5.6 kb SalI-NorI fragment was subcloned into the pPNT modified plasmid to give the targeting vector (Fig. 1A). Finally, the PGK-Thymidine Kinase cassette was inserted at the 3′ end of the vector to generate the final construct.

ES cell culture and generation of chimeric mice

ES cells from the CK35 line were provided by C. Kress (Kress et al., 1998) and were maintained as previously described (Campus et al., 1996). For electroporation of the ES cells, 20 μg of the targeting vector linearized using SalI was added to 1.6×10⁶ CK35 cells in phosphate buffer saline (PBS). Electroporation and selection of G418 and Ganciclovir-resistant colonies were performed as previously described by Colucci-Guyon and colleagues (Colucci-Guyon et al., 1994). Chimeric mice were generated from recombinant ES cells as described (Bradley, 1987).

Nucleic acid and protein analysis

Southern blot analysis of genomic DNA, extracted from ES cell clones or mouse tails, was performed following EcoRV digestion, blotting onto Hybond-N membranes (Amersham) and probed with an EcoRV-EcoRI DNA fragment located upstream of the homologous region (Fig. 1A,B).

Genotype analysis was performed by PCR amplification of genomic DNA using four oligonucleotide primers, two mapping within the junD gene: 5′-TGGCTCTTTGGACAGCAGCCGCCAAGCAAG-3′; 5′-GGCGGCTACGGCCCTCCTGCCATAGAGG-3′ and two in the lacZ gene: 5′-GACATCGAGCTGGAATATACGGGTGACATAG-3′, 5′-GACACCAGAACCAGATGTGTAGCGAC-3′. The size of the amplified bands corresponding to the wild-type or mutant alleles were 315 bp or 812 bp, respectively (Fig. 1C).

Northern blot analysis was performed by standard methods using total RNA extracted from adult mice tissues. RNA (20 μg/lane) were separated in 1.5% agarose gels, transferred to Hybond-N membranes (Amersham) and probed with c-Jun cDNA using random hexamer oligonucleotides as templates, in a 25 μl reaction volume containing 1 μl SuperScript II (GIBCO/BRL) reverse
transcriptase (RT) enzyme following the manufacturers’ instructions. Samples were diluted to 100 μl before PCR amplification. Samples omitting RT enzyme were used as negative (−RT) controls. Amplification was carried out in 25 μl reactions containing 1 μl cDNA and 1 μM oligonucleotide primers and 0.25 μl Taq polymerase (Promega). PCR was performed in a Perkin Elmer thermocycler and consisted of 30 cycles of 94°C for 1 minute, 54°C for 1 minute, and 72°C for 1 minute. PCR products (10 μl aliquots) were analysed by agarose gel electrophoresis. The primers used for PCR were: β-actin (5′-GACCTGACAGACTACCTCAT and 5′-AGACAGCAGCTTGTCGCAT), HPRT (5′-CTGTTGAAAGACCTCTCG and 5′-CACAGGACTAGAACACTGC), Hox.1.4 (Nantel et al., 1996), protamine 1 (Nantel et al., 1996), protamine 2 (Nantel et al., 1996), transition protein 1 (Nantel et al., 1996), calspemrin (Nantel et al., 1996), RT7 (5′-GTGTCTATGATGTAGGCCC and 5′-TATGTGCTCCTGTTACATGCC) and BMP8 (5′-AAGTCCGA- GATGGCTATGCG and 5′-CATGAAAGGCGTCTGGGAGC).

Staining and histological analysis

For X-gal staining, embryos or adult tissues were dissected, fixed in 4% paraformaldehyde/PBS for 20 minutes, washed three times in PBS, and then incubated at 32°C for 3 hours to overnight in a staining solution containing 2 mM MgCl2, 4 mM K3Fe(CN)6, 4 mM K3Fe(CN)6, 0.4 mg/ml 4-chloro-5-bromo-3-indolyl-b-D-galactopyranoside (X-gal) and 0.1% Triton in PBS.

For histological analysis, freshly dissected testes were fixed in Bouin’s fixative for 24 hours. They were then rinsed and embedded in paraffin. Sections (7 μm thick) were mounted, dewaxed and stained with Eosin/Hematoxylin before examination.

For X-gal staining of histological sections, either the tissues were fixed and stained prior to embedding in paraffin and sectioning (testes and brain), or animals were perfused, tissues removed, embedded in paraffin and sectioned (7 μm thick) prior to X-gal staining. Sections were counterstained with Eosin.

For the analysis of various parameters of epididymal sperm in adult mice, animals were killed and sperm removed from the epididymis, adult mice, animals were killed and immersed in the same fixative for 1 hour, and then mince d into small blocks (1 mm3) and postfixed for an additional hour at room temperature. Samples were then rinsed overnight at 4°C either in PBS or cacodylate buffer, postfixed for 1 hour at 22°C with ferrocyanide-reduced osmium tetroxide (Karnovsky, 1971), dehydrated with graded alcohols and embedded in Epon. Thin electron microscopy sections were counterstained with lead citrate and examined with a Philips CM 10 electron microscope at 60 kV (Institute A. Feyssard, CNRS, Gif-sur-Yvette, France).

Hormone analysis

Quantification of hormones was performed using commercially available kits following the manufacturer’s instructions; testosterone Coatria assay kit (BioMérieux, France); rat LH, rat FSH and rat GH using BIOTRAK radioimmunoassay kits (Amersham, UK); inhibin B dimer assay kit (Serotec, UK).

RESULTS

Targeted mutagenesis of the mouse junD gene

The junD gene was disrupted by homologous recombination in CK35 ES cells using a replacement targeting strategy (Fig. 1A). As the murine junD gene contains no introns, a region covering the entire coding sequence was replaced with a NLS-lacZ/PGK-neo8 cassette (Fig. 1A). The modified bacterial β-galactosidase

![Fig. 1. Targeted mutagenesis of the murine JunD locus. (A) Schematic representation of the wild-type junD allele, the targeting vector, and recombined mutant junD-lacZ allele. The transcribed sequences of the junD gene are represented by black (coding sequence) and white boxes (5′ and 3′ UTR). The NLS-lacZ cassette and the PGK-NEO8 selection cassette are also indicated. The position of the 5′ probe used for Southern blot analysis is shown, as well as the EcoRV-digested fragments of 14 kb (wild type) and 9.6 kb (mutant allele). Restriction endonuclease sites are indicated; C, Ncol; E, EcoRI; N, Ndel; O, NotI; S, Spfil; V, EcoRV. (B) Southern blot analysis of EcoRV-digested DNA from wild-type (+/+), heterozygous (+/−) or homozygous (−/−) mice. Hybridisation using the 5′ probe yielded bands corresponding to fragments of 14 kb for the wild-type allele (W) or 9.6 kb for the targeted allele (M). (C) PCR genotyping of progeny. Wild-type (+/+), heterozygous (+/−) and homozygous (−/−) mice were identified by the amplification of PCR products specific for either the junD wild-type allele (W, 315 bp) or the targeted allele (M, 812 bp).](image-url)
Expression of junD-lacZ in embryos and adult mice

We used heterozygous JunD+/− mice to document the expression of the NLS-lacZ transgene under the control of the endogenous junD promoter during embryonic development. No X-gal staining was detected in blastocysts prior to implantation. The earliest lacZ expression was detected in the ectoplacental cone at 7.5 days postcoitus (E7.5; Fig. 2A). At day E8.5, β-galactosidase activity was detectable only in small groups of cells in the yolk sac (not shown). Embryonic X-gal staining was observed as early as day E9.5 in the large blood vessels and the developing cardiovascular system (Fig. 2B). As embryogenesis progressed, there was a broadening of the lacZ expression pattern in phases. By day E10.5, extensive X-gal staining was observed along the central nervous system, the neural tube and somites, and in the developing musculature (Fig. 2C). There was additional expression in the developing limb bud, in the otic vesicle and the eye. By later embryonic stages (e.g. staining at E15.5, Fig. 2D), the expression was more widespread and roughly mirrored that seen in the adult animal. Hence, this cumulative expansion in phases resulted in a broad staining pattern at the end of development. At these later stages, nearly all the major organs were stained. However, the expression was not uniform; within each organ, lacZ expression was observed in particular cell types. Also, some cell types, notably the parenchymal cells of the liver, were almost devoid of staining.

Analysis of X-gal staining in heterozygous JunD+/− adults revealed a similarly wide pattern of expression. However, variations were observed in the intensity of staining. Particularly striking patterns were observed in the heart, kidney and brain (Fig. 3). The strong cardiac staining noted in early embryos persisted in adults (Fig. 3A). Examination of tissue sections indicated that many cells in the heart show a strong nuclear lacZ expression, including both cardiac and smooth muscle cells (Fig. 3B). In the adult kidney, X-gal staining was observed both in the medulla, where the blood vessels and the collecting ducts were stained, and in the cortex where the staining of the glomerular structures was clearly visible in histological sections (Fig. 3C,D). Analysis of X-gal staining in the brains of heterozygous animals revealed a striking pattern of expression in neuronal and glial cell populations, with particularly strong staining in the cerebellum, in the cortex and the hippocampus (Fig. 3G,H). lacZ expression was also detected in the testis (Fig. 3E), with staining of testicular interstitial cells, Sertoli cells and all germ cell populations, with the exception of spermatogonia (Fig. 3F). Staining was also observed in the epididymis, which was markedly above the low levels of background staining. Some tissues had notably lower expression levels; for example, in the liver, there was little staining except for the blood vessels or ducts (data not shown). The wide tissue distribution confirmed and extends previous results from northern blot and in situ analysis (Hirai et al., 1989; Ryder et al., 1989).

Phenotypic analysis of homozygous JunD−/− mutant mice

To test whether the broad expression pattern of JunD reflects diverse functions during development, we crossed heterozygous JunD+/− mice and analysed their offspring by Southern blot or PCR screening (Fig. 1B,C). These crosses...
yielded viable homozygous JunD−/− mice at the predicted ratio of wild-type (n=47), heterozygous (n=86) and homozygous (n=43) mutant offspring. Hence, despite the cumulative, phased expression of JunD during embryogenesis, JunD function is not essential for mouse development.

The homozygous JunD−/− mutant mice appeared similar to wild-type or heterozygous littermates. However, in most litters, the smallest animals were those with the homozygous JunD−/− genotype. Mutant and wild-type littermates were weighed and their growth rates compared (Fig. 4). At birth, the average weight of homozygous mice was indistinguishable from littermates (1.78±0.05 g compared to wild-type 1.77±0.02 g). However, with age the weights of the animals diverged and the average weight of homozygous mice was significantly reduced compared to wild-type (25.2±2.5 g; n=13) or heterozygous (12.7±4.9 ng/ml, n=3) or wild-type controls (13.9±3.3 ng/ml, n=3). Furthermore, analysis of GH levels in serum (6.2±1.7 ng/ml in younger (4 week old) litters also revealed a similar 30% reduction in both circulating GH in serum (6.2±1.7 ng/ml in Jun−/− animals, compared to 8.4±1.8 ng/ml in JunD+/− mice) and in total pituitary GH levels (8.3±1.4 μg in Jun−/− mice, compared to 11.5±1.8 ng/ml in JunD+/− mice). These results suggest that reduced growth hormone levels may contribute to the postnatal growth defect of the JunD−/− mutant mice.

The surprisingly mild mutant phenotype could be due to a compensatory upregulation of the other Jun genes in JunD−/− animals. We investigated this hypothesis by northern blot analysis of jun gene mRNA levels. As expected, there was no detectable JunD mRNA in the brain, kidneys, lungs, heart, stomach, testis and skeletal muscle of homozygous JunD−/− mice (Fig. 5A and data not shown), confirming that our mutagenesis created a null allele. Also, fibroblasts derived from JunD−/− embryos showed a complete absence of JunD protein by immunoblot analysis (Fig. 5B). The faint band seen in −/− lanes was due to mild cross-reactivity of the anti-JunD antibodies with the c-Jun protein (D. Lallemand, personal communication). Furthermore, we observed no changes in the levels of c-jun or junB mRNA levels in the tissues of homozygous JunD−/− mice (including stomach, lungs, brains, kidneys, heart or testis, Fig. 5A and data not shown), compared to control animals. Likewise, there were no changes in the protein levels of c-Jun or JunB in fibroblasts isolated from JunD−/− embryos (Fig. 5B). These results confirm that we have created a null allele for JunD and that this does not cause a dramatic compensatory upregulation of the other jun genes.

**Reproductive defects in homozygous JunD−/− male mice**

During attempts to establish a breeding colony, we noticed reduced offspring rates in cages of JunD−/− mice. Therefore, we systematically tested the reproductive capacity of homozygous mice of both sexes with wild-type mates. Homozygous JunD−/− female mice showed no severe reproductive defects and produced litters of approximately normal size (average litter size = 5.6, n=27 compared to 6.0, n=23 for wild-type females). In contrast, when JunD−/− male
mice were mated with wild-type females approximately 25% failed to produce any litters over a 2-month breeding period. Furthermore, in the remaining mice, there was a drop in fertility with age; more than half the mice mated normally when young (average litter size = 5.9, n=21), but ceased to produce litters as they grew older (Fig. 6A). No such behaviour was observed in heterozygous mice. Similar observations were found in colonies of a pure (129/Sv) or mixed (129/Sv¥×C57/B6) genetic backgrounds. We focused subsequent experiments on the group of animals that failed to give any litters.

We studied the frequency of copulations of these males over a 2-week period. Observation of the behaviour of these animals in the presence of wild-type females in oestrus, or superovulated females, revealed that they failed to exhibit any mating behaviour or vaginal plugs, whereas control male littermates engaged immediately in mounting behaviour. We performed a detailed histological examination of the testes of these sterile animals to search for structural abnormalities of the reproductive tract. A subset of homozygous mice that failed to mate displayed an abnormal testicular histology. Of the 13 sterile animals examined, 5 showed clear testis defects, whereas the others appeared to be histologically normal. A comparison of several spermatogenic parameters is shown in Table 1. No significant differences were observed in testes weights. The epididymal sperm analysis revealed that the sterility phenotype was heterogeneous and that homozygous mutant mice fall in two classes; group I exhibited oligo-astheno-teratospermia in which most spermatozoa showed frequent head and flagellum abnormalities, whereas group II had sperm of normal concentration and morphology, but with a dramatically diminished sperm motility (asthenospermia) (Table 1).

Light microscopy analysis of the seminiferous tubules of group I sterile mice revealed a striking absence of flagella in the lumen of the tubules (Fig. 6D,E). Detailed quantification of the different cell types in mutant mice tubules revealed that the numbers of Sertoli cells, spermatogonia, early spermatocytes and round spermatids were not affected at any stage of spermatogenesis (Fig. 6F,G). However, in stage VII tubules, the total absence of the flagella in the mutant animals correlated with a marked decrease in the number of late spermatid heads located near the lumen (Fig. 6F).

Further characterisation using light microscopy and electron microscopy revealed abnormalities in head and flagellum structures during spermatogenesis. For example, in stage V tubules, the clustering heads of late spermatids inserted inside the seminiferous epithelium showed an abnormal hammer-like shape (Fig. 7A). This flattening of the head was the most frequent malformation observed and was also seen at the ultrastructural level (Fig. 7B). However, the condensation of the nucleus appeared normal. Spermatogenesis appeared to

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**Table 1. Spermocytogram of homozygous JunD−/− mutants and wild-type mice**

<table>
<thead>
<tr>
<th></th>
<th>Wild-type JunD+/+ males</th>
<th>Homozygous JunD−/− males</th>
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<tbody>
<tr>
<td></td>
<td>n=2</td>
<td>Group I</td>
</tr>
<tr>
<td>Weight of animal (g)</td>
<td>30.5±0.5</td>
<td>23.8±5.8</td>
</tr>
<tr>
<td>Weight of testes (mg)</td>
<td>72±4</td>
<td>61±9</td>
</tr>
<tr>
<td>Total sperm number (average)</td>
<td>5.15×10⁶</td>
<td>0.54×10⁶</td>
</tr>
<tr>
<td>Sperm motility (%)</td>
<td>5±5.5</td>
<td>0</td>
</tr>
<tr>
<td>Head abnormalities (%)</td>
<td>5.5±1.5</td>
<td>86.7±3.8</td>
</tr>
<tr>
<td>Flagella abnormalities (%)</td>
<td>19.5±3.5</td>
<td>96.0±5.7</td>
</tr>
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homozygote JunD indicated a significant increase in inhibin B levels in sterile spermatogenic process. Quantification of serum levels analysed the levels of circulating hormones that regulate the microtubules.

cytoplasmic masses (compare Fig. 7E and F). This irregularly tail, the periaxonemal cytoplasm bulged out, forming irregular of the cell cytoplasm to form the future proximal region of the spindle. When the flagellum merged out such as radial spokes and dynein arms (Fig. 7D). At the final phase of spermiogenesis, late spermatids present in the tubules showed more flagella defects. When the flagellum merged out the cell cytoplasm to form the future proximal region of the tail, the periaxonemal cytoplasm bulged out, forming irregular cytoplasmic masses.

Figure 7. (A) Immunofluorescence staining of microtubules, monitoring MTB expression in late spermatids. (B) Western blot analysis of JunD expression in late spermatids. (C) Immunohistochemistry of c-Jun expression in late spermatids. (D) Immunohistochemistry of JunD expression in late spermatids. (E) Immunohistochemistry of JunB expression in late spermatids. (F) Immunohistochemistry of c-Jun expression in late spermatids.

DISCUSSION

JunD differs from the other two mammalian Jun proteins in terms of its expression pattern, regulation by mitogens and stress, and its transactivation capacity (Hirai et al., 1989; Kallunki et al., 1996; Pfarr et al., 1994; Ryder et al., 1989). We have generated a null allele for the junD gene by replacing the coding region with a modified NLS-lacZ gene, enabling us to document the JunD expression pattern and the phenotype of junD−/− animals. Our results are in marked contrast with studies mutating the genes for c-jun or junB. JunD is dispensable for embryonic development, but critical for the maintenance of normal male reproductive functions. These results offer insights into redundant and tissue-specific functions of the individual Jun members.

Expression of JunD during embryonic development and in adult tissues

Analysis of heterozygous junD-lacZ embryos revealed the appearance of broadening, cumulative waves of expression during development. These phases were additive in that, once expression was observed, it persisted until adulthood. Each successive phase appeared to follow the initial stages of organogenesis, suggesting a role in the maintenance of specific cell lineages once the commitment to differentiation is established. JunD expression is highest in differentiated cells such as myoblasts, epithelium and postmitotic neurons. This is consistent with earlier studies suggesting that JunD functions in growth inhibition (Pfarr et al., 1994). A role for JunD in the maintenance of specific organ functions is also suggested by the age-related sterility phenotype observed in adult males. As the other two Jun proteins also exhibit specific expression patterns during organogenesis (Wilkinson et al., 1989), we can begin to appreciate how development may be associated with shifts in the ratios of different Jun-containing AP-1 dimers.

The expression analysis in adult animals confirms and extends earlier Northern blotting results (Hirai et al., 1989; Ryder et al., 1989). The JunD expression was widespread, but not ubiquitous. There was a specific pattern of expression in different organs and cell lineages, with notable differences in differentiated cell types in organs such as kidney and testes (Fig. 3). Furthermore, in some tissues, expression was very low, e.g. in the fetal liver and the extraembryonic tissues. This is interesting in light of the tissue defects observed in c-Jun and JunB mutant embryos (Hilberg et al., 1993; Schorpp-Kistner et
al., 1999). The junD-lacZ mice will be invaluable for future detailed analysis of junD expression patterns, and characterising overlapping expression patterns with other jun and fos genes.

**JunD expression is dispensable for development**

Despite the broad expression pattern of JunD in many cell lineages, mice lacking JunD developed normally and appeared relatively healthy, unlike mice lacking the other jun genes (Hilberg et al., 1993; Johnson et al., 1993; Schorpp-Kistner et al., 1999). Despite our observations that there is no upregulation c-jun and junB gene expression in JunD−/− mice, it is possible that a functional redundancy could account for the lack of a developmental phenotype. There are several well-documented examples of genetic redundancy amongst multi-gene families of transcription factors. For example, the functional redundancy of the myoD family of myogenic regulatory factors (Rudnicki et al., 1993) or the upregulation of the bZip CREM factor explaining the mild phenotype of CREB−/− mice (Hummler et al., 1994). For the Jun family, it is possible that phenotypes are only apparent in restricted cell types where the expression patterns of the different Jun proteins do not overlap. The low levels of JunD in the liver and extraembryonic tissues may explain the hepatogenic defects of c-Jun−/− embryos (Hilberg et al., 1993) or placental defects in mice lacking JunB (Schorpp-Kistner et al., 1999). The recent observation that JunD interacts with menin the product of the MEN1 tumor suppressor gene suggests that these mice will be useful in understanding menin-associated neoplasias and other JunD-related pathologies (Agarwal et al., 1999). The 30% reduction in the levels of circulating growth hormone likely contribute to the reduced postnatal growth. Furthermore, preliminary results suggest an intrinsic proliferative defects in cells lacking JunD (data not shown). Growth defects have been reported for a number of mice with disruption of genes associated with AP-1 and the cell cycle (e.g. c-fos−/− (Johnson et al., 1992), cyclinD1−/− (Sicinski et al., 1995), Rb-family members (Lee et al., 1996)).

**Mutation of the junD gene affects male reproductive functions**

We observed specific defects in the reproductive function of JunD−/− male mice, indicating tissue-specific functions for JunD-containing AP-1 dimers. The sterility phenotype consists of a combination of characteristics, including both sexual behaviour and spermatogenesis. Our results suggest that the functions of JunD dimers in the pituitary and the testis are essential to maintain normal testes function. There are likely multiple factors that contribute to this complex phenotype. We have shown that changes in hormone levels and reduction in testes-specific transcription may account for some of the observed infertility. We observed a heterogeneity between homozygous JunD−/− males, with a clear deterioration in reproductive capacity with age. These differences could not be explained by genetic background as we observed the same phenotype even in a pure inbred 129/Sv colony. Variability of the mutation penetrance has been described in several gene targeting studies; e.g., exencephaly in a subset of p53−/− embryos showed (Sah et al., 1995); and variable, age-related sterility phenotypes in BMP8 gene knockouts (Zhao et al., 1996, 1998).

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**Fig. 6.** Characterisation of the sterility phenotype of homozygous JunD−/− male mice. (A) Reduced fertility of homozygous JunD−/− mice. The percentage of homozygous JunD−/− mice capable of reproducing decreased sharply with age (triangles), while the control heterozygous animals (squares) showed no reduced fertility. (B-E) Light microscopy images of wild-type (B,C) or JunD−/− mutant (D,E) mouse testis histological sections stained with Hematoxylin-Eosin. At low magnification (×10 images B,D), the gross testes morphology was similar in wild-type in mutant animals. However, in mutant animals, the lumen of the tubules were often empty (D). This is clearly visible in high power (×40 magnification) images (C,E) of stage VII tubules. In JunD−/− mutants less late spermatids were visible and the luminal region was strikingly devoid of flagella and mature spermatozoa (E). (F,G) Quantification of different cell populations in tubules at stage VII (F) or stage X (G) of spermatogenesis. The cell numbers per high power field (×40 magnification) were determined for spermatogonia (goni), spermatocytes (cyte), early spermatids, late spermatids and Sertoli cells. Stage VII tubules showed a significant reduction in the number of late spermatids in JunD−/− mice (red bars), compared to fertile wild-type mice (black bars).
Although the JunD<sup>−/−</sup> phenotype is unlike the embryonic lethality of other jun gene knockouts (Hilberg et al., 1993; Johnson et al., 1993), it resembles features observed in some fos gene mutations (Baum et al., 1994; Brown et al., 1996; Gruda et al., 1996; Johnson et al., 1992; Paylor et al., 1994). All published studies of fos family genes disruption have led to viable mice with tissue-specific phenotypes. Disruption of the fosB gene caused defects in maternal nurturing behaviour (Brown et al., 1996). Mutation of the c-fos gene resulted in the bone remodelling disease osteopetrosis (Grigoriadis et al., 1994; Johnson et al., 1992). These c-Fos<sup>−/−</sup> mice also displayed variable defects in male reproduction, include reduced mating behaviour and a block in spermatogenesis (Baum et al., 1994; Johnson et al., 1992). These results are remarkably similar to our observations with JunD<sup>−/−</sup> mice. Male animals lacking JunD also have a reproductive defect that consists of both behavioural and spermatogenic elements, suggesting that these defects may reflect selective functions for JunD/c-Fos dimers. This is supported by the overlap of c-Fos and JunD expression patterns in postmeiotic cells (Alcivar et al., 1991; Schultz et al., 1995). Hence, JunD<sup>−/−</sup> mice display some features of the pleiotropic c-Fos<sup>−/−</sup> phenotypes and imply tissue-specific roles for JunD/c-Fos dimers in maintaining normal spermatogenesis and reproductive functions.

The block in spermatogenesis upon JunD disruption appears not to be a cell autonomous defect, as haploid sperm are transmitted to offspring at equivalent frequencies as wild-type sperm. Crosses between heterozygous JunD<sup>+/−</sup> males and wild-type females generated both JunD<sup>+/−</sup> and wild-type offspring with equal numbers (e.g. 53 heterozygotes: 52 wild-type) and crosses between heterozygous animals generated all three genotypes at predicted frequencies.

JunD can now be added to a growing number of genes that affect male fertility (Elliott and Cooke, 1997). Ordering these
genes on regulatory pathways during spermatogenesis presents a formidable goal for future studies. Genes whose mutation affects mouse fertility can be divided into several classes of phenotypes. These include phenotypes that are predominantly behavioural (e.g. SP4 (Supp et al., 1996)), those affecting spermatogenesis fertilization capacity (e.g. genes for sperm-1 or SP4 (Supp et al., 1996)), those affecting cell proliferation and maintaining adult spermatogenesis (Zhao et al., 1996), and those affecting motility and morphology of epididymal sperm in relation to puberty in mice. (Elliott and Cooke, 1997). Several features of the JunD sterility phenotype resemble aspects of human reproductive pathology suggesting that these animals may contribute to our understanding and treatment of human infertility.

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**REFERENCES**


Colucci-Guyon, E., Portier, M. M., Dunia, I., Paulin, D., Pournin, S. and others. (1997) and is important for the maintenance of female germine stem cells (Ting and Spradling, 1998).

Human infertility may affect as much as 2-7 % of the population and is often ascribed to idiopathic abnormalities in sperm numbers (azoospermia or oligospermia) and sperm motility. Very few genes associated with human azoospermia have been identified (Reijo et al., 1995) and the genetic basis for human male sterility remains unclear (Elliott and Cooke, 1997). Several features of the JunD sterility phenotype resemble aspects of human reproductive pathology suggesting that these animals may contribute to our understanding and treatment of human infertility.

**Fig. 8.** Analysis of gene expression in testes of sterile JunD+/− mice. The expression of genes involved in spermatogenesis was determined using an RT-PCR assay. Total RNA was isolated from the testes of two wild-type animals (+/+ ) and two sterile mutant animals (−/−). The expression levels of several genes were examined by PCR following treatment with reverse transcriptase (lanes 1-5, +RT). The expression of β-actin and HPRT were included as positive controls. Amplification of samples not treated with reverse transcriptase (lanes 6-10, −RT) or water alone (lanes 5 and 10) served as negative controls. The expression analysis includes the bacterial lacZ gene used for insertion into mutagenesis, and spermatogenesis-related genes protamine 1, protamine 2, Transition protein 1, Hox1.4, calsperrin, RT7 and BMP8.


