Chromosomal localization of the zinc finger protein 15, *Zfp15*, on Mouse Chromosome 4

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Species: Mouse
Locus name: Zinc finger protein 15
Locus symbol: *Zfp15*
Map position: *Zfp15* is localized on mouse Chromosome (Chr) 4: centromere–*D4Bir11*–7.4 ± 2.7–***Zfp15***–1.1 ± 1.1–*D4Mit4*–17.0 ± 3.9–*D4Bir16*–7.4 ± 2.7–(*D4Mit9, D4Bir20*)–4.3 ± 2.1–*D4Bir21*–10.6 ± 3.2–*D4Mit11*–5.4 ± 2.4–*D4Bir23*–3.2 ± 1.8–*D4Bir24*–8.5 ± 2.9–(*D4Mit13, Pnd, D4Bir25, D4Mit14*)–1.1 ± 1.1–*D4Mit42*–6.4 ± 2.5–(*Dvl, Rnr4*)–telomere.
Method of mapping: *Zfp15* was localized by haplotype analysis of 94 progeny from an interspecific backcross, (C57BL/6J × *M. spretus*)F_1 × C57BL/6J [1].
Molecular reagents used for mapping: The *Zfp15* probe was obtained by polymerase chain reaction amplification of a 552-bp fragment from mouse pituitary cDNA with primers designed on the basis of the rat *Zfp15* cDNA sequence [2]. The primers amplify 465 bp of coding sequence, outside of the conserved zinc finger regions, corresponding to the last 154 amino acids, and 87 bp of the 3′ untranslated region. The RT-PCR product was cloned into the pGEM4Z vector and sequenced to confirm its correspondence with the rat *Zfp15* cDNA.
Allele detection: A *Bgl*I polymorphism was detected in mouse genomic DNA with the *Zfp15* probe, resulting in an *M. spretus*-specific restriction fragment of 15 kb and a common restriction fragment of 24 kb. The mapping was confirmed with a *Bam*HI polymorphism, resulting in two *M. spretus*-specific restriction fragments of 8.9 and 6.6 kb and two common fragments of 18 and 5.5 kb.

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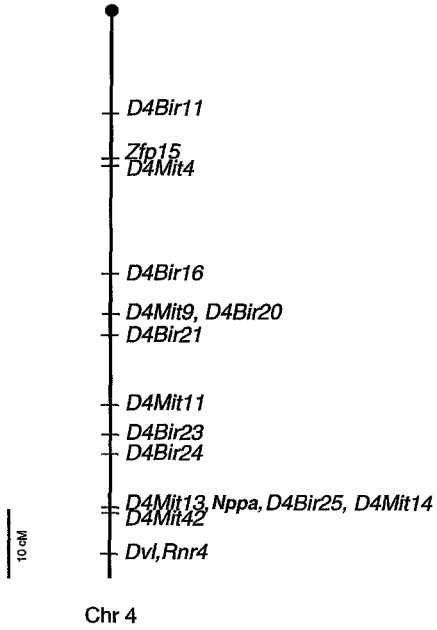

Fig. 1. *Zfp15* maps on mouse Chr 4 proximal to *D4Mit4*.

Discussion: Zfp15, formerly called Zn-15, is a transcription factor that binds to a highly conserved DNA-binding site within the GH promoter between the proximal and distal Pit-1 binding sites. Its unique DNA-binding domain consists of three $CysX_{2-4}CysX_{11-16}HisX_{3-6}His$ zinc fingers in the context of 15 highly conserved zinc fingers. It has been shown that Zfp15 acts synergistically with Pit-1 to activate the GH promoter. In contrast to Pit-1, Zfp15 shows no tissue specificity; it has been found in many tissues including pituitary, spleen, and heart [2]. There are no endocrine defects known in the region of Chr 4 where *Zfp15* is localized.

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Localization of sequences related to the human RAD6 DNA repair gene on mouse Chromosomes 11 and 13

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Species: Mouse
Locus name: Ubiquitin conjugation enzyme E2B-related sequences 1 and 2
Locus symbol: *Ube2b-rs1, Ube2b-rs2*
Map position: *Ube2b-rs1* is localized on mouse Chromosome (Chr) 13: centromere–*D13Bir2*–8.7 ± 2.9–*D13Bir4*–3.2 ± 1.8–*D13Mit4*–11.8 ± 3.3–*D13Bir12*–2.1 ± 1.5–*D13Mit10*–5.3 ± 2.3–*D13Bir13*–3.2 ± 1.8–*D13Bir14*–7.4 ± 2.7–*D13Mit8*–1.1 ± 1.1–*D13Mit9*–4.4 ± 2.1–*D13Bir18*–5.5 ± 2.4–*D13Bir19*–9.9 ± 3.1–(*D13Mit31,* ***Ube2b-rs1***)–1.1 ± 1.1–*Rnr13*–telomere. *Ube2b-rs2* is localized on mouse Chr 11: centromere–*Erbb*–12.3 ± 3.7–(*Adra1, Pad1*)–3.2 ± 1.8–(*Csfgm, Sparc*)–1.0 ± 1.0–(*Myhs, D11Mit5*)–2.0 ± 1.4–(*Rpo2-1, Asgr1*)–5.6 ± 2.4–*Tcf2*–3.9 ± 2.2–***Ube2b-rs2***–15.9 ± 4.0–*Erba*–5.4 ± 2.4–*Gh*–telomere.
Method of mapping: *Ube2b-rs1* was localized by haplotype analysis of 91 progeny from an interspecific backcross, (C57BL/6J × *M. spretus*)F_1 × C57BL/6J [1]. *Ube2b-rs2* was assigned by haplotype analysis of 96 progeny from an intraspecific backcross (DF/B-*dfldf* × CASA/Rk)F_1 × DF/B-*dfldf* [2].
Molecular reagents used for mapping: The mouse brain cDNA clone, MBL 12-900, is homologous to the human RAD6B gene (HHR6B). A 900-kb *Eco*RI fragment containing the complete open reading frame was used for mapping. This is referred to as the Hhr6b probe [3].
Allele detection: In mapping *Ube2b-rs1*, a *Bam*HI polymorphism was detected in mouse genomic DNA hybridized with the Hhr6b

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probe, resulting in an *M. spretus* specific restriction fragment of 3.3 kb, and common bands of 16.8, 11, and 2.8 kb. The mapping was confirmed with a *Hin*dIII polymorphism, resulting in an *M. spretus* specific restriction fragment of 2.1 kb and common bands of 21.3, 12.2, and 1.5 kb. In mapping *Ube2b-rs2,* an *Ssp*I polymorphism was detected in mouse genomic DNA hybridized with the Hhr6b probe, resulting in a CASA/Rk-specific band of 5.7 kb, DF/B-specific bands of 4.3 and 1.5 kb, and three common bands of 3.1, 1.9, and 1.6 kb. The mapping was confirmed with a *Bgl*I polymorphism resulting in a CASA/Rk-specific band of 14 kb, a DF/B-specific band of 9.5 kb, and three common bands of 16, 7.3, and 2.1 kb.

Discussion: The ubiquitin-conjugating enzyme encoded by the DNA repair gene RAD6 is involved in numerous cellular processes in *Saccharomyces cerevisiae,* such as sporulation, damage-induced mutagenesis, and post-replication repair [4]. The binding of a ubiquitin-activating enzyme (E1) activates ubiquitin and initiates the multi-step process. The activated molecule is then transferred to a ubiquitin-conjugating enzyme (E2), which ligates ubiquitin to its target protein, sometimes with the help of a ubiquitin protein ligase (E3). Once ubiquitination of a protein is accomplished, it is signaled for stabilization, (re)folding, or degradation. The human homologs of RAD6 are ubiquitin-conjugating enzyme E2B (UBE2B) and ubiquitin-conjugating enzyme E2A (UBE2A), also known as HHR6B and HHR6A. These human proteins are sufficiently conserved to permit functional substitution for the repair and mutagenesis pathways in yeast [5]. UBE2A has been previously mapped to human Xq24-25 and mouse Chr X [6]. UBE2B was localized on human Chr 5q23-31 [6], while the murine homolog, *Ube2b,* was assigned to the central portion of Chr 11 by fluorescence in situ hybridization (FISH) analysis with a cocktail of genomic clones [E.M.E. Smit and A. Hagemeijer, unpublished results]. Mapping data from two backcrosses show that two related genes of *Ube2B* exist in the mouse. *Ube2b-rs1* (related sequence 1) maps to a region of Chr 13 with homology to human Chr 5q and may represent the real gene. *Ube2b-rs2* (related sequence 2) maps to a region of Chr 11 with homology to human Chr 17 and most likely represents a pseudogene. Further studies will be required to resolve this issue.

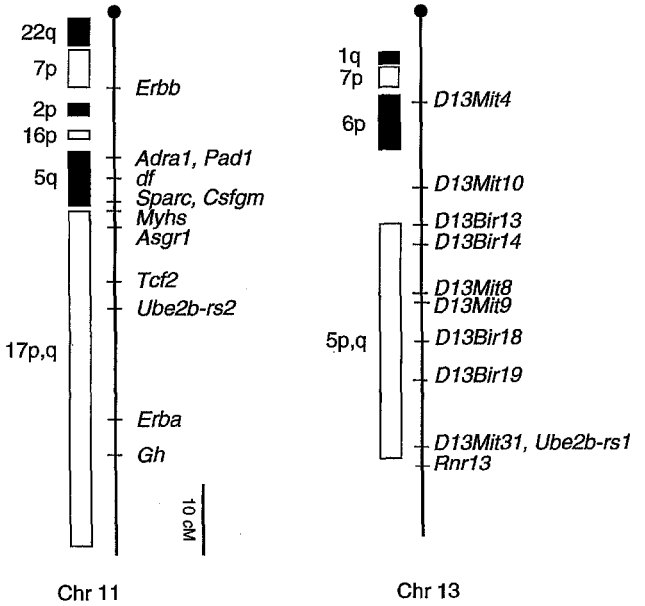

Fig. 1. *Ube2b-rs1* and *Ube2b-rs2* are localized to mouse Chrs 13 and 11 respectively. These represent two related sequences homologous to the yeast RAD6 gene. The mapping of *Ube2b-rs1* to mouse Chr 13 is in a region homologous to human Chr 5. This is consistent with the mapping of UBE2B to human Chr 5q. *Ube2b-rs2* maps to a region of mouse Chr 11 with homology to human Chr 17 and therefore most likely represents a pseudogene.

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Genetic mapping of the β-arrestin 1 and 2 genes on mouse Chromosomes 7 and 11 respectively

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Species: Mouse
Locus names: β-arrestin 1 and 2
Locus symbol: *Arrb1* and *Arrb2*
Map positions: centromere–*D7Was12*–5.3 ± 2.1 cM–*Arrb1*–2.6 ± 1.5 cM–*Calc*–telomere; and centromere–*Trp53*–2.6 ± 1.5 cM–*Arrb2/Nos2*–2.6 ± 1.5 cM–*Erba/Erbb2*–telomere (Fig. 1)
Method of mapping: (C3H/HeJ-*gld* × *Mus spretus*)F_1 × C3H/HeJ-*gld* interspecific backcross mice [1–3].
Database deposit information: MGD Accession numbers MGD-CREX-237 (*Arrb1*), MGD-CREX-238 (*Arrb2*). Genbank accession numbers M91589 (rat *Arrb1* cDNA) and M91590 (rat *Arrb2* cDNA).
Molecular reagents: *PCR products corresponding to nucleotides 333–1321 of a rat Arrb1* cDNA and nucleotides 425–1413 of a rat *Arrb2* cDNA [4].

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