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Identification of an X-linked member of the *Odc* gene family in the mouse

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The mouse ornithine decarboxylase gene is part of a dispersed family of at least 14 related loci (1,2). Eight *Odc* loci have been assigned to 7 different autosomes (3,4), although the actual structural locus has not been identified.

Recent mapping of the mouse genome has exploited the sequence diversity apparent between inbred strains and feral species, notably *Mus spretus* (5). This diversity, expressed as restriction fragment length polymorphism, together with the unique segregation pattern of X-linked loci, has facilitated assignment of molecular markers to the mouse X chromosome (6). Figure 1 shows how F_1 progeny from reciprocal crosses between C57BL/6JRos (B) and wild-derived *M. musculus* from Denmark (D) have been used to identify an X-linked member of the *Odc* gene family. This assignment demonstrates the power of the mapping technique, as a single X-linked band can be distinguished from multiple autosomal bands.

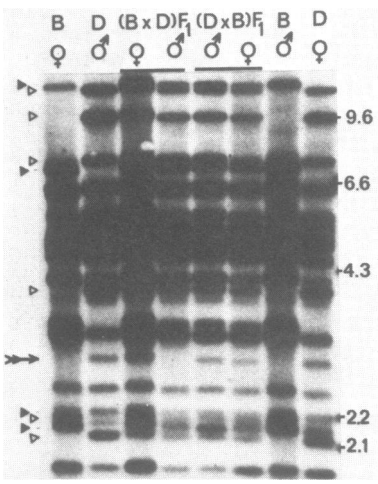

Figure 1. *Southern analysis of* BglII-*digested genomic parental and progeny DNAs hybridized to a cDNA for mouse ODC. Bands originating from the inbred (▶) or wild-derived parent (▷) are present in the progeny of both crosses, regardless of sex, except for a 2.7 kb band (⇾) missing from the BXD F_1 . This fragment specifically defines a locus on the D X chromosome, which is not inherited in the progeny of the D sire. The 7.0 kb B X-linked fragment, identified in a* M. spretus *cross (data not shown), is obscured by autosomal fragments.*

Although less divergent evolutionarily than *M. spretus*, the *M. musculus* stock remains a potent source of restriction variation. Unlike *M. spretus*, the use of *M. musculus* as the wild-derived parent allows for reciprocal F_1 crosses, so that unique X-linked fragments originating from either the wild or inbred genome may be discerned.

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