MAPPING THE FSH RECEPTOR AND LH RECEPTOR GENES IN SHEEP AND DEER

412

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Restriction fragment length polymorphisms (RFLPs) were identified in sheep and deer using ovine cDNA probes for the follicle-stimulating hormone receptor (FSHR) and the luteinizing hormone receptor (LHCGR). FSHR and LHCGR were closely linked in sheep and neither receptor was linked to the Booroola fecundity gene (*FecB*). The estimated genetic distance between the receptors in sheep was 0 cM and no recombinants were detected (18 observations). Both receptors were also closely linked in deer (4 recombinants from 122 observations) and the estimate of genetic distance was 3.3 cM. Linkage between the receptor genes and comparison of the genetic maps of both sheep and deer assigns FSHR to sheep chromosome 3. Sequence analysis showed that the mammalian LHCGRs and FSHRs are more similar to each other than to mammalian thyroid-stimulating hormone receptor (TSHR). Based on evidence from mammalian evolution, these data suggest that TSHR and the LHCGR/FSHR arose from a common ancestral gene by a process of chromosomal duplication. Subsequent duplication of the region containing the LH/FSH receptor and functional divergence could have given rise to the two gonadotrophin receptors present in mammals today.