Evaluation of hybrids between Pere David's deer (Elaphurus davidianus) and red deer (Cervus elaphus) as resource for genetic linkage mapping

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Male and female F1 hybrids between Pere David's deer and red deer are fertile and have been backcrossed to red deer to produce substantial numbers (n > 200) of 1/4 Pere David's deer progeny. To evaluate the potential of these interspecies hybrid pedigrees for genetic linkage mapping, we compared David's deer and red deer for protein and RFLP markers. Of the 45 protein loci examined, 19 showed a fixed difference between Pere David's deer (n = 5) and red deer (n = 5) while a further three loci were polymorphic in red deer but not in Pere David's deer. To date, 10 of the 12 ovine or bovine DNA probes examined in deer have identified restriction fragment length differences between red deer (n = 3) and Pere David's deer (n = 3) with between two and six of the 12 restriction enzymes used. Seven probes were polymorphic with one enzyme, MspI. The two probes not revealing polymorphism hybridised to cervine repeated sequences.

We conclude that Pere David's deer and red deer hybrids will be highly informative for genetic linkage mapping in deer and that they represent a unique resource for genetic studies within the ruminants.