Setting up a *Cervus* genotyping kit based on a automated fluorescent multiplex PCR for a rapid characterization of the genetic diversity in several deer populations.

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Microsatellite loci are highly conserved among related species (Kühn *et al*, 1996) such as cattle and sheep (Moore *et al*, 1992). Transfer of a large number of polymorphic microsatellites between families of the Artiodactyla order has been demonstrated several times (Engel *et al*, 1996; Kuhn *et al*, 1996, Slate *et al*, 1998 and Roed, 1998). Therefore such a multi-allelic system should be useful to study the genetic diversities of populations.
This study was developed on four different deer species (Rusa deer, Eld deer, Swamp deer and Vietnamian Sika deer). A set of 38 microsatellites derived from bovine and ovine origin were chosen matching two criteria, (i) known to amplify in other deer species (Red deer) and (ii) showing an interesting polymorphic level as described in different previous studies (Slate *et al*, 1998 and Talbot *et al*, 1996). From these 38 screened markers, 30 gave a product of amplification in the 4 deer species (78.9 %) of which 14 to 20 (40 to 60%) were polymorphic depending on the species. Using 12 microsatellites polymorphic in the 4 species, we set up a unique multiplexe PCR optimized for annealing temperature and reagent concentrations. The 12 primer sets were labelled with 3 different fluorochromes depending on the allelic range for each species. The automatic analysis was performed using a ABI 377 sequencer and the PE Genotyper software. This method for parentage testing or genotyping gave good and reproducible results for the 4 studied species as well as for several other tested deer species and subspecies. This tool could be considered as a first generation “Cervus” genotyping kit useful for a rapid characterization of the genetic diversity .