FORENSIC DNA TYPING IN MOOSE (ALCES ALCES) IN CANADA

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Moose are the largest members of the deer family in North America. This species is a highly prized big game mammal that has an important cultural and economic impact in many communities. This project involves the analysis of DNA from over 900 moose from across Canada. Moose samples were collected from the Yukon, Alberta, Quebec and New Brunswick. The moose DNA was interrogated using 12 microsatellite markers and one sex typing marker. These panels of markers were used in two multiplexed reactions. Multiplex one consists of: Rt5, BM203, Rt9, BM1225, BM4513 and Rt24. Multiplex two consists of: FCB193, Sika Amelogenin, Rt1, BM888, BL42, Rt30 and BM848. Analysis of the genotypes using Genepop, indicates that the markers used are in Hardy-Weinberg equilibrium, none of the loci are genetically linked and that there is a substantial amount of genetic structure in this species (Fst=0.1138). Further analysis with programs such as FSTAT and Structure support the finding that genetic structure exists in Canadian moose, especially between the Eastern and Western populations. Analysis also shows that these markers are appropriate for forensic use. These tests and databases have already been used in a forensic capacity to detect and prosecute individuals for illegal taking of moose. Casework examples of how DNA results were used to: 1) convict an individual of the illegal killing of a moose with a recreational vehicle and 2) convict an individual of illegal hunting of moose, will also be presented. Development and use of this technology improves the protection and management of this species in Canada.