Low variability on the Y chromosome of lynxes *(Lynx lynx)* in Europe

Testing the efficiency of Y chromosome markers for studies of male polymorphism and migration in the Eurasian lynx

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Summary

The Eurasian lynx *(Lynx lynx)* is a large carnivore that mostly lives in forest habitats. Following the last glaciation, the lynx had probably colonized most of the forested parts of Europe. From the 18th to the 20th century, lynx populations in Europe experienced a dramatic, mostly hunting-induced, decline. In Central Europe, lynx populations probably went completely extinct, whereas refugia in Fennoscandia and in the Carpathian mountains remained. Following legal protection, the Northern European lynx population is currently expanding. In Central Europe, reintroduction programmes in e.g. Switzerland and the French Vosgues mountains have led to the recolonization of several countries around the Alps.

The Eurasian lynx is a species of high conservation interest. Gaining more knowledge about effective population size and inbreeding in the Scandinavian lynx population is an important conservation goal. One major management issue is whether gene flow from the large and more variable populations in Eastern Europe via Finland into Scandinavia exists.

Previous genetic studies have shown that gene flow between Scandinavia and Finland is low or non-existing, but the task has not been completely solved. It is known that male lynx migrate further than females and genetic studies using the Y chromosome have proved to contribute interesting information about a species' male population history and migration patterns. Yet, such studies are comparatively new and only few examples of other species than humans exist.

In this study, seven regions on the lynx Y chromosome were screened for polymorphism - in total 2324 basepairs (bp), 1810 bp (78%) in introns, the rest within the *SRY* gene and other exon regions. A combined approach of sequencing and screening for single stranded conformation polymorphism (SSCP) was used. 105 (male) lynx samples from Norway, Sweden, Finland, Latvia, Estonia, Switzerland and France were analysed.

The analyses suggest that all individuals had identical Y chromosome haplotypes. I present two complementary explanations for this: one can be overall low genetic variability of the Eurasian lynx. The other explanation comprises several molecular mechanisms with the general effect that the Y chromosome, as a non-recombining element with low effective population size, exhibits only little variation between closely related populations.

As one of the first population genetic studies using Y chromosome markers in a non-human species, this investigation reveals that it can be very difficult to detect any Y-linked variation – even if well over 2000 bp in individuals from a relatively large geographic area are screened. The study does not allow inferences about recent male migration, but it shows that Y chromosome studies may not be as easily applicable for conservation genetic analyses as previously assumed.

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