

CONSERVATION STATUS OF THE FINNISH GREY PARTRIDGE (*Perdix perdix lucida*)

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ABSTRACT

UIMANIEMI, L., LUMME, J., PUTAALA, A. and HISSA, R.: CONSERVATION STATUS OF THE FINNISH GREY PARTRIDGE (*Perdix perdix lucida*). The conservation status of Finnish Grey partridge population was studied by sequencing 377 nucleotides of mitochondrial (mt) control region I. European Grey partridge has distinct maternal lineages in Finland and France. Individuals from Finnish natural populations represent subspecies *Perdix perdix lucida* and French population subspecies *Perdix perdix perdix*. High divergence between these subspecies indicates separation already during Middle pleistocene. Within Finnish populations no genetic variation was found. The genetic structure of captive partridges from Finland and Sweden was compared to that of natural populations in Finland. Finnish captive stock contains "French" lineage among individuals used for restocking. The "French" mtDNA has not been detected among "wild" birds in Finland. The genetic constitution may have been deteriorated because of mixing with the Swedish and even the French stocks. As an implication for conservation we conclude that the farm stocks of grey partridge used for restocking and supplementary breeding should always be founded from local populations. Then possible released individuals represent population typical to each region.

1. INTRODUCTION

The European Grey partridge (*Perdix perdix*) is a bird of open arable lands. It reaches its northernmost limit at Tyrnävä, Finland. Originally the Grey partridge has arrived to Finland from Carelian Isthmus, Southeast Finland, in the beginning of 1800 century (MERIKALLIO, 1958). At the same time there has been also introductions of the Grey partridge to Finland. As introduction sources literature mentions Sweden and also some Middle European countries. The species has decreased in numbers in its whole distribution area during last decades. In Finland the number of the Grey partridge has decreased from 15000 pairs to 3000-5000 breeding pairs. Once continuous distribution area of the species is more fragmented nowadays.

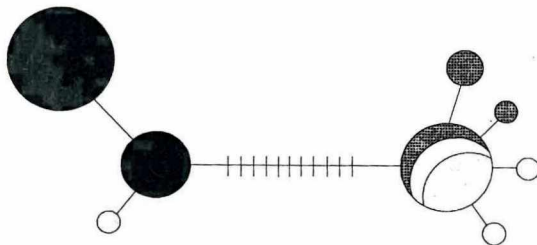
The main reason for the declining of the species is changes in agriculture. Due to modern type of harvesting and the use of herbicides there are not enough suitable habitats and food for the species. Despite declining of the species the Grey partridge is still a hunted species in most of its distribution area.

The aim of this study was to evaluate the conservation status of the Finnish grey partridge population by sequencing 377 nucleotides of mitochondrial (mt) control region I. High mutation rate on mtDNA lineages and haploid mode of inheritance make mtDNA an excellent tool for constructing phylogenies and time scales relating molecular lineages even below species level. Because of its mode of inheritance, mtDNA is sensitive to bottlenecks in population size and to population subdivision (WILSON *ET AL.*, 1985).

2. MATERIAL AND METHODS

We studied three wild populations from Finland: Tyrnävä, Kauhava and Jokioinen. There were five samples from each population. Also five samples from Finnish captive stock were studied. From Sweden we got egg samples from captive stock. From France we got 11 liver samples from shot wild birds (**Figure 1**).

For analyses we used blood, liver and egg samples. From tissue samples we extracted total DNA and from eggs mtDNA. No sign of nuclear copies were found. We amplified 377 nucleotides of mitochondrial control region I with PCR. Sequencing was done with both radioactive and automated sequencing method. Sequences were aligned and analysed.



- Tyrnävä, Finland, wild birds
- Jokioinen, Kauhava, Southern Finland, wild birds
- Oulu, Finland, captive birds
- France, wild birds
- Tranås, Sweden, captive birds

Figure 1: The sampling locations of the European Grey Partridge (*Perdix perdix*)

3. RESULTS AND CONCLUSIONS

Sequencing 377 nucleotides of mitochondrial control region I of the European grey partridge from Finland and France reveals distinct maternal lineages in the species. Individuals from Finnish natural populations represent subspecies *Perdix perdix lucida* and French population subspecies *Perdix perdix perdix*. These two subspecies diverge from each other by 12 point mutations, mainly transitions. This divergence is high within a species ($d = 0.031$) indicating separation during Middle Pleistocene. Already in Finland the northern and southern populations have drifted. Within Finnish populations no genetic variation was found. The genetic structure of captive partridges from Finland and Sweden was compared to that of natural populations. Sequencing of captive farm individuals reveals that both lineages exist among individuals used for restocking, both in Sweden and in Finland. Even if the supplementary stocking has continued quite long, the "French" mtDNA has not been detected among "wild" birds in Finland.

SIIVONEN (1957) suspected that introductions with wrong material may have been deteriorated genetic constitution of original Finnish Grey partridge population already in 1957. This study provides excellent conservation genetic lessons from supportive introductions.

Based on these preliminary results we present following conservation genetic conclusions (**Figure 2.**):

1. Finnish partridge population represents the *Perdix perdix lucida*, which differs by 12 point mutations from the western European *Perdix perdix perdix*.
2. Supportive breeding has been made by wrong material, i.e., by Swedish stocks representing the western subspecies *Perdix perdix perdix*.
3. The genetic constitution of Finnish grey partridges may have been deteriorated because of mixing with the Swedish and even French *Perdix perdix perdix* stocks.
4. Restocking programs should be stopped immediately. Restocking could be continued only by proper bird material, but it has been demonstrated that birds do it better themselves.



Figure 2. The minimum spanning network of the Grey Partridge. Each tick mark represents one point mutation. Each population has been marked with the particular shading and the size of the circle describes number of the individuals included to the circle. There are two distinct main lineages in this network.

REFERENCES

- SIIVONEN, L. (1957): Peltopyy – ja rusakkokantojen vaihteluista ja niiden perussyistä sekä katojen torjumisesta. *Suomen Riista* **11**: 7-28.
- MERIKALLIO, E. (1958): Finnish birds. Their distribution and numbers. *Soc. Pro Fauna Fenn., Fauna Fennica* **5**: 53 - 54.
- WILSON, A.C., CANN, R.L., CARR, S.M., GEORGE, M., GYLLENSTEN, U.B., HELM-BYCHOVSKI, K.M., HIGUCHI, R.G., PALUMBI, S.R., PRAGER, E.M., SAGE, R.D. and STONEKING, M. (1985): Mitochondrial DNA and two perspectives on evolutionary genetics. *Journ. Biol. Linn. Soc.* **26**: 375-400.