Testing the presence of a barrier to nuclear gene flow between two distant mitochondrial lineages of the bank vole (Myodes glareolus) in central finland

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TESTING THE PRESENCE OF A BARRIER TO NUCLEAR GENE FLOW BETWEEN TWO DISTANT MITOCHONDRIAL LINEAGES OF THE BANK VOLE (*MYODES GLAREOLUS*) IN CENTRAL FINLAND

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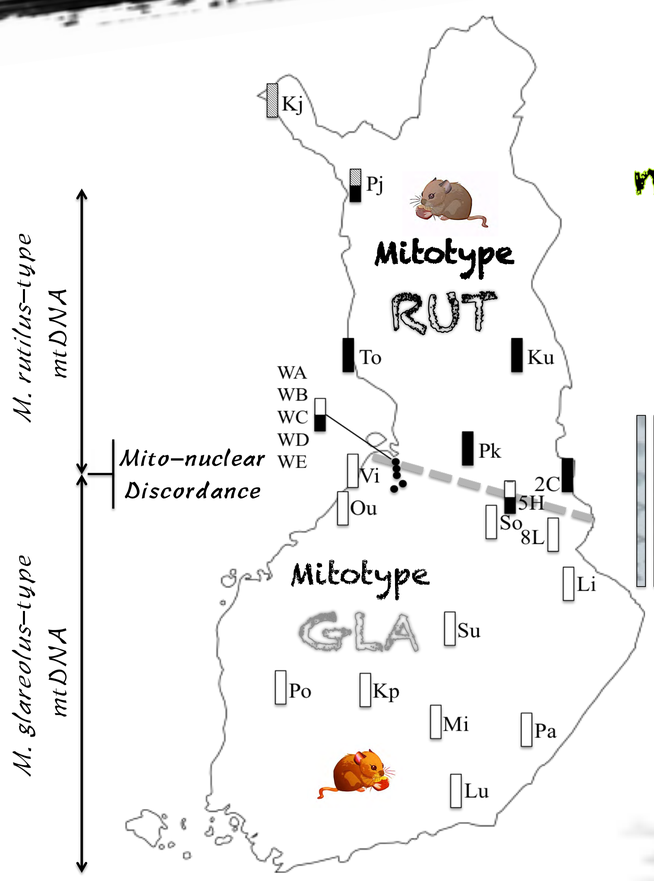
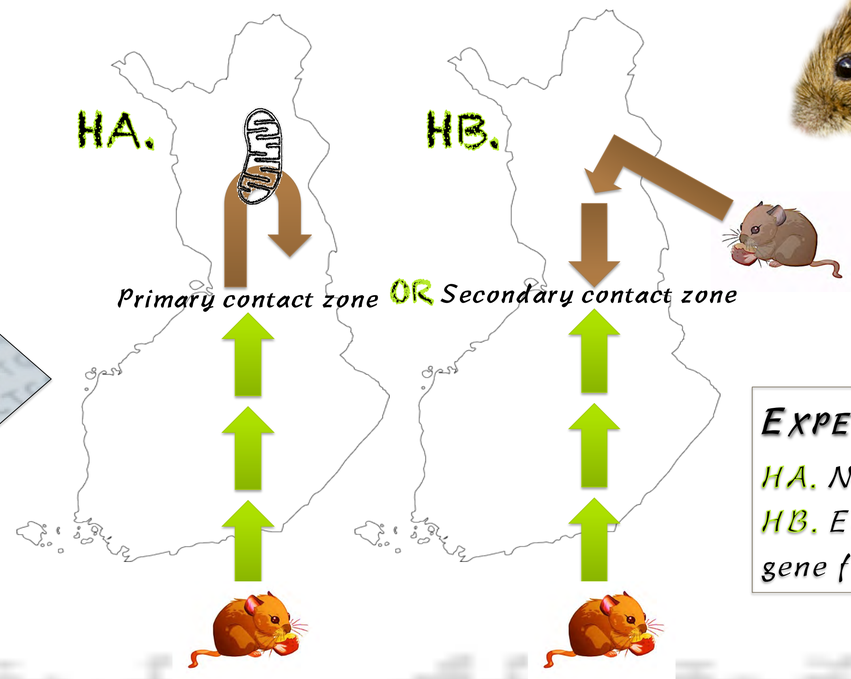
STATE OF THE ART



Bank vole mitotypes: Origin & dispersal along Finland ?

442 specimens of *M. glareolus*
17 microsatellite loci
Cytochrome *b* gene sequences

TWO HYPOTHESES ABOUT FINLAND COLONISATION



Bank vole, *Myodes glareolus*

EXPECTATIONS

HA. No barrier to nuclear gene flow
HB. Evidence of a barrier to nuclear gene flow

A. ***'One colonisation event hypothesis'*** A population carrying the mitotype GLA colonised Finland. Later, mitochondrial introgression events occurred with *M. rutilus* leading to the introgressed mitotype RUT.

B. ***'Two colonisation events hypothesis'*** The contact zone was formed by secondary contact after a period of geographic isolation. GLA and RUT populations colonised Finland independently, and the introgression occurred before the colonisation of Finland. We expected to observe two mitochondrial lineages in any cases but two nuclear populations only under the hypothesis B.

RESULTS

Nuclear population structure

① ***Genotypic differentiation between sites:***

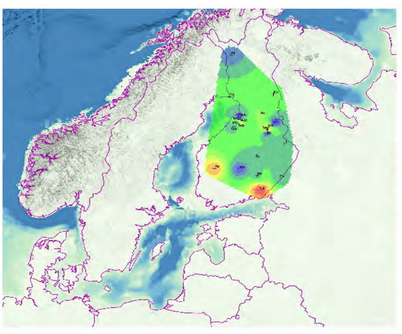
☑HB

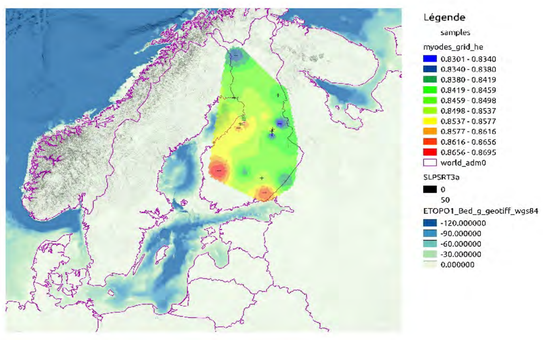
- Sites from distinct mitotypes are more differentiated than sites within each mitotype
- Sites from larger distance are also more differentiated

② ***Projection of indices of allelic richness (A) & estimated heterozygosities (He) along Finland:***

☑HA

- Highest genetic diversity in the South
- Genetic diversity lower northward
- ➢ But no relationships with geographical distances



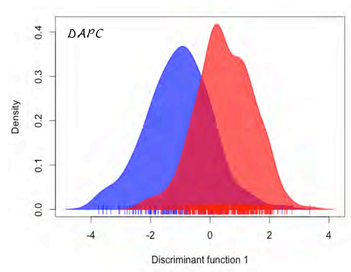


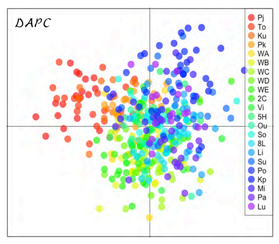
Estimating nuclear clusters among Finnish bank voles

① ***PCA & DAPC:***

☑HA

- No genetic differentiation
- ➢ Only a slight differentiation along the latitudinal axis

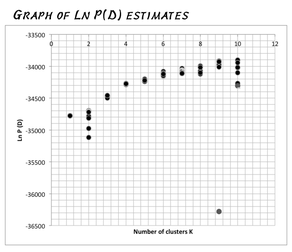


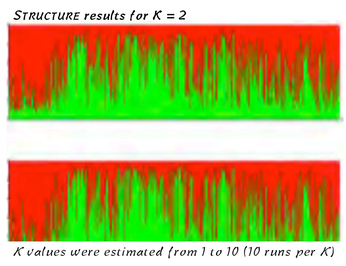


② ***STRUCTURE:***

☑HA

- No distinct genetic clusters
- ➢ Only a very slight signal distinguished the Northern sites from the rest



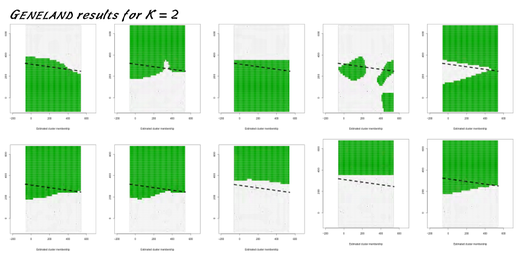


K values were estimated from 1 to 10 (10 runs per K)

③ ***GENELAND:***

☑HB

- Different spatial positions of clusters in all run
- ➢ Genetic discontinuity between GLA and RUT almost in all runs



④ ***Isolation By Distance analyses:***

☑HB

- Highly significant patterns
- ➢ The genetic differentiation (F_{ST}) is correlated with the geographic distances, which means that the more geographically distant specimens will be from each other, the more genetically differentiated.
- ➢ These IBD patterns suggest the occurrence of a slight barrier to nuclear gene flow

IN PROGRESS

The next step of this study is to apply methods that **investigate changes in neutral genetic clines to detect break in allelic frequencies** and finally, identify which hypothesis best explains the evolutionary history of Finnish bank voles.

CONCLUSION

Difficult to identify which hypotheses best explained the origin and dispersal of Finnish bank vole mitotypes because results support both hypotheses

HA. No distinct genetic clusters — OR — HB. Slight barrier to nuclear gene flow

Anyway, if there is a barrier, it is very weak compared to the abrupt changes in mtDNA.