

The genomic consequences of 10,000 generations of isolation of Orkney voles

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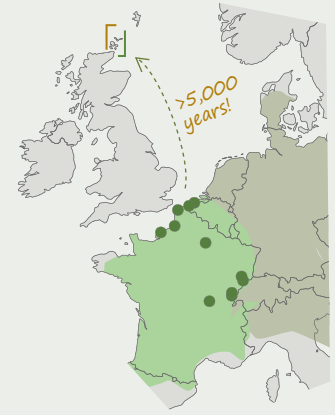
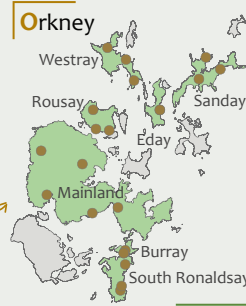


Common vole *Microtus arvalis*

Habitat: open meadows; farmland
Distribution: widespread in Europe

- Distinct genetic lineages in European continent
- Orkney closest to Belgium/Northern France coast, in Western lineage¹
- Orkney voles introduced by Neolithic farmers as food² Went through strong **bottleneck** and recovered **Isolated** for >5,000 years since introduction
- Genome resequencing of 22 Orkney voles + 11 continent + 3 *Microtus obscurus* as outgroup

Voles are abundant and big up there

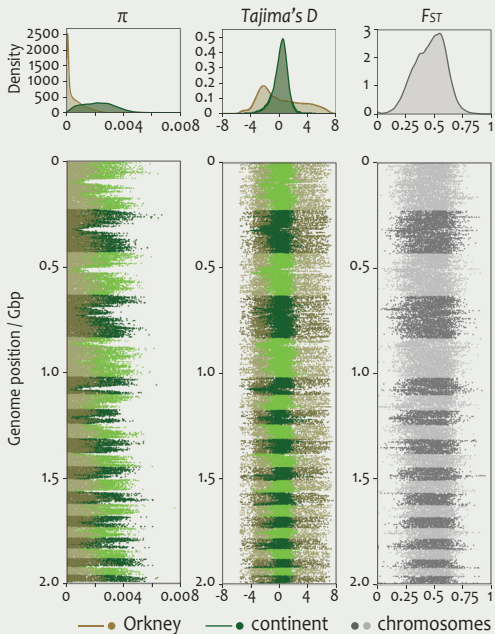


In Short

The **genome** of Orkney voles is dominated by **genetic drift** after bottleneck and isolation. They live well despite **fixed deleterious alleles** and genome-wide **relaxed selection**.

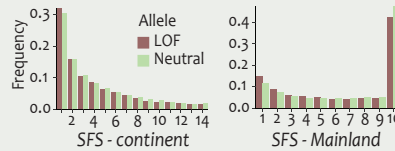
Genetic Drift

Extreme Genomic Landscape



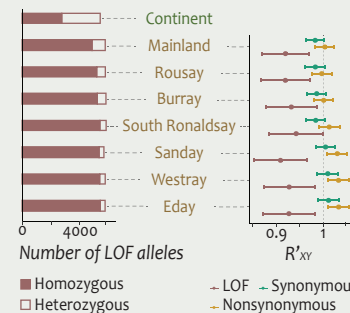
- $\pi \rightarrow 0$ • Reduced genetic diversity
- $Tajima's D \leftarrow 0 \rightarrow$ • Signatures of both population contraction **AND** expansion
- $F_{ST} \rightarrow 1$ • Highly divergent from the source lineage, median = 0.47

Mutation Load



*Functional impact of SNPs annotated with SnpEff³

- High fixation rate of loss-of-function (LOF) alleles in Orkney



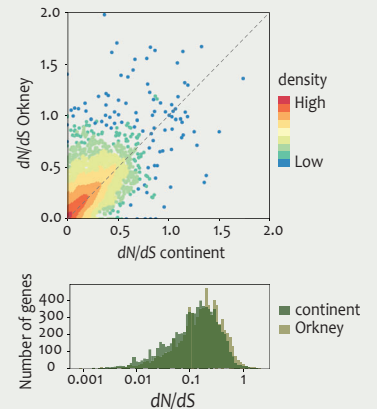
*Standard error of R'_{xy} from jackknifing of 100 blocks

- >80% LOF alleles homozygous in Orkney
- Limited purging of LOF alleles ($R'_{xy} < 1$)

BUT
no sign of fitness loss observed

How do they still live so well?

Relaxed Selection



*dN/dS calculated with KaKs_Calculator⁴

- dN/dS ratios increased for 21%
- Widespread relaxed selection

Signals of hard sweep on genes:

*Window based, XP-EHH⁵ and other parameters, outliers detected with DBSCAN⁶

- Orkney
 - immune response
 - high density kept by humans
- continent
 - lipid and hormone metabolism
 - selection for small body size

Relaxed positive selection made the Orkney voles big?

1. Martinková, et al. *Molecular Ecology* 2013
2. Romaniuk, et al. *Royal Society open science* 2016
3. Cingolani, et al. *Fly* 2012
4. Wang, et al. *Genomics, Proteomics & Bioinformatics* 2010
5. Simonson, et al. *Science* 2010
6. Schubert, et al. *Acm Transactions on Database Systems* 2017