

Local Adaptation in Europe

Alan R. Rogers

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In this lecture, we focus on loci for which population differences are large.

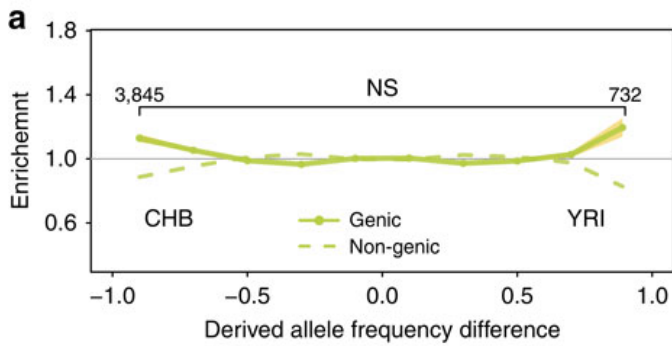
How did these differences evolve?

Based on Key et al (2016) doi:10.1038/ncomms10775

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Divergent loci are enriched with genes

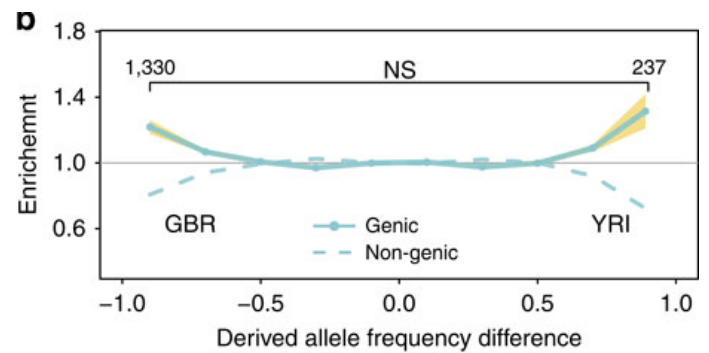


Left and right extremes: loci at which China and Africa have very different allele frequencies.

These are *more* likely to be genic, *less* likely to be non-genic.

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Divergent loci are enriched with genes



Also true in comparison between Great Britain and Africa.

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Why?

Two hypotheses

- ▶ Selection for locally-advantageous alleles underlies the most extreme population differences.
- ▶ Background selection (Charlesworth 1994)

Background selection: harmful mutations

Harmful mutations arise in genes, survive for awhile, then die out.

In a given chunk of chromosome, some haplotypes are doomed.

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Background selection: the lucky subset

The future belongs to haplotypes that are free of deleterious mutations.
 This lucky subset is smaller than the population as a whole.
 The smaller the lucky subset, the greater the effect of genetic drift.

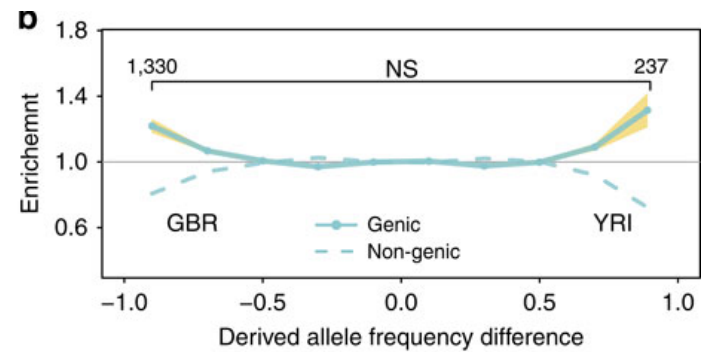
Background selection: genic versus non-genic regions

In non-genic regions, harmful mutations seldom arise.
 The lucky subset is the entire population.
 Genetic drift is stronger in genic than in non-genic regions.

Background selection: population differences

Genetic drift is stronger in genic than in non-genic regions.
 Drift increases differences between populations.
 Populations should differ more in genic than in non-genic regions, even without local adaptation.
 This might explain why divergent loci are enriched with genic DNA (Coop et al 2009).

This pattern is consistent with both hypotheses



Local adaptation, or background selection? We need to look at ancient DNA.



Ust'-Ishim: a 45-ky-old modern man from W Siberia

Lived just after the out-of-Africa bottleneck.

If the Europe-Africa differences arose by drift, Ust'-Ishim's DNA should look European.

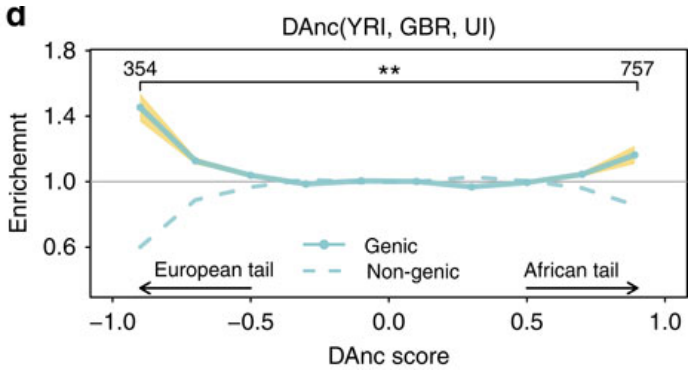
If local selection, Ust'-Ishim should look African.

Key et al (2016) developed a statistic, D_{Anc}, which compares European and African allele frequencies to that of Ust'-Ishim.

D_{Anc} = -1 ⇒ big difference between populations, and Ust'-Ishim looks African.

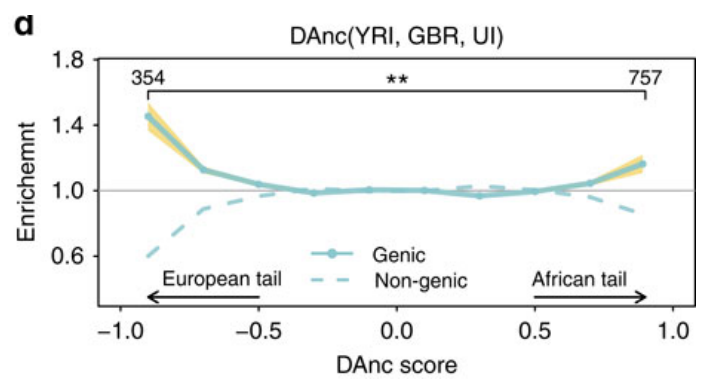
D_{Anc} = +1 ⇒ big difference between populations, and Ust'-Ishim looks European.

Case for local adaptation



Ust'-Ishim looks African at left but European at right.
 Left side: evolutionary changes happened since 45 kya, and *after* the bottleneck.

Case for local adaptation



Recent evolutionary changes in Europe enriched for genic regions.
 Probably not drift, because population was large. Must be local adaptation.

Further evidence

- ▶ The European (but not the African) tail is enriched with sites that are strongly conserved in other organisms.
- ▶ Also enriched with regulatory sites.

This is as expected if European (but not African) population was adapting to a new environment.

Not consistent with background selection.

Where did these local adaptations arise?

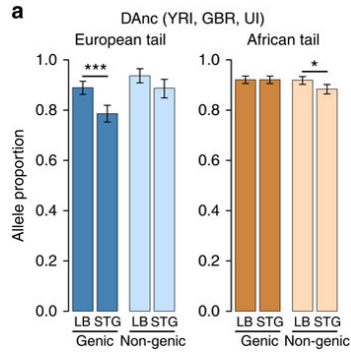
Europe is a palimpsest of three populations:

1. Mesolithic foragers
2. Neolithic farmers from the Middle East
3. Indo-European pastoralists from Russia

How did these populations contribute to adaptive evolution in Europe?

Comparison with two ancient genomes

- ▶ Loschbour: an 8 ky-old Mesolithic forager.
- ▶ Stuttgart: a 7 ky-old Neolithic farmer.



Where did these adaptive alleles come from?

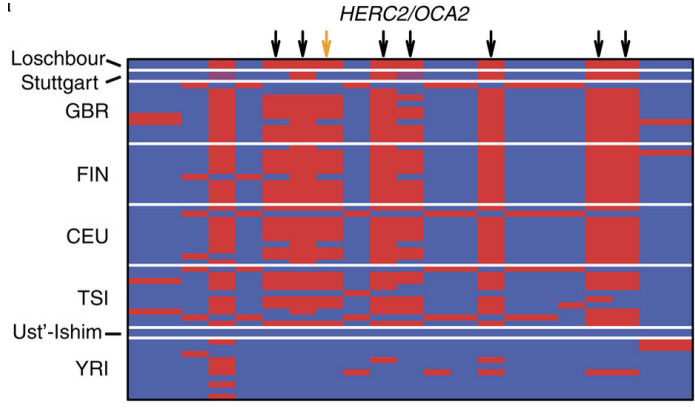
Mesolithic foragers (LB) contributed more to the European tail than did Neolithic farmers (STG).

No difference in African tail.

No difference in non-genic regions.

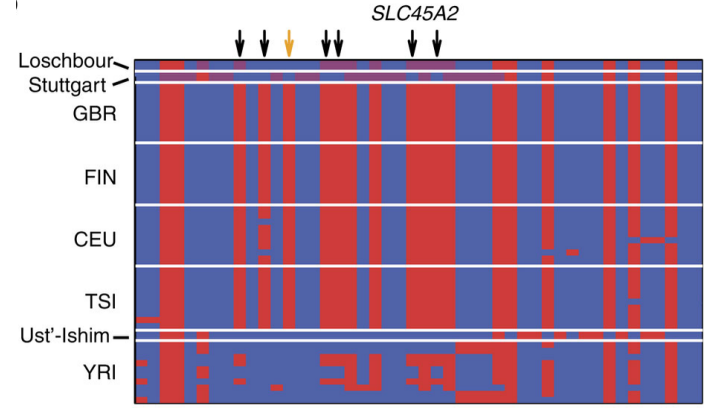
Many European adaptations originated in Mesolithic foragers.

HERC2: blue eyes



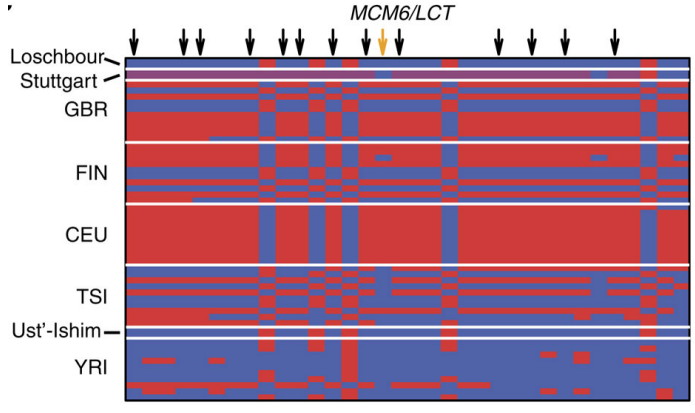
Modern allele similar to Loschbour ⇒ arose on Mesolithic chromosome.

SLC45a2: pale skin



Modern allele similar to Loschbour ⇒ arose on Mesolithic chromosome.

LCT: lactase persistence



Modern allele similar to Stuttgart farmer ⇒ arose on Neolithic chromosome.

Summary

- ▶ Loci that differ greatly between continents are often in or near genes.
- ▶ In Europe, these genic differences arose within past 45 kya, probably by adaptation to local environments.
- ▶ Mesolithic foragers contributed many adaptive alleles to the modern European population, even though they contributed only a minority of neutral DNA.