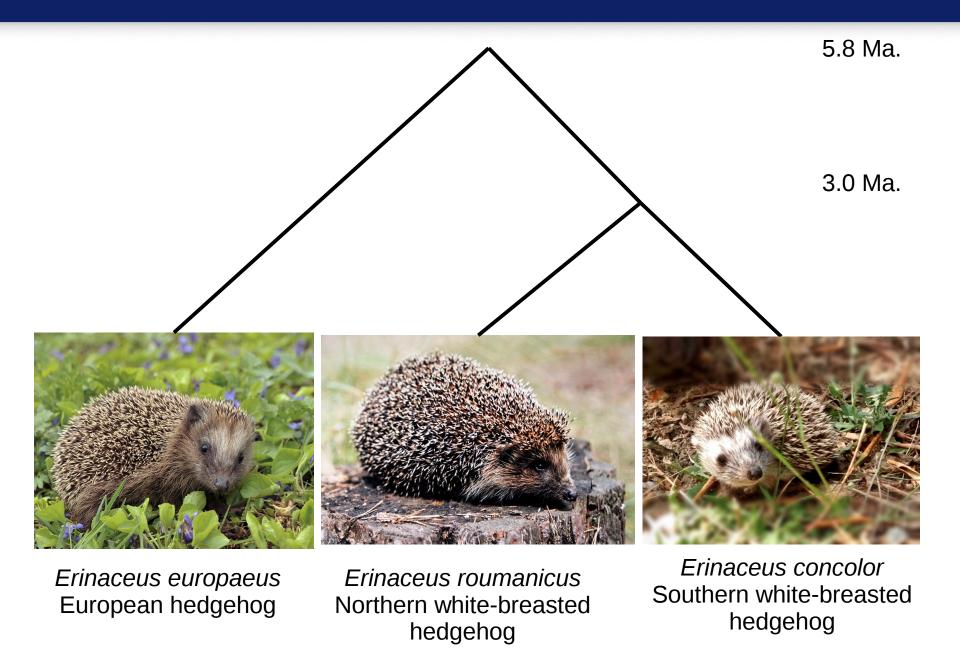
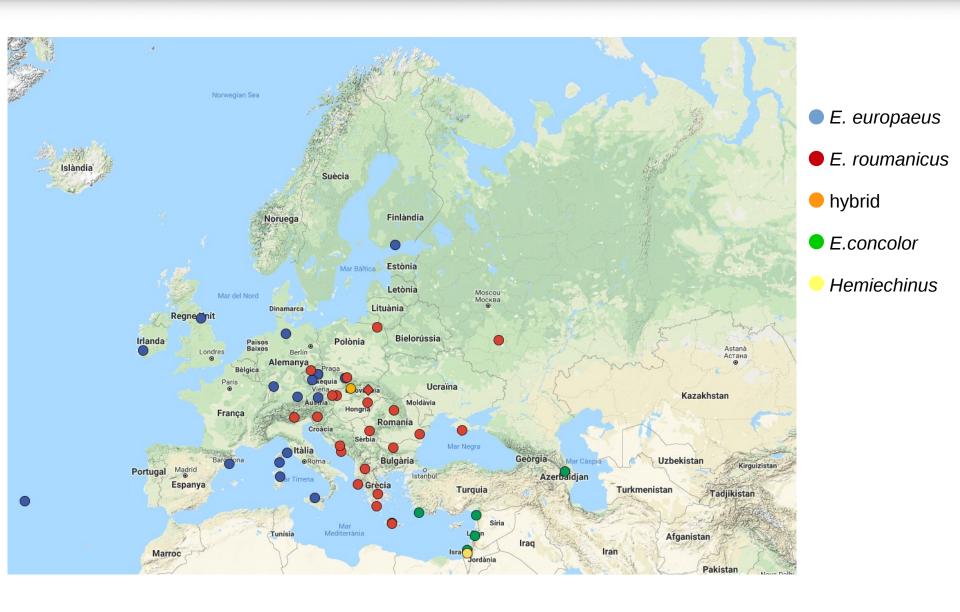


Secondary contact of hedgehogs in central Europe

Kristýna Eliášová, J. Ignacio Lucas Lledó*, Pavel Hulva, Barbora Černá Bolfíková

* e3 (Population genomics)





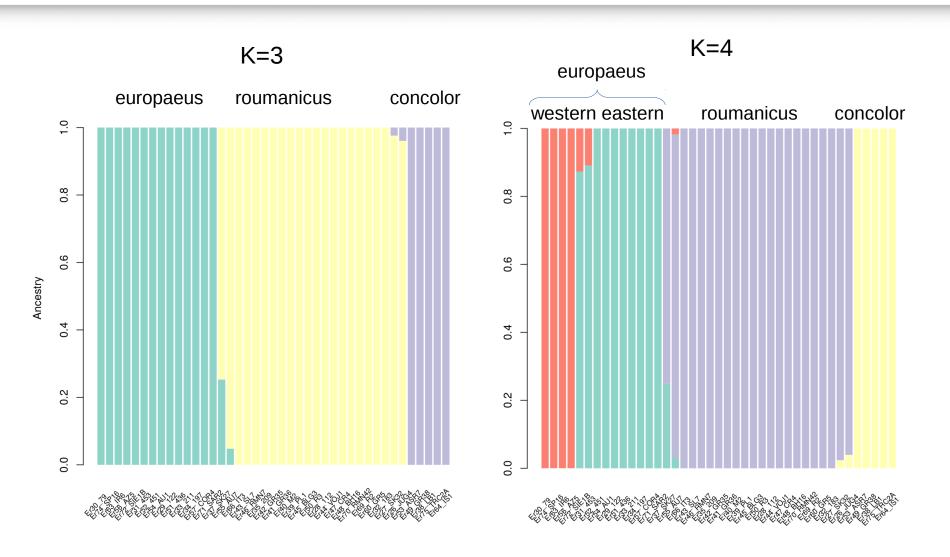
Goals

- Check classic model of post-glacial colonization.
- Quantify hybridization.
- Does natural selection determine the fate of introgressed variation?

Methods

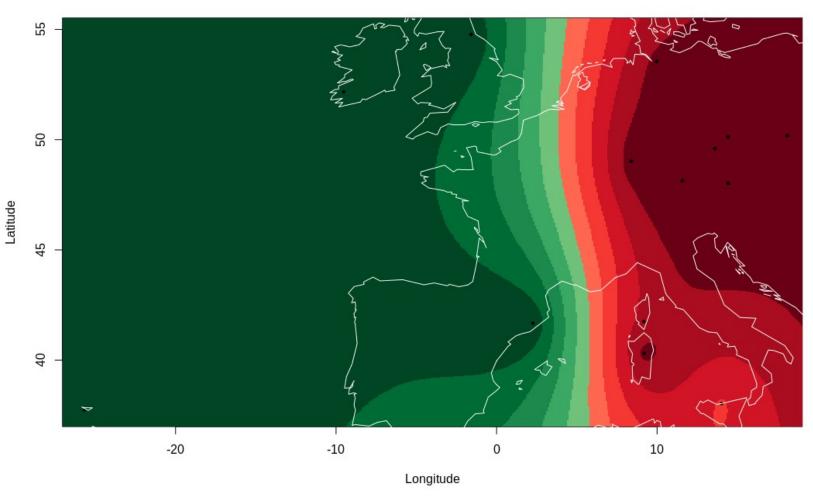
- Restriction-Associated DNA (RAD) sequencing
 - ~100,000 SNPs in 16 eur., 25 rou., 5 con., 1
 Hem.
- Model-based ancestry estimation (Admixture).
- Geographically informed ancestry estimation (TESS3).
- Inference of local blocks of admixture (LAMP).
- Test of historical introgression (ABBA/BABA test).

Results. Admixture.

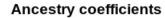


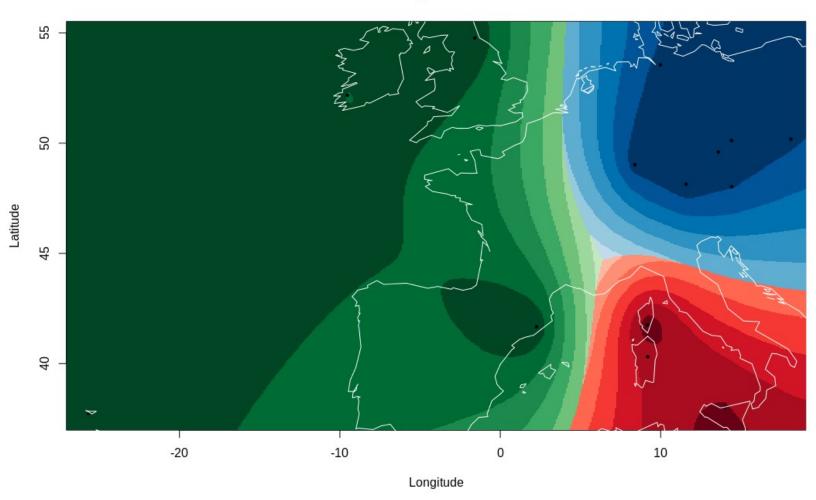
Results. TESS3. *E. europaeus*, K=2.



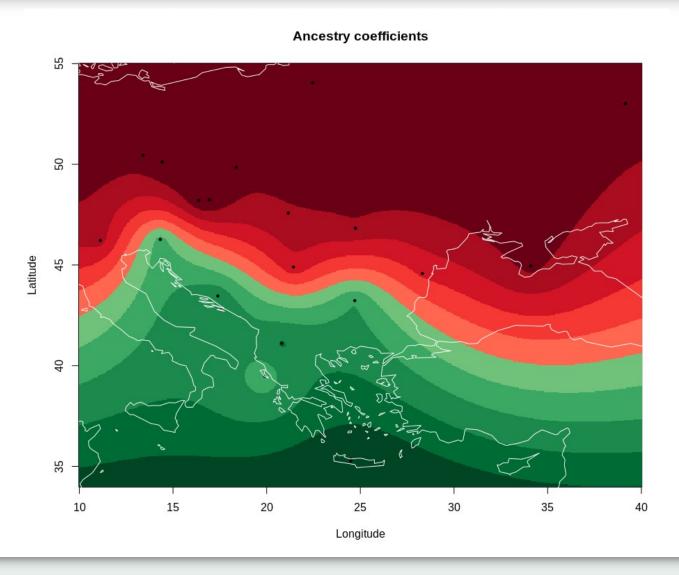


Results. TESS3. *E. europaeus*, K=3.

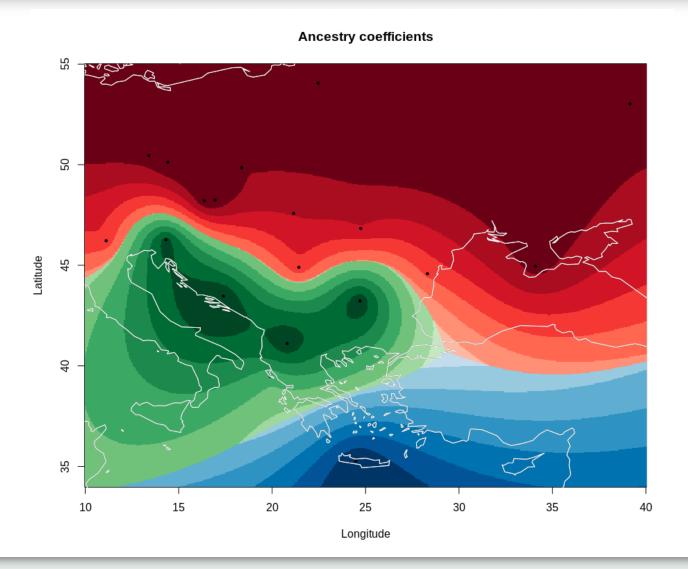




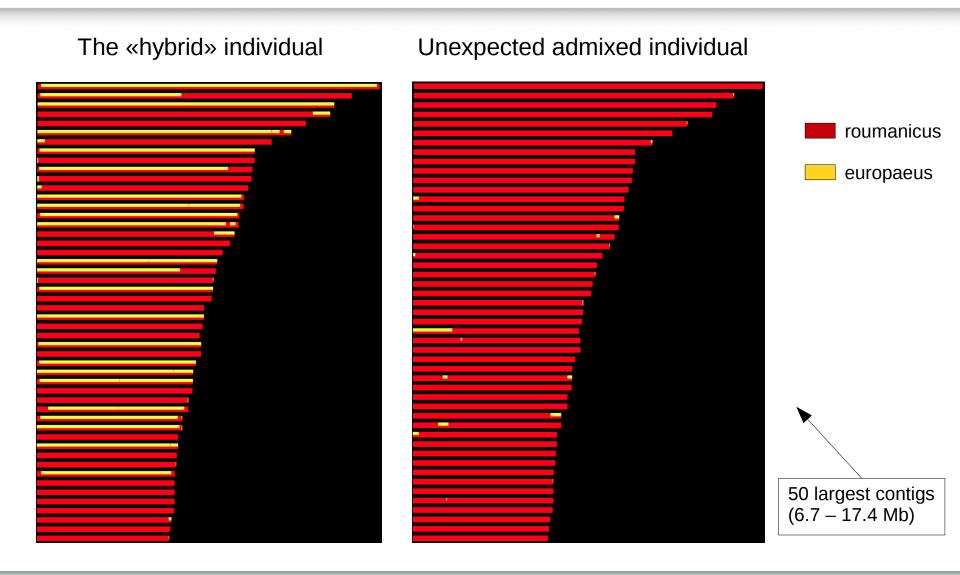
Results. TESS3. *E. roumanicus*, K=2.



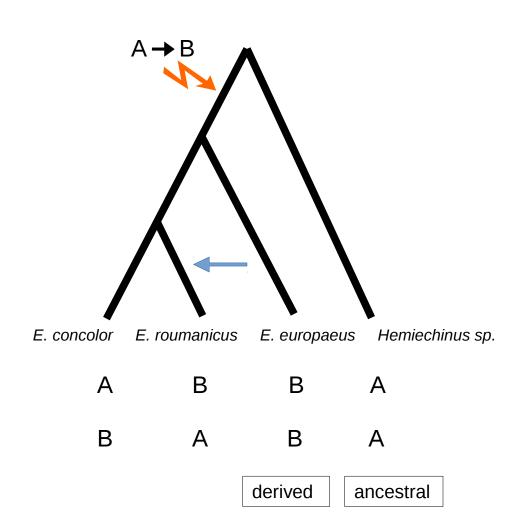
Results. TESS3. *E. roumanicus*, K=3.



Results. Genomic blocks of ancestry (LAMP).



Results. ABBA/BABA or D-test of introgression.

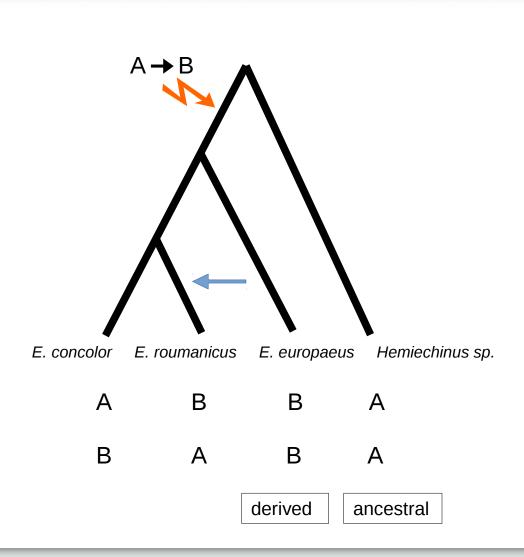


In the absence of introgression between *E. europaeus* and *E. roumanicus*, incomplete lineage sorting would produce a similar number of sites with the ABBA and the BABA patterns.

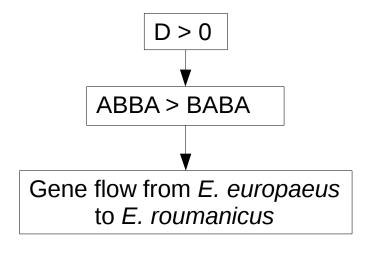
D-test compares the frequency of both patterns.

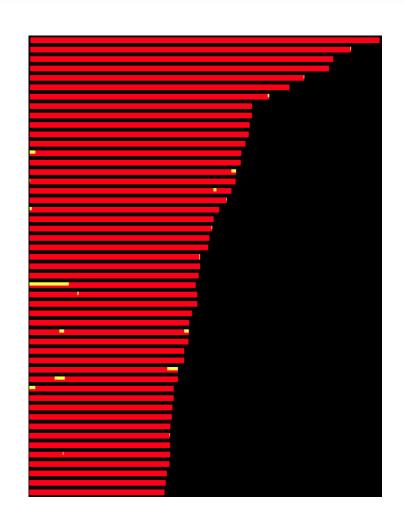
f statistics quantify the portion of the genome affected by introgression.

Results. ABBA/BABA or D-test of introgression.



D (±S.E.) p-value Num. sites	0.154 (±0.018) 3.1E-18 99365
f f HOM f	0.0432 0.0395 0.0234





Introgressed variants may be neutral, deleterious or beneficial.

If they are neutral, they must be lost randomly.

If natural selection governs the fate of introgressed variation, independent signals of introgression should be associated in the genome.

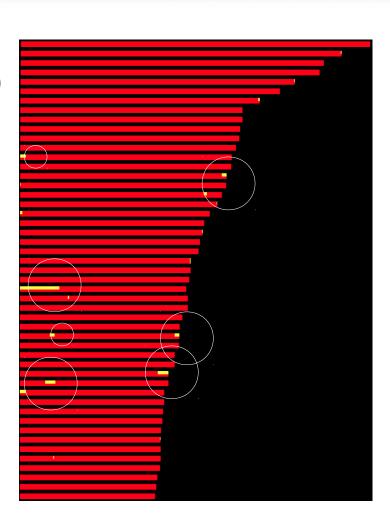
admixed blocks

$$D = 0.372 (\pm 0.138)$$

p-value = 0.0072

$$f = 0.104$$

 $f_{HOM} = 0.106$
 $f = 0.059$



E. roumanicus background

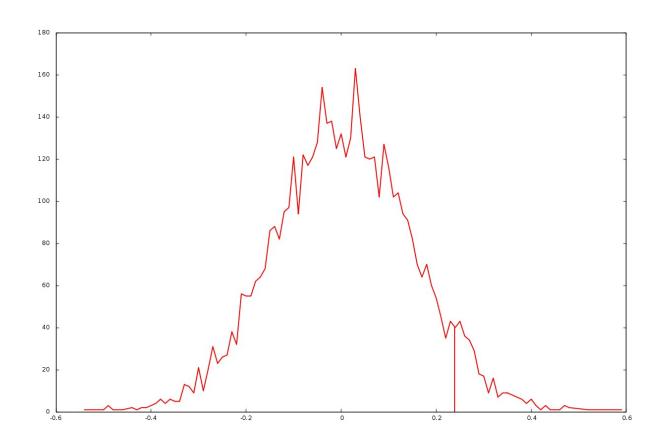
$$D = 0.133 (\pm 0.020)$$

p-value = 1.25E-11

$$f = 0.037$$

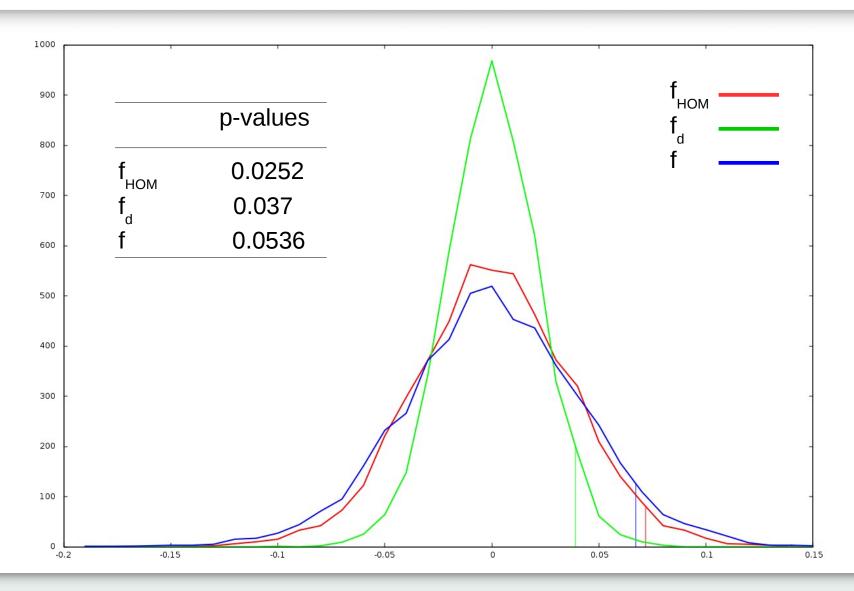
 $f_{HOM} = 0.034$
 $f_{d} = 0.020$

Are differences significant?



Null distribution of the difference in *D* statistic between admixed genomic blocks and rest of the genome, obtained by shuffling the admixed regions of individual Er55.

p-value: 0.0608



Conclusions

- Support for the classic model of post-glacial colonization.
- Detection of low levels of hybridizacion, both historical and recent, in the central European contact zone.
- Evidence that natural selection determines the fate of the introgressed variation.

Acknowledgements

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