Signatures of selection in transcriptomes of lizards adapting in parallel to cool climate

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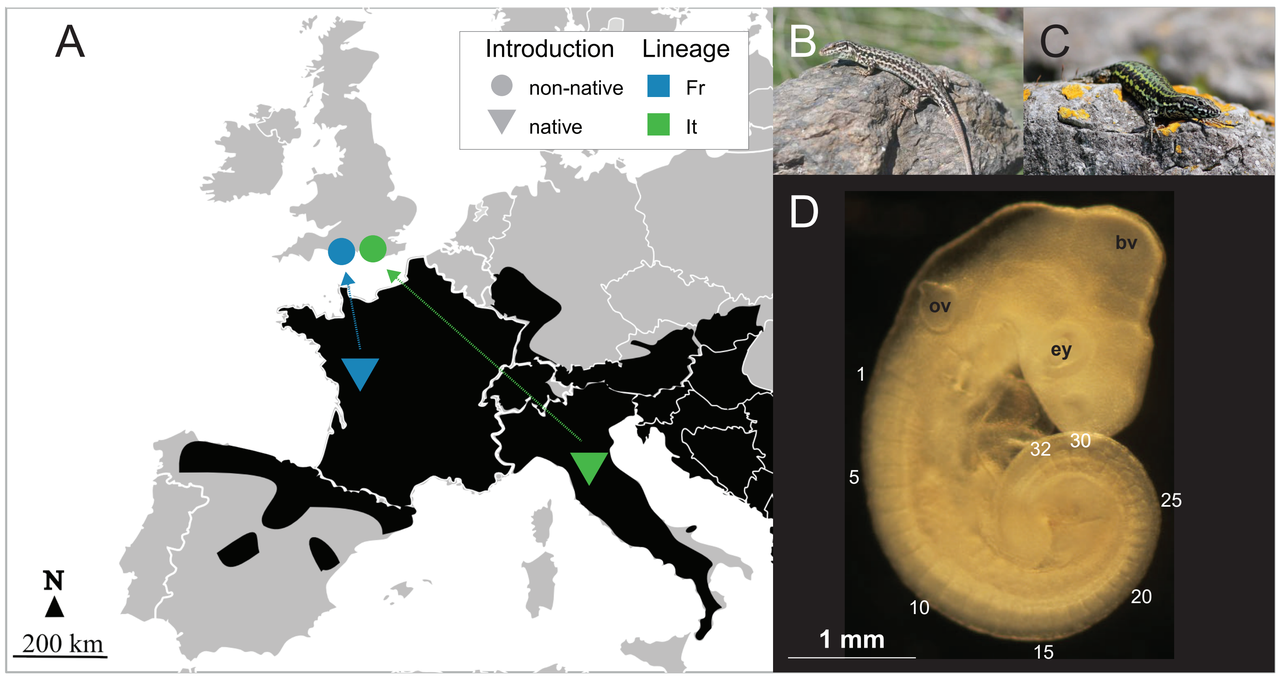
Background

Rapid adaptation to cool climate



In the 20th century, common wall lizards (*Podarcis muralis*) from Italy and France were introduced to England, north of their native range [1]. Non-native populations of both lineages have adapted to the shorter season and lower egg incubation temperature by increasing the rate of embryonic development [2].

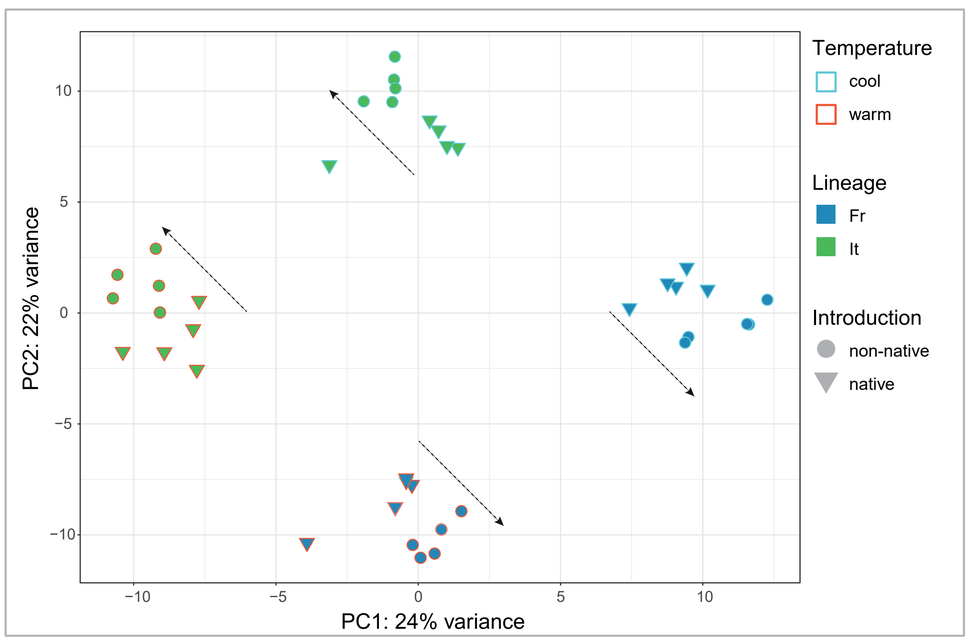
We applied transcriptome sequencing to early embryos of native and non-native lizards of both lineages and asked:

1. **Is parallel adaptation in developmental rates accompanied by signatures of directional selection in gene expression profiles of early embryos?**
2. **If yes, do non-native populations of both lineages adapt convergently, i.e., are the same genes differentially expressed?**

Experimental design

RNA-Seq of lizard embryos

- Gravid females from native (France and Italy) and non-native (England) sites were collected.
- Their clutches were split and eggs were incubated at cool or warm temperatures.
- Embryos at the 31 (±1) somite stage were sacrificed and their RNA was sequenced.
- We applied a 2x2x2 experimental design with factors ‘temperature’, ‘lineage’, ‘introduction’.
- To assess and compare the effect of introduction, we divided the dataset into 4 subsets (Fr-cool, Fr-warm, It-cool, It-warm).

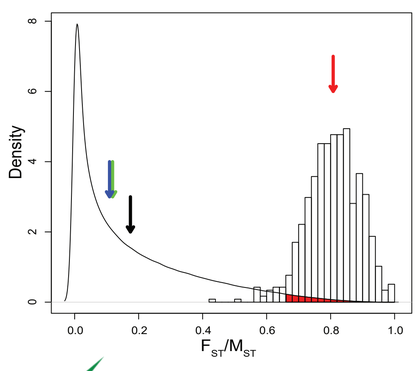


Principal component analysis of gene expression profiles. Dashed arrows indicate that at a given temperature, native lizards show more similar expression profiles than samples from non-native lizards.

Result ①

Do we find signatures of selection in gene expression profiles?

- For each transcript, we calculated M_{ST} values [3], analogous to F_{ST} values.
- We used F_{ST} markers derived from 13 microsatellite loci to simulate M_{ST} values under neutral evolution.
- Comparison of MST values expected under neutral evolution and MST values (graph) of differentially expressed genes between native - non-native (bars):



Red arrow: average observed MST of DEG_{intro}
Green arrow: average observed MST of all transcripts
Blue arrow: average observed F_{ST}
Black arrow: average simulated neutral M_{ST}
The 2.5% tail of the neutral M_{ST} distribution is shaded in red.

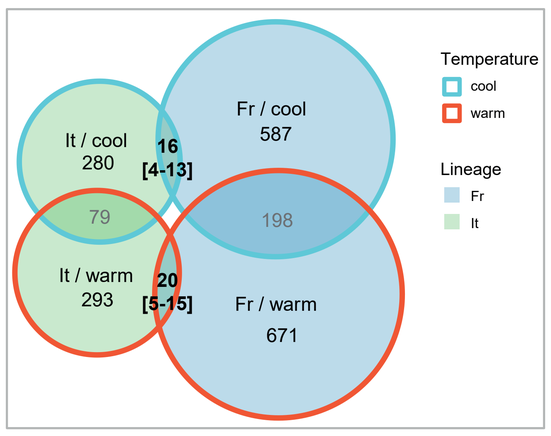
We find almost three times as many genes showing expression patterns under directional selection as expected under a scenario of neutral evolution.

✓ Robust signal of directional selection in embryonic transcriptomes

Result ②

Do we find convergence between the two lineages?

- We looked for genes that are differentially expressed following introduction to England (DEG_{intro}) in the 4 data subsets.



Overlaps between gene sets [and 95% CI expected by chance] are shown in intersects. We find a substantial overlap in DEG_{intro} within lineages at different temperatures, but **only very limited overlap between the Italian and French lineage**.

In addition, only half of the 36 genes differentially expressed in both lineages showed a consistent direction of expression change.

✗ Very limited signal of convergence in gene expression profiles.

BUT we find significant similarity between gene funtionalities (GO terms)

Category	Number of GO terms Fr	number of GO terms It	Observed similarity	95% CI of simulated similarity
BP	*10*	*14*	*0.2356*	*0.0645-0.1641*
MF	*12*	*13*	*0.1072*	*0.0408-0.1071*

✓ Convergence on the level of gene function.

Repeatability of evolution?

✓ French and Italian lizards both adapted to cool climate by increasing developmental rates.

✗ Underlying gene expression profiles are largely divergent,

✓ but similar functional pathways are used.

References

1. Michaelides et al., Mol Ecol 24, 2702 (2015).
2. While et al., Proc Biol Sci 282 (2015).
3. Whitlock, Mol Ecol 17, 1885 (2008).

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