Gene flow relates to evolutionary divergence among populations at the range margin

BACKGROUND

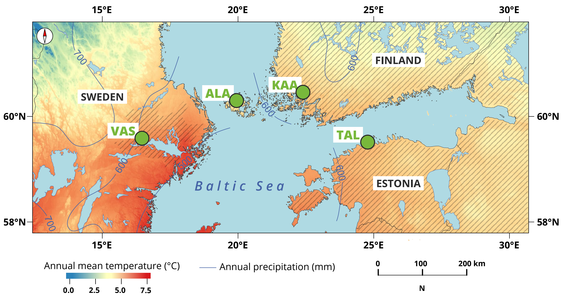
Morphological differentiation between populations resulting from local adaptations to environmental conditions is likely to be more pronounced in populations with increasing genetic isolation.

In a previous study a positive clinal variation in body size was observed in isolated Roesel's bush-cricket, *Metrioptera roeselii*, populations, but was absent from populations within a continuous distribution at the same latitudinal range. This observational study inferred that the expression of climate-induced phenotypic effects were related to gene flow.

METHODS

To disentangle genetic versus environmental drivers of population differences in morphology, we measured **four different physical traits in wild-caught individuals from the two most distinct latitudinally-matched pairs of populations** occurring at about 60°N latitude in northern Europe, characterised by either restricted or continuous gene flow, **and corresponding individuals raised under laboratory conditions**.

STUDY SITES WITHIN THE RANGE OF *M. ROESELII* IN NORTHERN EUROPE WHERE NYMPHS AND ADULTS WERE SAMPLED

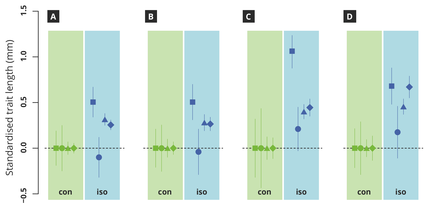


The populations KAA and TAL are situated in the species continuous distribution range and connected via Russia in the east; VAS and ALA are isolated population sites. Hatched area shows range in 2010.

RESULTS

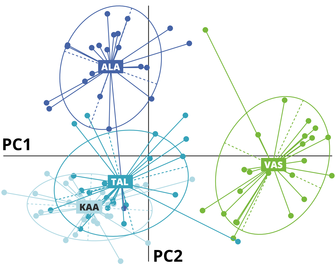
Individuals that originated from the genetically isolated populations were always bigger (femur, pronotum and genital appendages) when compared to individuals from latitudinally-matched areas characterised by continuous gene flow between populations. The magnitude of this effect was **similar for wild-caught and laboratory-reared individuals**. We found that previously observed size cline variation in both male and female crickets was **likely to be the result of local genetic adaptation** rather than phenotypic plasticity.

THE ESTIMATED MEDIANS AND 95% CREDIBLE INTERVALS FOR THE LENGTHS OF MORPHOLOGICAL TRAITS OF *M. ROESELII*



The estimated medians and 95% credible intervals for the lengths of morphological traits of M. roeselii. (A) Males grown in the field or (B) reared in the laboratory and (C) females grown in the field or (D) reared in the laboratory. Squares – hind femur, circles – forewing, triangle – pronotum, diamond – cerci/ovipositor. Individuals originated from the sites of the continuous species range (con) and isolated sites (iso) located about 60°N latitude in northern Europe. Values on the y-axis are standardised relative to the estimates from the continuous populations, which are set to zero for each trait.

GENETIC DISTANCES BETWEEN INDIVIDUALS SAMPLED IN 2008



Genetic distances between individuals sampled in 2008 examined by a Principal Coordinates Analysis (PCoA). Ellipses indicate credible distribution of the individuals into different clusters.

CONCLUSIONS

Our findings strongly **suggest that restricted gene flow is important, influencing the frequency of alleles that participate in climate-induced selection** and resulting in them favouring larger phenotypes in isolated populations at colder latitudes.

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