Connectivity and dispersal potential of *Dinocras cephalotes* populations (Plecoptera): A population genetic case study in the Sauerland region

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Progress Report!

Background

To understand the impact of human alterations on freshwater ecosystems, information about the species connectivity and diversity are essential (→ implications for planning and management). Genetic methods can improve the accuracy of dispersal models which use geo-referenced environmental data. With molecular data, morphospecies can be validated and migration between populations estimated with greater precision.

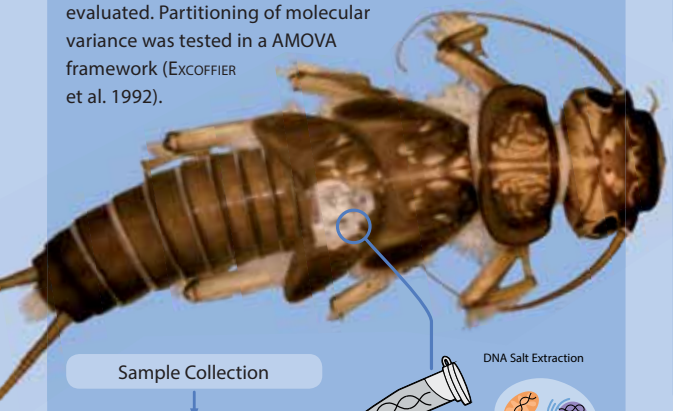
In this project, we focus on the population connectivity and genetic diversity of the stonefly *Dinocras cephalotes* (Plecoptera) in the Sauerland region. We analysed over 300 samples from 29 populations for the mitochondrial marker *Cytochrome c Oxidase 1* (CO1) and the nuclear *Wingless* gene. In addition, microsatellites have been developed *de novo*, which will provide additional information regarding the dispersal potential of *D. cephalotes*. A central aim of the project is to compare the results obtained from the genetic data with the results obtained from GIS models.

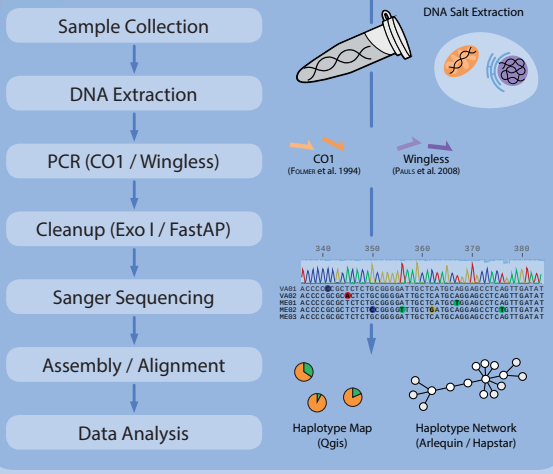
Research Questions

- What is the dispersal potential of *D. cephalotes*?
- Do we find isolated populations?

Material and Methods

To access the diversity and connectivity of *D. cephalotes* populations, two variable molecular markers were used: A 658 bp fragment of the mitochondrial barcoding gene CO1 and a 400 bp fragment of the nuclear Wingless gene were sequenced and evaluated. Partitioning of molecular variance was tested in a AMOVA framework (Excoffier et al. 1992).





Results

Two diverse haplotype groups were found for the mitochondrial marker CO1, which differed by 5% p-distance (Fig. 1A). Only few pairwise population comparisons had significant F_{ST} values (uncorrected mean F_{ST}= 0.192, σ = 0.078, p = 0.05, n = 32 of 406). The nuclear Wingless gene shows only a single haplotype group that is shared between all sampled specimens (Fig. 1B).

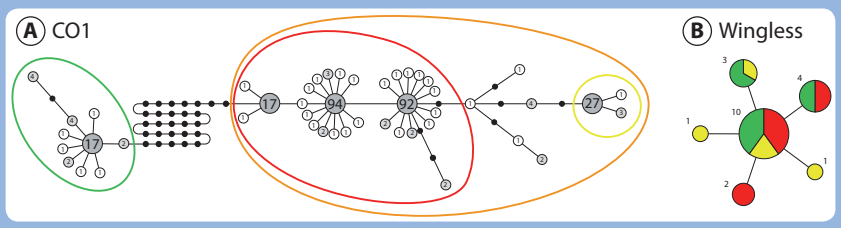


Figure 1: Minimum Spanning Network of the mitochondrial marker CO1 and the nuclear gene Wingless (numbers indicate the number of specimens with the respective haplotype, dots represent hypothetical haplotypes). **A** Network of 307 CO1 sequences. Three haplotype groups were identified, indicated by circles. **B** Wingless network with 21 sequences. The sequences were obtained from 2 populations (Fig. 2 ✱), covering the 3 haplotype groups found in the CO1 network (indicated by color).

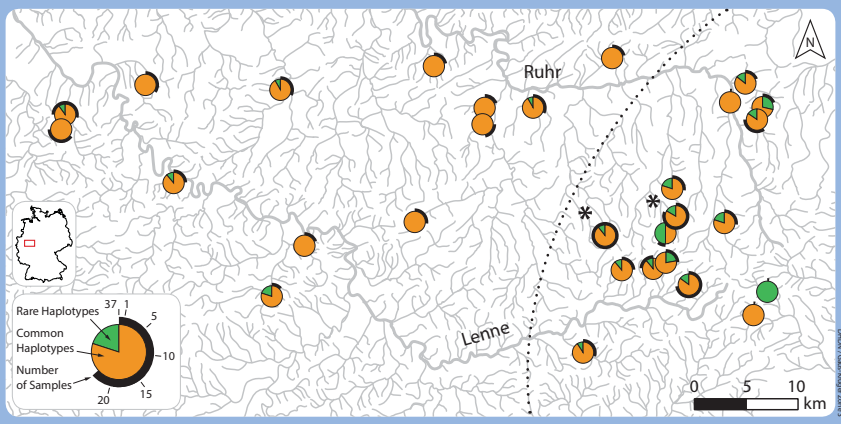


Figure 2: Haplotype map of 320 *D. cephalotes* samples for the marker CO1. The samples cluster into two main haplotype groups, separated by p-distance of 5%. Results of an AMOVA calculation revealed a weak but significant difference in variation between the eastern and western populations (dotted line, Phi_{CT} = 0.065, p < 0.001). No significant difference was observed among populations from Ruhr and Lenne catchments.

Discussion

The 5% p-distance between the main CO1 haplotype groups could be explained by:

1. Independent evolution of populations in glacial refugia, now in secondary contact.
2. Speciation → no gene flow between the two haplotype groups (*cryptic species*).

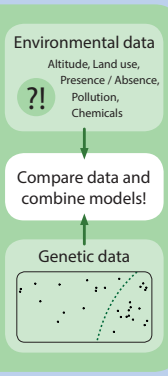
To test these hypotheses the Wingless marker was sequenced, which is affected by recombination as it is a nuclear gene. As the individuals from all CO1 haplotype groups share a single Wingless haplotype, we reject Hypothesis 2 (i.e. no cryptic species). Furthermore, the geographical distribution of haplotypes suggest that *D. cephalotes* has a good dispersal potential and gene flow is present. However, we need independent and fast evolving markers such as microsatellites to test the population connectivity in more recent times.

Conclusion and Outlook

- *D. cephalotes* seems to have good dispersal abilities and populations are interconnected.

Ongoing research:

- Test results with microsatellite markers.
- Obtain distant *D. cephalotes* samples to find the geographical origins of the two haplotypes groups.
- Compare the results obtained from the genetic data with the results obtained from GIS models.



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Sources

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