GLOBAL CHANGE AND GENETIC IMPACT OF INVASIVE SPECIES

The case of invasive and native *Arion* slugs in Switzerland

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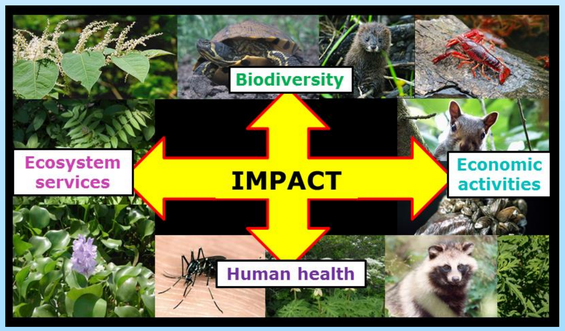
Background and rationale

CLIMATE CHANGE AND INVASIVE SPECIES

- climate change and invasive species represent two of the greatest threats to biodiversity and the provision of valuable ecosystem services
- combined, the complexity of the interaction of these two global drivers increases dramatically
- ***climate change impacts are likely to facilitate the introduction, establishment and spread of invasive species***

IMPACT OF INVASIVE SPECIES



SPANISH SLUG (*ARION VULGARIS*)

- belongs to one of the 100 most invasive species in Europe
- causes large economic costs in agriculture
- introduced to Switzerland in 1955
- **its impact on native fauna is still unclear:** populations of closely related species decline when *A. vulgaris* is introduced to the region

Research questions

The Swiss native slug *A. rufus* used to be widely distributed, but is now confined to natural habitats, mainly at higher altitudes, to where *A. vulgaris* is spreading.

Arion vulgaris and *A. rufus* are difficult to distinguish based on their external morphology. There have been some reports of intermediate morphological forms, suggesting that hybridization might occur.

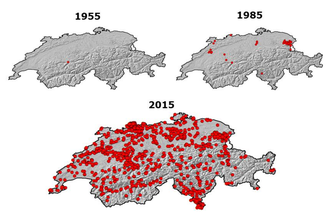
IS THE DECLINE OF NATIVE *A. RUFUS* LINKED TO THE SPREAD OF INVASIVE *A. VULGARIS?*

DOES THIS INVOLVE INTROGRESSIVE HYBRIDIZATION?

Materials and methods

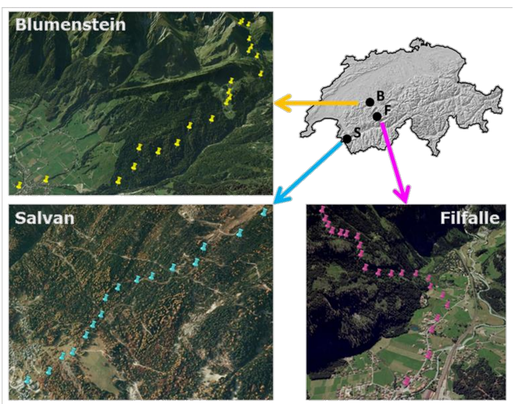
- sampling along three altitudinal transects
- over 600 *Arion* sp. individuals
- genotyped with 15 microsatellite markers
- Bayesian admixture analysis

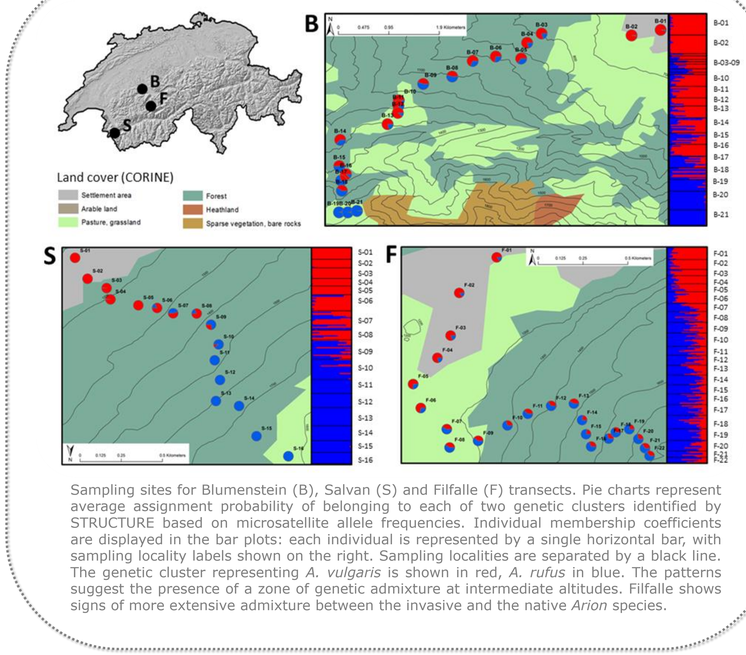
Arion vulgaris is present in the lowlands and is spreading into the mountains.



Top: distribution of *A. vulgaris* in Switzerland in 1955, 1985 and 2015.

Right: sampling locations along altitudinal transects in Blumenstein, Salvan and Filfalle.





Sampling sites for Blumenstein (B), Salvan (S) and Filfalle (F) transects. Pie charts represent average assignment probability of belonging to each of two genetic clusters identified by STRUCTURE based on microsatellite allele frequencies. Individual membership coefficients are displayed in the bar plots: each individual is represented by a single horizontal bar, with sampling locality labels shown on the right. Sampling localities are separated by a black line. The genetic cluster representing *A. vulgaris* is shown in red, *A. rufus* in blue. The patterns suggest the presence of a zone of genetic admixture at intermediate altitudes. Filfalle shows signs of more extensive admixture between the invasive and the native *Arion* species.

Results and conclusions

- *A. vulgaris* is predominant in the lowlands, *A. rufus* is mainly at higher altitudes
- we provide evidence of various degrees of admixture between the two species at locations of contact
- hybridization might be indeed involved in the displacement of *A. rufus*
- without specific conservation action, *A. vulgaris* will probably further expand its range, which is likely to be assisted by global change impacts

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