

The genetic dynamics of the Great Crested Newt (*Triturus cristatus*) populations : Insights for effective conservation strategies



AUTHORS




BEAUMARIAGE Anaïs (1), ATTAQUE Alix (1), PIGNEUR Lise-Marie (1), GRAITSON Éric (2), MICHAUX Johan (1)
 (1) Laboratoire de génétique de la conservation (GeCoLab), Université de Liège, Chemin de la Vallée 4, 4000 Liège, Belgique. Anaïs.beaumariage@gmail.com
 (2) Natagora, Rue des Muses 1, 5002 Namur, Belgique.

INTRODUCTION

The Great Crested Newt (*Triturus cristatus*) is a key indicator of aquatic ecosystem health. Despite widespread across Eurasia, the urodele faces challenges such as habitat fragmentation which can lead to genetic isolation, reduced its adaptive capacity and threaten amphibian survival.

➤ **Connecting populations and preserving their genetic diversity** are crucial for their conservation.

This study addresses global conservation challenges from a genetic perspective by focusing on the populations of Great Crested Newts in Belgium, with the specific goals of :

- 
 Assessing the current **structure** of populations
- 
 Evaluating **gene flow**
- 
 Estimating indicators of **genetic diversity**

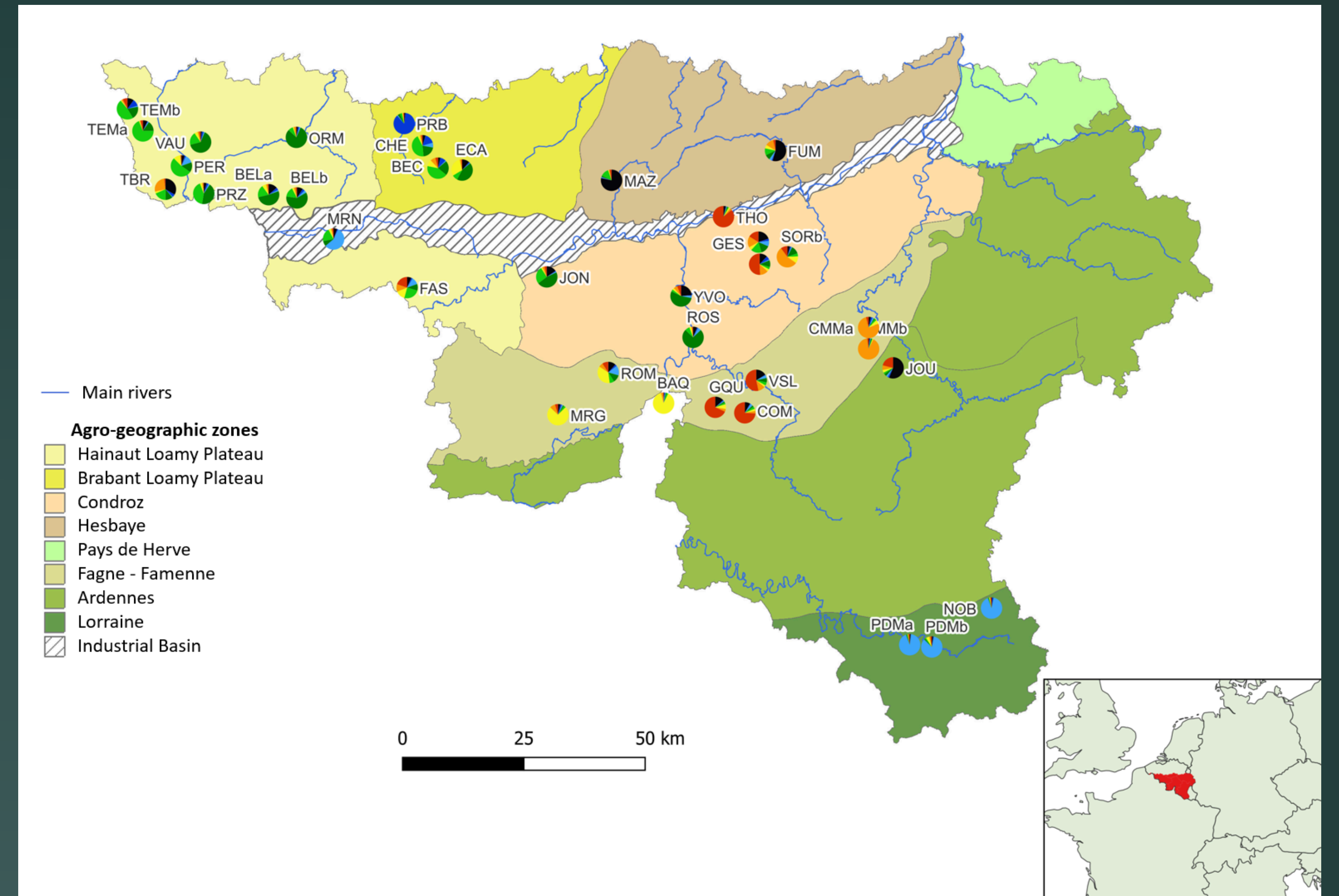
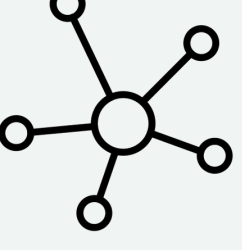
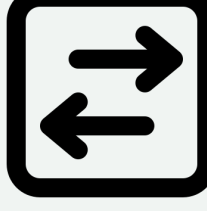
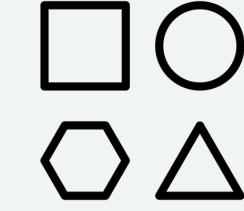


FIGURE 1
 Representation of the average affiliation of each station to the eight genetic groups in Wallonia (Belgium). Circular diagram shows the average percentage of belonging to the different groups.

METHODOLOGY

Buccal DNA from 540 individuals from widely distributed stations in Wallonia were analyzed using eight microsatellite markers.

- 
Population structure
 STRUCTURE software
- 
Genetic differentiation indices
 Fixation index : G_{st}
 Allelic differentiation : D_{jost}
- 
Diversity indices
 Allelic richness
 Inbreeding

ANALYSIS

- Diversity
- ◇△ Diversity

The highest genetic diversity indices were found in stations in the loamy region (with a few exceptions). Cases of inbreeding were rare and well localized.

- Making possible to target populations requiring priority management measures such as translocations
- Saving as a priority isolated populations with low indices of genetic diversity

ANALYSIS

Samples with insufficient signals were excluded, leaving 444 samples for further analysis.

Structuration

Genetic structuring showed heterogeneity, with lineages from the loamy region genetically distinct from other Walloon populations. Eight clusters were identified to explain the distribution of individuals (Figure 1).

Genetic differentiation

Genetic differentiation was low among individuals from stations in the loamy region. Gene flow between populations was limited, particularly with geographically distant populations. Geographical distance played a key role in the observed gene flows : our data indicated that proximity of ponds favors essential genetic exchanges.

- Establishing networks of ponds is recommended to facilitate the movement of newts and thus gene flow.

CONCLUSION

Our goals were to analyze the genetic structuring, diversity, and gene flows within the populations of an emblematic amphibian species : the Great Crested Newt.

Although a portion of the studied populations exhibits promising genetic characteristics, it is crucial to **continue conservation efforts** to ensure a sustainable future for amphibian species.

Our study highlights the need to **pursue an integrated approach** that considers genetic dynamics to develop effective conservation strategies.



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ACKNOWLEDGEMENTS

