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Genomic-based health-screening of reintroduced Emys orbicularis

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1. Background

Species reintroductions are considered promising strategies for limiting biodiversity erosion. Yet, translocations of captive-bred individuals into the wild rely on their capabilities to adapt to new conditions. Genomic-based health-screening of gut microbiome can provide important insights into eco-evolutionary adaptations. Indeed, the communities of microorganisms coinhabiting an animal are highly driven by environmental factors and ultimately influence individual fitness.

2. Objectives

Within our project Emys-R (<u>www.emysr.cnrs.fr</u>), where we investigate best practices for European pond turtle (Emys orbicularis) reintroductions, we establish guidelines for health screenings in this species. We infer whether changes in diet between captivity and after translocation affect the turtles' microbiome. Further, we hypothesize that turtles with most diversified microbiomes are less infected with pathogens and have better fitness.

3. Methods

We screen the gut microbial community of E. orbicularis from different breeding facilities via fecal samples, cloacal and combined oral-cloacal swabs, using a shotgun metagenomic approach.

4. Results

We aim at defining 1) an original index of individual health based on the microbial composition, complementary to biometric and genetics indices; 2) guidelines for sampling techniques in the field and 3) the most appropriate diet prior translocation for ensuring best adaptive capacities of the individuals after translocation.

5. Conclusion

As the connection of the microbiome and host health are of high importance, equipping hosts with set of beneficial bacteria and creating conditions to maintain that flora can be integrated in continuous health screenings of translocated species as an efficient tool to ensure long-term reintroduction success of captive-bred individuals.

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