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Make visible the invisible: Optimised development of an environmental DNA metabarcoding tool to characterise trematode parasitic communities



Philippe Douchet, Jérôme Boissier, Stephen Mulero, Hubert Ferté, Margot Doberva, Jean François Allienne, Eve Toulza, Kévin Bethune, Olivier Rey

Contacts: philippe.douchet@univ-perp.fr
olivier.rey@univ-perp.fr

IHPE, Univ Montpellier, CNRS, IFREMER, Univ Perpignan Via Domitia, Montpellier, France

- Trematoda** →
- Ubiquitous over all marine and freshwater ecosystems
 - 44.000** estimated species (14% described) ¹
 - Key organisms in **ecosystem functioning** ²
 - 100 species involved in **human and livestock diseases**
 - Important number of cryptic species ³
 - Difficult to tract in natural environments

→ **Need to develop new tools for a better assessment and understanding of the structure and dynamics of trematode diversity**



In silico primers design and evaluation of the trematode metabarcode

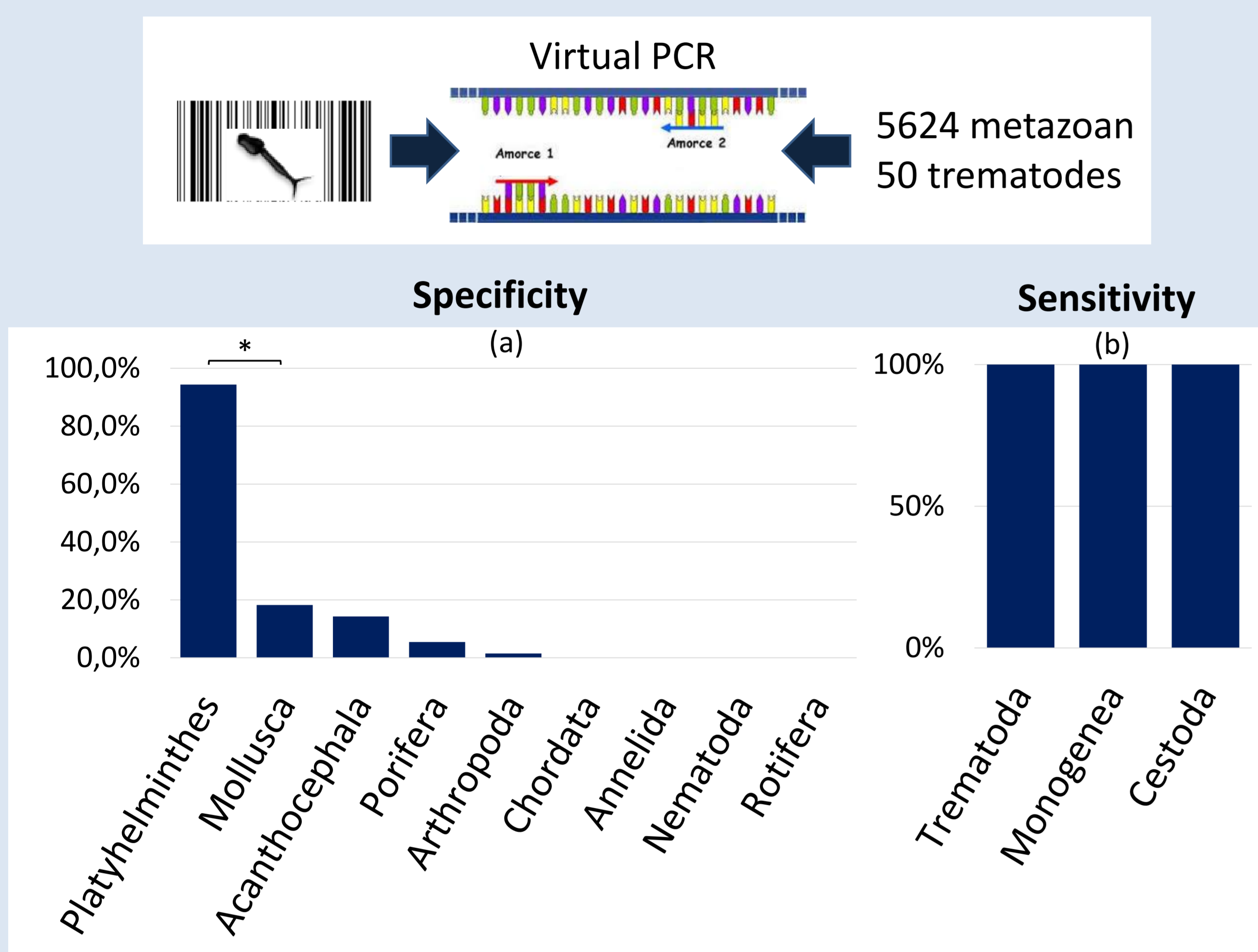


Figure 1. Percentage of sequences amplified by virtual PCR (a) per phylum and (b) per class of Platyhelminths when allowing up to 3 mismatches between each primer and the targeted sequences. *: Fisher's exact test p-value < 0.001

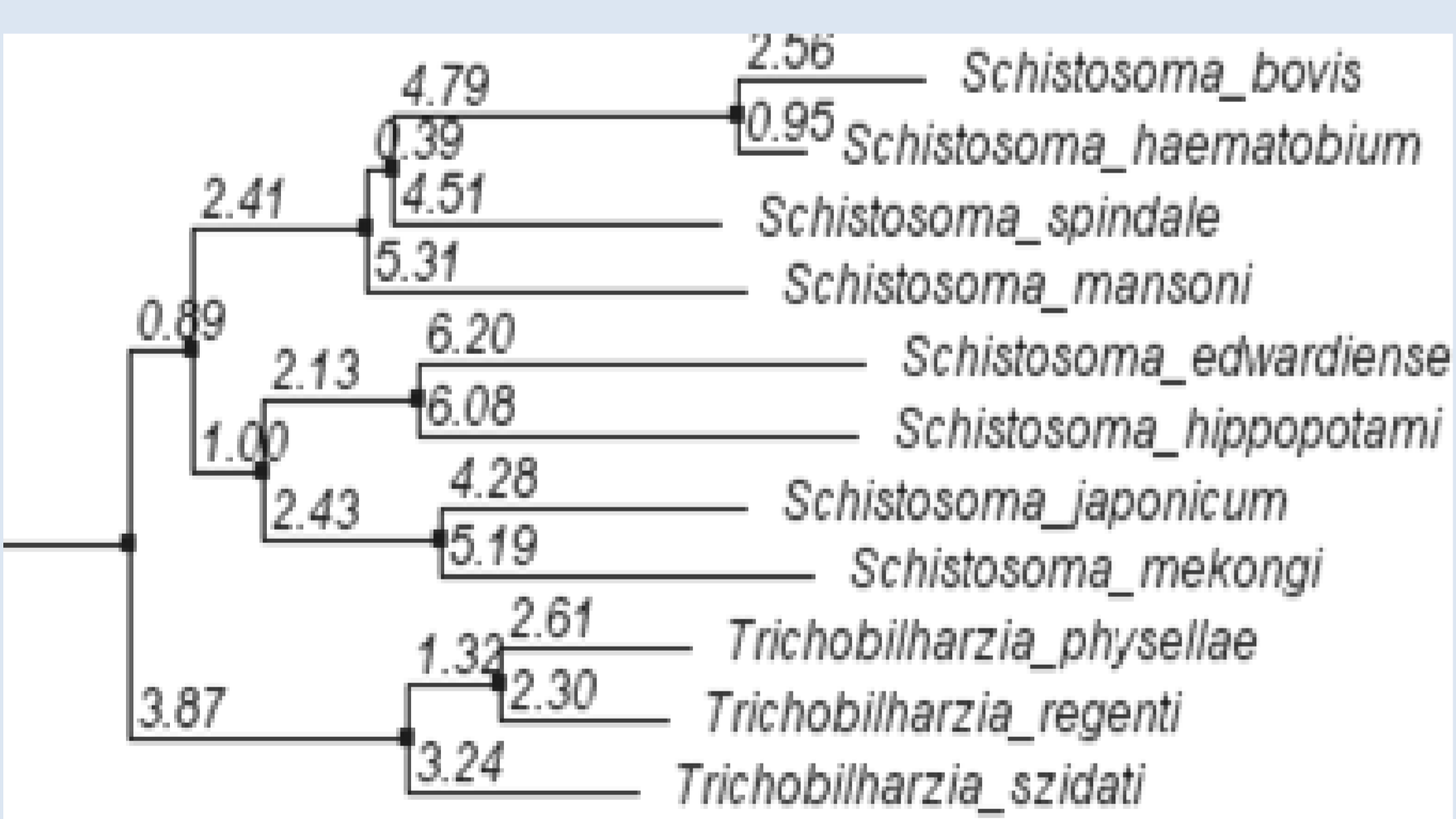


Figure 2. Partial phenetic tree illustrating the resolution of the trematode metabarcode within the Schistosomatidae family. The numbers on each branch indicate the percentage difference in nucleotides between amplicons of the different trematode species

In vitro validation of the metabarcode efficiency to detect and identify trematodes

Mock communities
DNA pool of 28 trematode species

Detection & identification score : **100%**

In natura comparative analysis between a classical trematode species characterisation and our eDNA-based monitoring method



Figure 3. Pictures of the four sites sampled in in this study (Occitanie region; southern France)

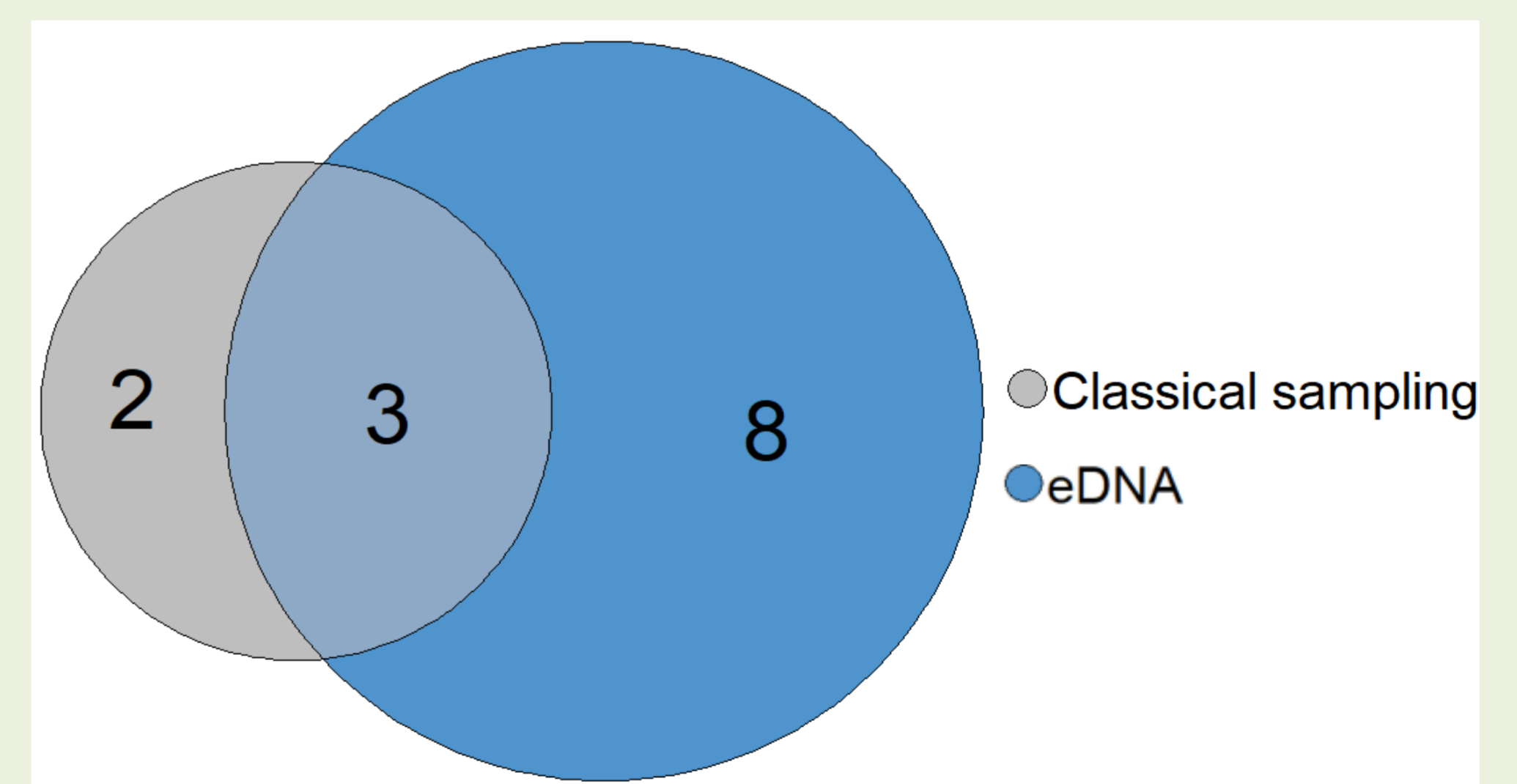
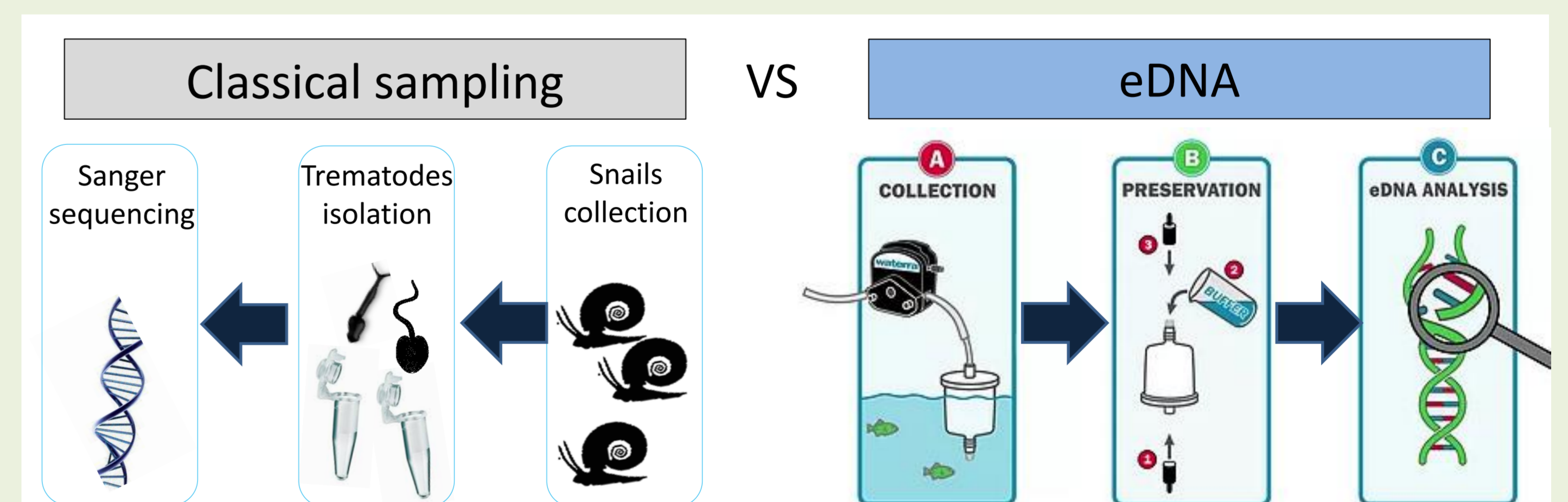


Figure 4. Number of trematode species characterised in field by classical sampling (in grey), by eDNA monitoring (in blue), and by both over the four sites sampled in this study

This new eDNA-based metabarcoding tool open new perspectives for fundamental and applied studies in conservation, sanitary survey, and field ecology

Références: 1- Carlson et al., *Proceedings of the Royal Society B: Biological Sciences* 287, n° 1939 (2020)
2- Dougherty et al., *Conservation Biology* 30, n° 4 (2016)
3- Poulin, *Biology Letters* 7, n° 2 (2011)