Association of some genetic markers with parasitic infection in stickleback (*Gasterosteus aculeatus*)

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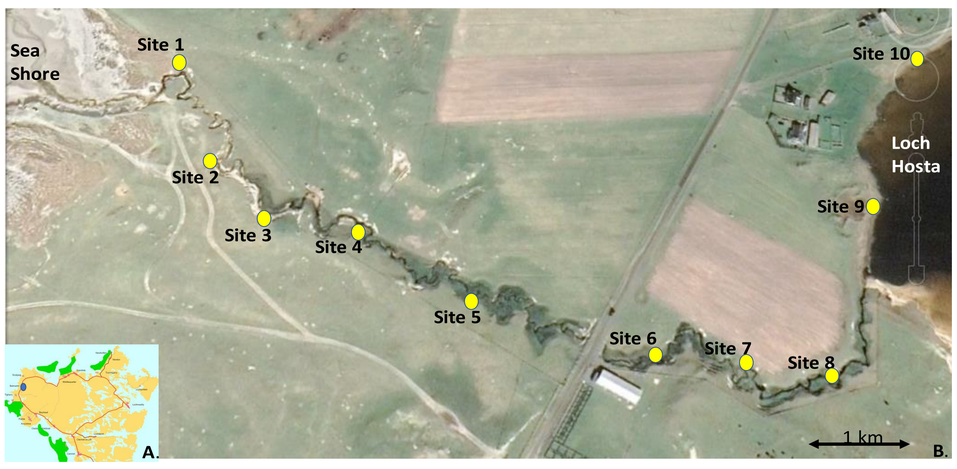
Background

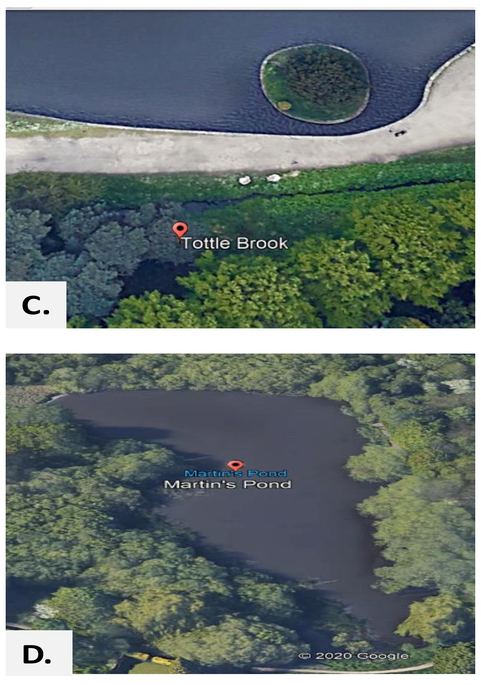
- **Parasites are potential agents of selection which might affect traits of taxa to drive adaptive changes in natural populations[1].**
- **The strength and prevalence of parasite-mediated selection in nature largely relies on reduction of host fitness (reproduction or survival) and host genetic variation[2].**
- **Few studies revealed the genetic basis of parasite resistance in fish and other animals[3].**
- **Identification of adaptive loci or genes involved in parallel divergence of stickleback is the prerequisite to map the genetic basis of an individual trait evolved by natural selection.**

Major Objective

To investigate abundance of two macro-parasites (*Gyrodactylus* sp. and *Diplostomum* sp.) and their association with genotypes at candidate loci (Eda, PPARA, WNT7B and NLRC5) in both artificial and natural conditions.

Methodology





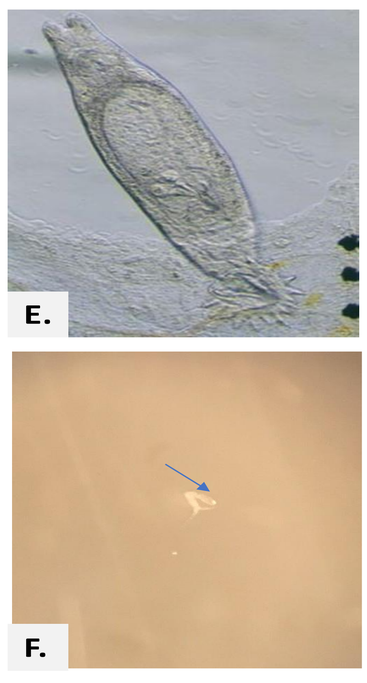


Fig.1 Collection sites of stickleback for parasites A. Map of United Kingdom B. Hosta stream hybrid zone, North Uist, Scotland (natural) C. Tottle Brook and D. Martin's pond, Nottingham (experimental) including images of E. *Gyrodactylus* sp. and F. *Diplostomum* sp.

- **216 sticklebacks were collected from Hosta stream, North Uist, Scotland.**
- **Natural infection status was assessed by counting *Gyrodactylus arcuatus* (ectoparasite) and *Diplostomum* sp (endoparasite).**

Fig. 2 Different armour phenotypes in the hybrid zone and lab-crossed fish: A) Completely plated fish with continuous row of plates (CM) B) Partially plated fish with discontinuous row of plates (PM) and 3) Low plated (LM) fish.

- **In captive condition, two experiments were conducted to investigate infection patterns –**
  - **a) 100 fish for the ectoparasite (*G. gasterostei*) artificially infecting the F2 generation of marine x freshwater crosses and**
  - **b) 90 fish for the endoparasite (*D. pseudospathecum)* infecting lab-raised F1 fish from the already admixed Hosta hybrid zone on North Uist.**
- **All fish were genotyped using SNPs based PCR-RFLP method at four candidate loci (Eda, PPARA, WNT7B and NLRC5) to determine the effects of genotypes on natural and artificial infection pattern.**

Results

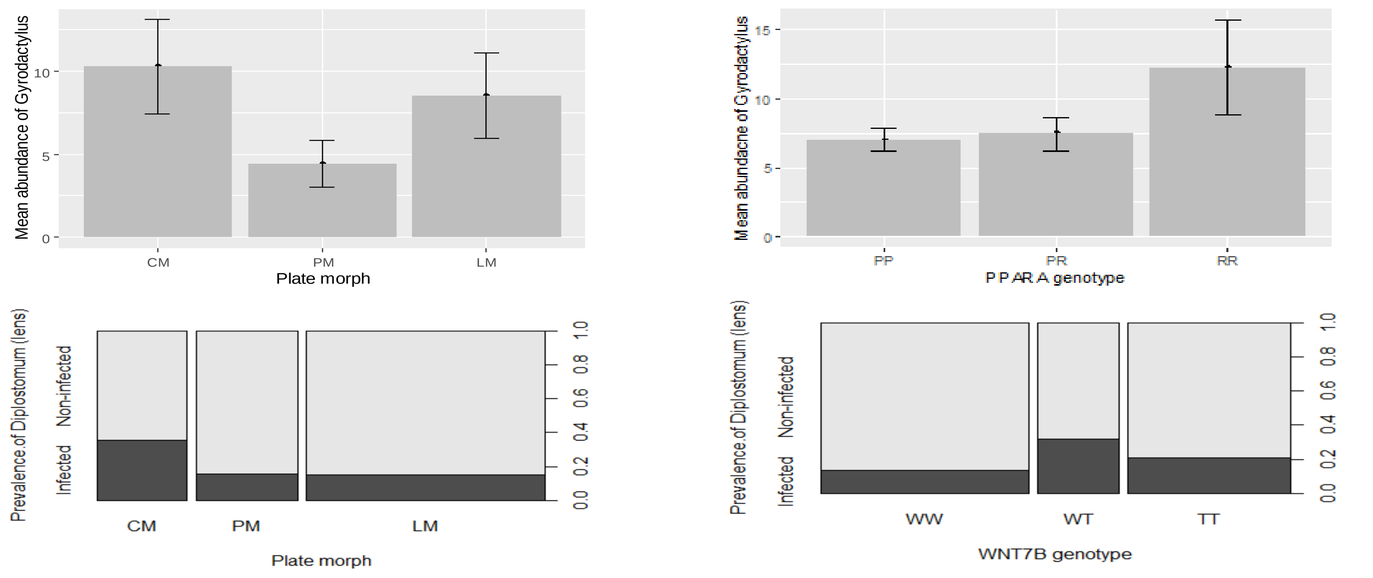


Fig. 3 Phenotype and genotypes of ectoparasite and endoparasite infected fish in natural conditions.

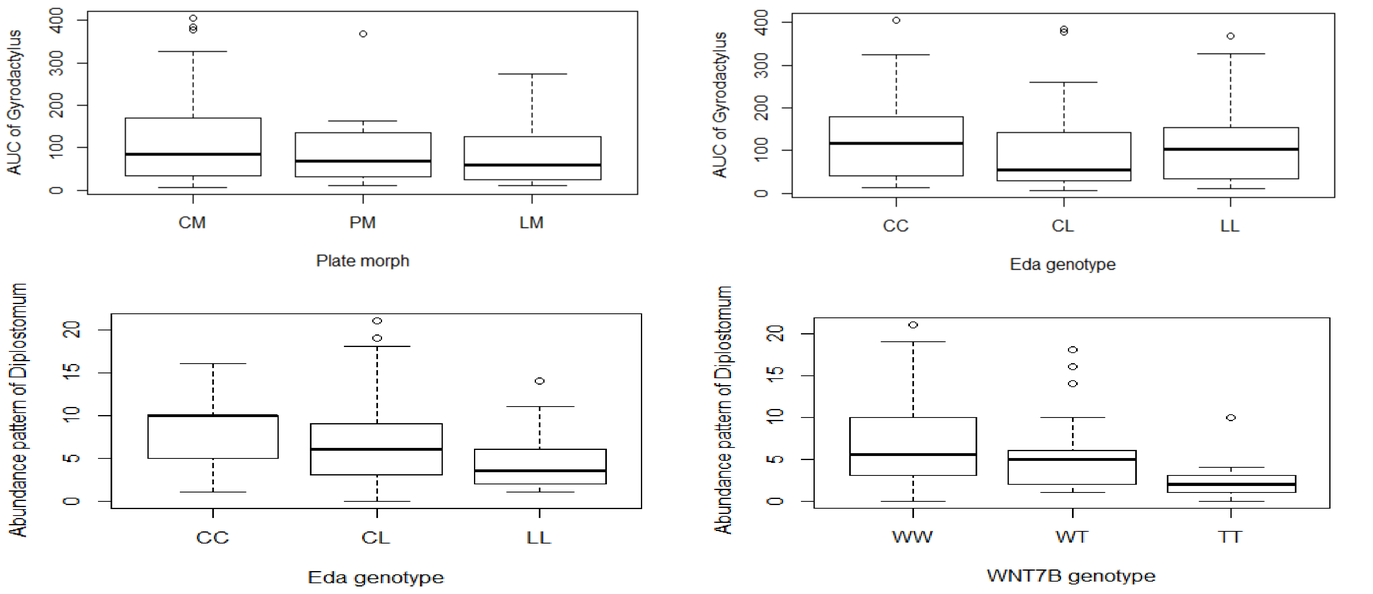


Fig. 4 Phenotype and genotypes of ectoparasite and endoparasite infected fish in experimental conditions.

- **The completely plated phenotype experienced the highest parasite burden while partially plated had the lowest in both wild and experimental fish.**
- **Eda genotype was constantly associated with both types of parasites in experimental condition.**
- **WNT7B genotype was also associated with endoparasite abundance in both natural and experimental conditions while PPARA genotype with ectoparasite in natural condition.**

Conclusion

- **The strong association of parasite abundance with selected candidate genes has implication in elucidating the genetic regions underlying adaptation to infection.**
- **This findings suggest the role of parasite-mediated ecological selection in nature.**

References

1.MacColl, A.D., 2011. The ecological causes of evolution. *Trends in Ecology & Evolution*, *26*(10), pp.514-522.

2. Little, T.J. and Ebert, D., 2000. The cause of parasitic infection in natural populations of Daphnia (Crustacea: Cladocera): the role of host genetics. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, *267*(1457), pp.2037-2042.

3. Brown, E.A., et al. 2013. Detecting genes for variation in parasite burden and immunological traits in a wild population: testing the candidate gene approach. *Molecular Ecology*, *22*(3), pp.757-773.