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## commentary

## The impact of host dispersal on parasite biogeography

Understanding the diversification of species remains a topic of primary interest in the field of biogeography (Faria et al. 2014). Typically, this involves studies investigating species' dispersal capabilities and the identification of geographic barriers to their movements. While free-living organisms display a broad range of mobility, parasites spend a portion of their life cycles on or within one or more host species. Parasite dispersal and geographic diversification may, therefore, be intimately connected to host vagility and the connectivity of host populations (Blasco-Costa and Poulin 2013).

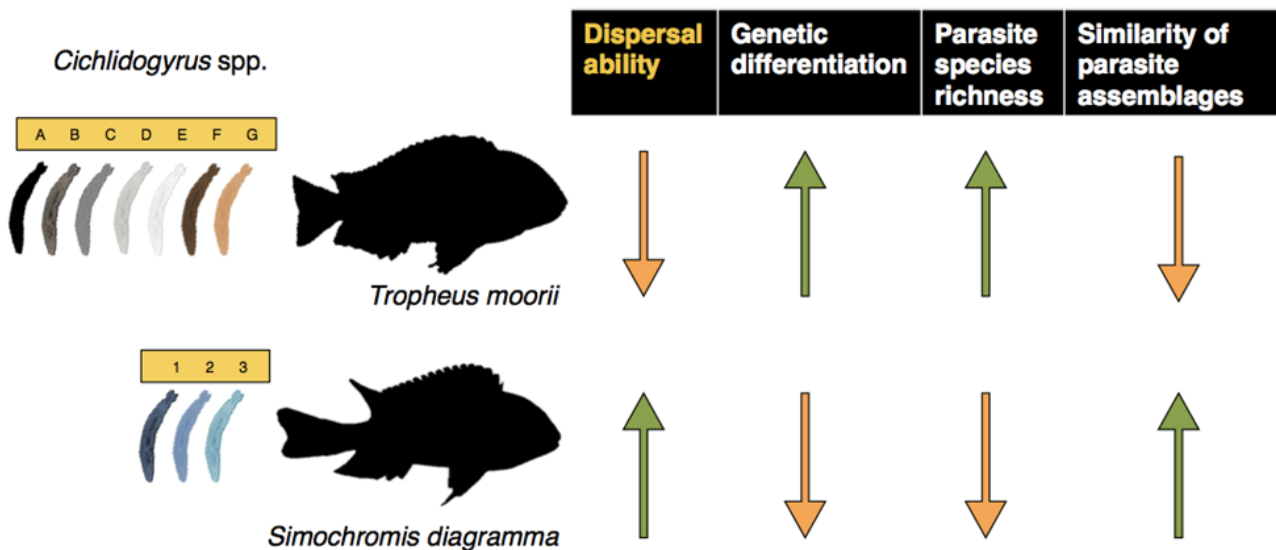
A recent study by Grégoir et al. (2015) examined the relationship between host dispersal and parasite diversity to determine whether host characteristics influence parasite diversification. Their study compared ectoparasitic monogean *Cichlidogyrus* species richness and assemblage composition in sympatric *Tropheus moorii* (low dispersal ability) and *Simochromis diagramma* (high dispersal ability) cichlid populations from the southern end of Lake Tanganyika in Zambia. Levels of host genetic differentiation were used to confirm relative cichlid dispersal abilities. Hermaphroditic *Cichlidogyrus* species were identified by morphological analyses of male reproductive structures. The authors compared host dispersal ability to overall parasite species diversity and the similarity of parasite species assemblages among hosts collected from different geographic locales. The system they selected was ideal for testing host–parasite biogeographic hypotheses because these monogean are highly host-specific and have direct life cycles without intermediate hosts, and the two sympatric hosts possess differing dispersal capabilities.

Genetic differentiation among geographic areas was strong for *T. moorii*, but weak for *S. diagramma*, consistent with previous inferences (Meyer 1993), revealing a greater likelihood for parasite gene flow among populations of *Cichlidogyrus* infecting *S. diagramma*. *Tropheus moorii* was infected by seven *Cichlidogyrus* species while

*S. diagramma* was infected by three species. The authors hinted at the possibility of limited host connectivity inducing allopatric parasite speciation, but did not directly address this in their study. Parasite species assemblages differed among populations of *T. moorii*, but were similar among the more vagile *S. diagramma*, consistent with the hypothesis that the structure of *Cichlidogyrus* species assemblages is driven by host mobility (Figure 1). These patterns remained consistent when *T. moorii* from two geographically distant sites were excluded.

By revealing how host characteristics may influence the diversification and allopatric speciation of parasites, Grégoir et al. have provided a system with numerous possibilities for future investigation. Utilizing molecular data to confirm *Cichlidogyrus* species, in addition to morphological identification, could provide complementary data that contribute to the identification of cryptic species, infer host-specificity and coevolution, reveal patterns between speciation and environment, and add to our understanding of host biodiversity (Huysse et al. 2005; Poulin and Keeney 2007; van Steenberge et al. 2015). Parasite gene flow analyses, as Grégoir et al. mention, would show whether limited host dispersal corresponds to decreased parasite gene flow and increased genetic differentiation among populations, potentially elucidating how parasite allopatric speciation could occur in this system.

Although cichlid host characteristics and dispersal may drive ectoparasite diversity, seemingly separate parasite populations may experience connectivity if less mobile cichlids are able to occasionally overcome potential geographic barriers, or if the parasites themselves have other means of dispersal. An apparently isolated parasite population may therefore be able to infect hosts from other areas. Infection success could yield information on the specificity of host–parasite interactions for previously geographically isolated populations of conspecific hosts, clarifying the relationship between ecological and geo-



**Figure 1.** A schematic of results from Grégoir et al. (2015), showing cichlid species *Tropheus moorii*, a host species with low dispersal, infected by a large number of *Cichlidogyrus* species, whose assemblages also differed among host populations. In contrast, *Simochromis diagramma*, a host with a high dispersal capacity, is infected by a smaller number of *Cichlidogyrus* species, whose assemblages are similar among hosts from different geographic areas. Distinct *Cichlidogyrus* morphotypes referenced in Grégoir et al. (2015) are represented by differing colours.

graphic barriers to parasite infection (Locke et al. 2010). Using experimental infections to investigate parasite transmission among cichlids from different geographic areas might demonstrate early stages of population-level host specialization. For example, many geographically separated *T. moorii* populations are predominately parasitized by different *Cichlidogyrus* species. While this is probably the result of low host mobility and regional exposure to parasites, are the dominant parasite species from different regions able to infect hosts from other areas equally well? If not, parasites may be evolving specificity for regional host populations, a trend that can lead to parasite speciation. The same methods could also be used to examine host specificity and the potential for host switching in this system, allowing further insight into the likelihood of speciation (King and Cable 2007).

The Grégoir et al. (2015) study is exemplary for advancing our biogeographical understanding of factors influencing species diversity and host–parasite interactions. Given that low levels of host dispersal lead to variation in parasite species diversity and assemblages, they could also drive parasite speciation as populations within hosts restricted to specific geographic areas diverge. Testing the specific mechanisms driving diversifi-

cation within a system can reveal how current patterns of biodiversity have evolved. Prospective studies that thoroughly account for parasite species identification with morphological and molecular approaches, and assess host and parasite populations, will strengthen and advance our perspective on the processes of diversification and speciation.

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