Parasite Population Genetics: Illustrated Uses in the Environmental and Conservation Sciences

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Juvenile steelhead trout


Screw Trap (ODFW)

ABSTRACT

The field of parasitology has much to offer environmental studies that examine health, biodiversity, and conservation problems. In particular, population genetic studies of parasites can contribute to epidemiological studies of medical or veterinary importance and aid in conservation designations for endangered host populations. Here we provide three examples of how data on the genetic structure of parasite populations can be utilized in the environmental and conservation sciences.

1) First, we used life cycle patterns of parasites to understand gene flow potential among parasite populations.

Gene flow has been shown to play a key role in the dispersal and persistence of drug resistance genes (an emerging problem in many human and livestock parasites). The results indicate that life cycle patterns will be helpful in predicting the spread of drug resistance.

2) The second example involves the use of parasite population genetics to support host populations that are designated as populations of conservation concern (e.g., ESUs-Evolutionary Significant Units).

Some parasite species are intricately intertwined with their hosts in terms of population dynamics. Such parasite species should mimic their host's historical population processes, thus, providing independent evidence for biogeographic or genetic separation among host populations.

3) An extension of the use of parasites as biological tags is the third example.

Some parasites will have more genetic subdivision among populations than their hosts. The genetic information in highly subdivided parasite populations can be exploited to indicate the origin of commercially important hosts species. For example, the freshwater origin of Pacific salmon caught at sea may be determined more accurately with assignment tests using the parasite genetics than with the host genetics.

STUDY 1-Published

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Little is known about what controls effective sizes and migration rates among parasite populations. Such data are important given the medical, veterinary, and economic (e.g., fisheries) impacts of many parasites. The autogenic-allogenic hypothesis, which describes ecological patterns of parasite distribution, provided the foundation on which we studied the effects of life cycles on the distribution of genetic variation within and among parasite populations. The hypothesis states that parasites cycling only in freshwater hosts (autogenic life cycle, Fig. 1) will be more limited in their dispersal ability among aquatic habitats than parasites cycling through freshwater and terrestrial hosts (allogenic life cycle, Fig. 2). By extending this hypothesis to the level of intraspecific genetic variation, we examined the effects of host dispersal on parasite gene flow. Our a priori prediction was that for a given geographic range, autogenic parasites would have lower gene flow among subpopulations. We compared intraspecific mitochondrial DNA variation for three described species of trematodes that infect salmonid fishes (Fig. 3). As predicted, autogenic species (*Deropegus aspina* A & B, *Plagioporus shawi*) had much more highly structured populations and much lower gene flow among subpopulations than an allogenic species (*Nanophyetus salmincola)* sampled from the same locations (Fig. 3, Table 1). In addition, a cryptic species was identified for one of the autogenic trematodes (*Deropegus aspina* A & B). These results show how variation in life cycles can shape parasite evolution by predisposing them to vastly different genetic structures. Thus, we propose that knowledge of parasite life cycles will help predict important evolutionary processes such as speciation, coevolution, and the spread of drug resistance.

FIGURE 1

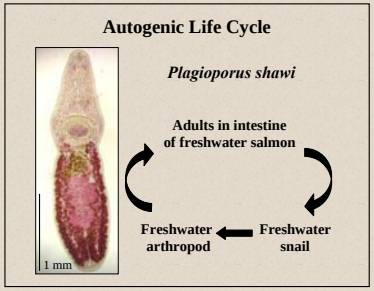
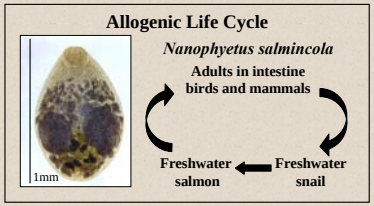


FIGURE 2



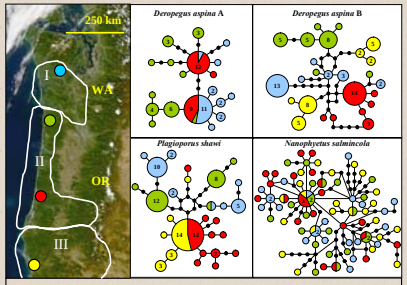


FIGURE 3

Sampling locations and mtDNA genealogical networks.

Rivers sampled in Washington (WA) and Oregon (OR) are shown as colored circles. White lines on the map indicate ESUs (I, II, III) for four salmonid species.

Each connection in a network is a single mutational step with black circles representing inferred haplotypes (a unique DNA sequence). Observed haplotypes are shown as colored circles, which indicate the geographic locations from which haplotypes were sampled. Haplotypes shared among locations are shown as proportional pie diagrams. Sizes of circles are proportional to the number of individuals (as indicated in the circles) with that haplotype; blank pie slices or circles indicate a single individual. **High gene flow results in a lack of structure as shown by the network of the allogenic *N. salmincola*. However, notice the strong geographic structure caused by low gene flow (i.e., related haplotypes are more likely found in the same subpopulation) for the autogenic species (*Deropegus aspina* A & B, *Plagioporus shawi).***

TABLE 1.
Genetic population subdivision and estimation of migration.

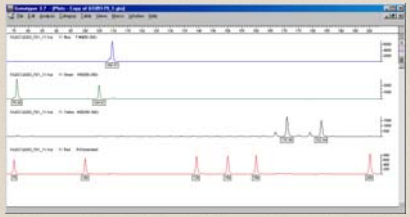
Φ_{ST} is a measure of genetic subdivision that ranges from 0 (no subdivision) to 1. Φ_{ST} > 0.15 indicates large amounts of genetic structure among subpopulations. N_em is the average number of immigrants into each subpopulation. N is the total sample size over 4 subpopulations. Asterisk (*) signifies Φ_{ST} values that are statistically significant (P < 0.0001) from 10,000 random permutations of haplotypes among populations; ns, P > 0.05.

Species	N	Φ_{ST}	$2N_em$
Autogenic			
***Deropegus aspina* A**	**66**	**0.172***	**0.76**
***Deropegus aspina* B**	**89**	**0.553***	**0.17**
Plagioporus shawi	**92**	**0.393***	**0.24**
Allogenic			
Nanophyetus salmincola	**91**	**0.013^{ns}**	**70.44**

STUDY 2-In progress

Four species of Pacific salmonids, *Oncorhynchus mykiss* (steelhead trout), *O. clarki* (cutthroat trout), *O. kisutch* (coho salmon), and *O. tshawytscha* (Chinook salmon) share similar ESU designations (Fig. 3). For some of these species, these ESUs represent federally protected populations under the Endangered Species Act. ESU III includes the Rogue River and Klamath basin. The northern border of ESU III is demarcated at Cape Blanco, OR and marks a biogeographic break for many organisms. ESU II includes coastal mountain streams and the Umpqua drainage. ESU II and ESU I are basically separated at the Columbia River. However, the boundaries of ESU I are generalized in Fig. 3 because it varies for the above salmonid species. There are more ESUs for these salmon, but our study focuses on these three. These ESUs are based on genetic, life history, and ecogeographic data of the fishes. The trematode *Plagioporus shawi* infects all of the above salmonid species. Dispersal of *P. shawi* among freshwater rivers is likely dependent on its fish hosts because salmonid fishes are the most mobile hosts in the life cycle of *P. shawi* (Fig. 1). Therefore, if the salmonid ESUs demarcate genetic boundaries for the fishes, then we predict than the salmonid ESUs should also mark major genetic subdivisions for the parasite *P. shawi*. It should be noted that the mtDNA data from *P. shawi* (Fig. 3) do not support the ESU designations. However, mtDNA is a single genetic marker. To test this hypothesis, we sampled more populations within each ESU and genotyped parasites at 9 microsatellite loci (Fig. 4). Preliminary data show unique microsatellite alleles for populations of *P. shawi* above and below the Cape Blanco split (between ESU II and ESU III) and thus, support the unique biogeographic history of this region and salmonid ESUs.

FIGURE 4



Electropherogram of three microsatellite loci from a single parasite. Microsatellites are segments of DNA that have repeat sequences (e.g., GATAGATA…). Individuals that vary in their repeat number for the same locus have different alleles. For example, this individual is a homozygote for the blue locus (109/109), and a heterozygote at the green (76/104) and black (170/182) loci. The red lane is a size standard. If there is subdivision among subpopulations, individuals from the same population will have similar alleles among the loci and subpopulations will differ in their allele frequencies.

STUDY 3-In progress

Pacific salmonids have freshwater distributions in the United States, Canada, and Russia. Because Pacific salmon are commercially important, each country would like to conserve their stocks. Thus, it is important to be able to identify the freshwater origins of sea-caught salmon. The fluke *Nanophyetus salmincola* has been used as a biological tag to indicate the freshwater origin of steelhead trout. The distribution of *N. salmincola* is restricted to Washington, Oregon, and northern California. Thus, the presence of this parasite in a fish indicates a United States origin. We would like to extend this concept to the level of the parasite's genetics in order to get a more precise location of origin. However, *N. salmincola* shows too much gene flow to make this feasible. Again, we focus this study on *P. shawi* because the mtDNA data (Fig. 3, Table 1) show high genetic subdivision. In this study, we will genotype both *P. shawi* and steelhead from four populations within ESU II. Because the steelhead salmon are from the same ESU, we expect little genetic separation among the populations. We will test to see if genetic data from *P. shawi* can assign individual steelhead back to their stream of capture with higher probability than the genetic data from the salmon populations. This study is important because it may indicate that more precise origins can be found than when using the fish genetics alone. Additionally, the concept and methods of this study will provide an illustrative example that could be applied to other host-parasite systems.

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