**Week 6: Population Genetics**

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| **16 Groups** | **74+ participants** |

**Summary:** Groups discussed papers that examined how coalescent theory (Eldon and Wakely 2006, *Genetics*) and how continuous vs. discrete spatial distributions (Bradburd et al. 2018, *Genetics*) affect genetic structure and differentiation.

**1.** **What are the implications for sweepstakes reproduction on how we model evolutionary processes in the ocean?**

* (SR) acts as a genetic bottleneck and can reduce genetic variation, increase relatedness, and produce more rare variants compared to expected genetic variation if each individual contributed to next generation, each of which may affect adaptive dynamics.
  + Increases amount of variability in number of viable offspring/recruits, which increases odds of multiple mergers in coalescent process.
  + If non-random (i.e., success is selected), could aid in local adaptation in short term, but reduced genetic variability could hamper adaptation in long term.
* SR violates assumptions of evolutionary processes and can produce bias in classical models
  + Wright-Fisher model is often used but assumes small variance in number of offspring and no SR, can also estimate inaccurately low effective population size. Also usually assume equal numbers of offspring and discrete populations.
  + Multiple mergers can lead to star phylogenies and violated neutrality tests, which is usually interpreted as population expansion, selective sweep, or purifying selection, but may not be.

**2. Given the complexity of marine dispersal dynamics, do you think we as a field should adopt Bradburd et al. approach for characterizing population structure?**

* While the Bradburd approach is useful framework for analyzing population structure in species with isolation by distance, it is not a universal panacea.
  + Maybe good to form hypotheses for populations whose structure is not known
  + Useful in finding population structure in systems shaped by clines, as models have both spatially explicit and non-spatial options.
  + Investigating multiple K’s can help identify large scale vs. small scale processes
  + Perhaps best if used in conjunction with other models.
* Assumptions of model are fairly rigid and may not be flexible enough for marine diversity, as spatial components of marine systems can be case specific.
  + Requires subjective assumptions which may limit generality of results.
    - Unsure whether bias affects applicability to real systems
  + Geographic distance correlated with dispersal, but this does not apply to many marine organisms (e.g., pelagic species with large ranges)
  + Model may not work with temporal congregations (e.g., breeding) or invasive populations
  + May not apply for chaotic patchiness across habitats
  + Physical properties like currents and geographic barriers should be taken into account

**3. Given the potential for high variance in reproductive success, overlapping generations, and a combination of continuous and discrete population structure, how should we sample for population studies? (Across space and cohorts)**

* Sampling scheme is critical and depends on species, environment, and question. The more knowledge about system, the more appropriate sampling design can be implemented.
  + To reduce bias, sampling designs should encapsulate spatial and temporal scales.
    - Fine temporal sampling given overlapping generations, short lived organisms, seasonality, temporal structure)
    - Fine spatial sampling around geographic breaks or microgeographic adaptation
    - If interested in rare alleles (as expected with SR or coalescence back to MRCA), need to sample extensively to increase likelihood of capturing.
  + Important to characterize underlying variance structures in data

**Key Unknowns:**

* Can we come up with optimal sampling guidelines, if sampling is dependent on question and system?