Mathematical Biology of Plant Diversity

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https://gregconradismith.github.io/

My collaboration with Josh Puzey at William & Mary combines mathematical modelling, statistical analysis and evolutionary genomics to investigate how genetic variation produces biological diversity. Monkeyflowers (Mimulus) provide a common experimental system for work spanning floral pigmentation, hybridization, genome duplication and gene regulation. Our joint publications connect mechanistic explanations of development with quantitative methods for interpreting genomic data.

Flower pigmentation and the origins of new patterns

Our 2021 collaboration with Arielle Cooley and colleagues identified MYB5a/NEGAN as a regulator of petal anthocyanin pigmentation. Genetic mapping, expression analysis and experimental manipulation linked this transcription factor to pigment production and showed that altering its expression affects the wider regulatory network.[1] Building on this biological framework, our 2023 study with Emily Simmons and Cooley developed a multigenerational Turing model that explicitly represents diploid inheritance in an activator–inhibitor gene network. The model reproduces the emergence of spotted hybrid offspring from parents with unpatterned petals, as well as variation in later generations. It offers a plausible mechanistic explanation for how combining parental alleles can yield new spatial patterns, and generates hypotheses for experimental testing.[2]

Hybrid genomes, gene expression and reproductive barriers

Our 2017 collaborative study showed that subgenome expression dominance can appear immediately in first-generation Mimulus hybrids, with stronger bias in a naturally established allopolyploid lineage.[3] In 2019, we developed a likelihood ratio test for changes in the relative expression of corresponding parental gene copies (homeologs) across conditions. Applied to leaf and petal RNA-seq data, the method helps distinguish shifts in the balance between gene copies from overall changes in expression.[4] Our 2021 work on hybrid seed development linked cross-direction-dependent seed failure to abnormal endosperm development and divergent epigenetic and imprinting states, illuminating an early barrier to hybridization.[5]

Population genetics of mobile DNA

In 2022, Ronald Smith, Puzey and I investigated why transposable-element counts vary so widely among individuals. Data from monkeyflowers and fruit flies showed variance far exceeding the mean. We developed a stochastic population-genetic model using a birth–death master equation and moment analysis. The results identified copy-and-paste proliferation, especially when proliferation and excision are nearly balanced, as a plausible source of this overdispersion; selection against total element load alone was unlikely to explain it.[6]

Selected joint publications

1. Zheng X et al. (2021). The regulatory network for petal anthocyanin pigmentation is shaped by the MYB5a/NEGAN transcription factor in Mimulus. Genetics 217:iyaa036. doi:10.1093/genetics/iyaa036.

2. Simmons ESG, Cooley AM, Puzey JR, Conradi Smith GD (2023). A multigenerational Turing model reproduces transgressive petal spot phenotypes in hybrid Mimulus. Bull Math Biol 85:120. doi:10.1007/s11538-023-01223-7.

3. Edger PP et al. (2017). Subgenome dominance in an interspecific hybrid, synthetic allopolyploid, and a 140-year-old naturally established neo-allopolyploid monkeyflower. Plant Cell 29:2150–2167. doi:10.1105/tpc.17.00010.

4. Smith RD, Kinser TJ, Conradi Smith GD, Puzey JR (2019). A likelihood ratio test for changes in homeolog expression bias. BMC Bioinformatics 20:149. doi:10.1186/s12859-019-2709-5.

5. Kinser TJ et al. (2021). Endosperm-based incompatibilities in hybrid monkeyflowers. Plant Cell 33:2235–2257. doi:10.1093/plcell/koab117.

6. Smith RD, Puzey JR, Conradi Smith GD (2022). Population genetics of transposable element load: a mechanistic account of observed overdispersion. PLOS ONE 17:e0270839. doi:10.1371/journal.pone.0270839.

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