Genomics and Bioinformatics Illuminate Speciation Patterns and Processes throughout Arid North America

A Works in the Works presentation by Dr. Christopher Blair, February 26, 2026

Despite their morphological differences, English mastiffs and Pomeranians are still *canis lupus familiaris*. What is it, then, which would constitute a speciation event? How gradually or suddenly does it happen, and how do changes in habitat correspond to divergences?

On February 26 Dr. Christopher Blair from the NYC College of Technology Biology Department/CUNY Graduate Center gave a talk about the mystery of speciation. Blair showed phylogenic trees or cladograms, with diagonal lines to the right unbreaking and perpendicular offshoots to the left signifying turtles, tuataras, etc. Monophyly trees showed a trait inherited from a common ancestor such as a red beak or an amniotic egg. Paraphyly trees showed a common ancestor and some (but not all) of its descendant lineages. Multicolored lines showed gene trees within species trees, leading to a photo of Blair or one of his monophyletic relatives, the chimp, gorilla and orangutan. Speciation events were indicated by the vertex of 45° forks in the road.

Blair's field is phylogeography, at the crossroads of molecular genetics, population genetics, phylogenetics, and historical geography. This field is tasked with the modest goal of figuring out *which* species branched out *when*. Massive genomic datasets show the interplay of geography and gene mutation leading to diverging lineages. Familiar maps onscreen show topographic barriers to genetic mingling, like rivers and mountain ranges.

As an example, Dr. Blair considered Phrynosomatidae, a family of spiny lizards, which has 9 genera and 148 species, including Sagebrush, Texas-Horned and Greater Earless lizards. At this point the talk pivoted to Blair and colleagues' work in genome sequencing. The GBS (genotyping by sequencing) flowchart showed DNA digested by restriction enzymes, followed by ligation of adapters, barcodes and primers. Next, gene targets are amplified, pooled and quantified, followed by next-generation sequencing (NGS) and alignment to a reference genome. Data is extracted as Single Nucleotide Polymorphisms (SNPs) and Presence/Absence Variations (PAVs). The nested acronyms show we are into the proverbial weeds, but Blair pays his audience a compliment with his confidence in our extremophilic fitness (surviving in harsher terrains of technicality!)

The takeaway message is that genomics and bioinformatics "uncover cryptic diversity across spatial and temporal scales." The research shows that speciation is bound up with space, place, and time spans, reaching back to another geological age. The matter of species delimitation, however, remains a subject of controversy, with differing views on what even constitutes a species. Blair's last slide shows this is NSF and PSC-CUNY funded research and he credits many biologist collaborators, City Tech postdocs and undergrad researchers: An evidently diverse gene pool fit for a deep dive.

Review by David Lee