Blind fish provide big insights

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Cavefish exhibit distinct behavioral (e.g. reduced sleep, reduced aggression), metabolic (e.g. increased fat stores), and phenotypic (e.g. reduced eyes, reduced pigment) traits despite gene flow with surface fish. Mexican tetras have also evolved cave-associated phenotypes multiple times and consist of two major lineages ("new" and "old") that like diverged 1-4 mya. The genetic underpinnings of many cave-associated traits are different among cave populations even within the new and old lineages, and we are examining divergent outlier loci between cave and surface fish within caves among these lineages to infer commonalities about the evolutionary process across multiple origins of the cave phenotype. To address these goals, we generated whole genome resequencing data from three cave populations and two surface populations, including surface and cavefish populations from both the new and old lineages. We also sequenced a closely related congener A. aeneus to serve as outgroups for polarizing changes in the A. mexicanus cavefish. In total, we have 45 resequenced genomes (7.3x-19x per individual aligned to the reference genome), and have thoroughly explored the relationships between populations, revealing extensive gene flow between new and old cavefish lineages, while the surface fish lineages remain distinct. This gene flow shapes how we interpret adaptation to the cave environment, and the interpretation of outlier loci, and will provide fruitful avenues for future research into gene-flow mediated adaptation.