Homing In On the Genetic Basis of Adaptive Pigmentation Differences in a New Vertebrate Model System

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A dazzling pallet of pigmentation is one of the most obvious features of life's diversity on Earth. Animal survival and reproduction depend on pigment patterns deployed for blending into surroundings, warning predators, dominating rivals and impressing potential mates. Variation in melanization among human populations is thought to reflect trade-offs between protecting against folic acid depletion and skin cancer, and producing essential forms of vitamin D. Given the importance of pigmentation, it is not surprising that scientists have already started investigating its genetic basis in a number of different models. In some cases (*e.g.*, domestic cats and zebrafish), pigment pattern types useful for genetic research have been generated by artificial selection or derived from laboratory mutants. Yet work on domesticated models provides limited insight for fully understanding the genetics of pigmentation in free-ranging natural populations. In a few systems (*e.g.*, beach mice), scientists have made advances in understanding the genetics of pigmentation in the wild, but such cases involve uniform changes in pigmentation with a very simple underlying genetic basis. Lacking are genetic investigations of complex, repeating patterns – stripes, spots and the like – which are often critical to adaptation in natural populations.

Combining geographic comparisons of pigmentation in threespine stickleback fish (across the Pacific Northwest) with genetic research in the laboratory, first author Dr. Anna Greenwood and senior author Dr. Katie Peichel (both in the Human Biology Division) help to fill this void in pigmentation research. Greenwood *et al.* quantitatively demonstrate that laboratory-raised sticklebacks from marine populations lack bars and are uniform in color, whereas sticklebacks from nearly every freshwater population are adorned with distinctive bars of melanin pigment. Replicate, parallel divergence of this kind is a hallmark of natural selection for adaptation to different environments: silvery, uniformly pigmented saltwater sticklebacks are well equipped to hide from predators in open marine environments, while barred freshwater sticklebacks blend into the weedy habitats of lakes and streams. Greenwood and Peichel also artificially crossed a marine stickleback to a freshwater stickleback; they then detected statistical associations in the second generation hybrid offspring between aspects of pigmentation and polymorphic genetic markers scattered across the genome. Using this approach, they found genomic regions on stickleback chromosome 1 and chromosome 6 which affect either the degree of barring or the darkness of pigment cells within individual bars; this, they speculated, could be similar to a two gene system underlying stripes in tabby cats. Intriguingly, the genomic regions that Greenwood and Peichel identified were found to contain candidate genes accounting for similar variation in other vertebrates, such as the *Gja5* gene that determines the *leopard* pigmentation variety of zebrafish. The authors' work shows that adaptive differences in repeating pigmentation patterns may arise due to multiple genes acting together to produce variation in a complex trait. Their work also establishes a new vertebrate model for pigmentation studies in the Pacific Northwest, which should allow local researchers to start linking newly discovered genes, and genes already known from domesticated vertebrates, to the variation in pigmentation seen in natural populations.

Greenwood AK, Jones FC, Chan YF, Brady SD, Absher DM, Grimwood J, Schmutz J, Myers RM, Kingsley DM, Peichel CL. 2011. The genetic basis of divergent pigment patterns in juvenile threespine sticklebacks. *Heredity* 107:155-66.

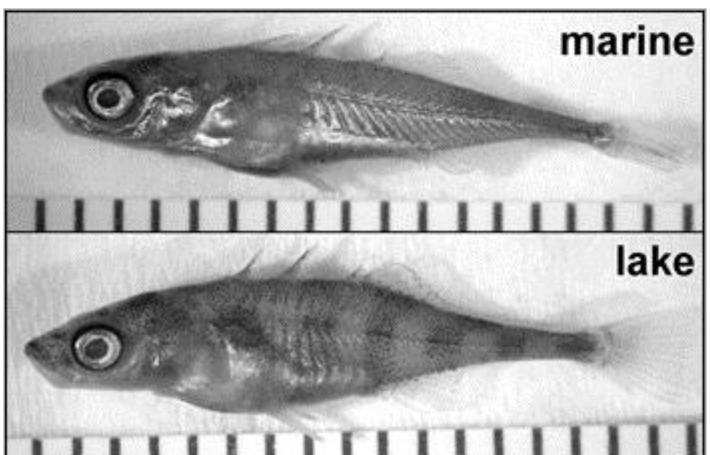

Image courtesy of Anna Greenwood

Juvenile sticklebacks from marine and lake environments exhibit divergent pigment patterns.