Melanic Coat Color Variation in Rock Pocket Mice (Chaetodius intermedius)

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Coat color variation in small mammals is a classic example of phenotypic variation in response to selection in different environments (Hoekstra and Nachman, 2005); many species closely match the color of the substrate in which they live. Examples of intraspecific color variation in rodents include the canyon mouse (Peromyscus crinitus), the deer field mouse (Peromyscus maniculatus), and the rock pocket mouse (Chaetodius intermedius) (Hoekstra and Nachman, 2005). The rock pocket mouse is one of the most studied models for phenotypic color variation.

Many studies have found coat color variation in the rock pocket mouse in deserts of the southwestern states (Nachman, Hoekstra, and D’Agostino, 2005). Authors have showed that C. intermedius coat color matched the color of the rocks on which the mice live (Nachman, Hoekstra, and D’Agostino, 2005). Several studies have found that most light-colored mice live on light-colored rocks, but in several geographic regions, they are melanic (black or brown) and live on dark-colored basalt lava (Hoekstra and Nachman, 2003; Hoekstra, Drumm, and Nachman, 2004). Furthermore, the pocket mice on volcanic lava with dark coats do not have banded hairs, whereas mice from nearby light-colored granitic rocks have light coats that do have banded hairs. This color polymorphism is a presumed adaptation to avoid predation from avian and mammalian predators (Nachman, Hoekstra, and D’Agostino, 2005). Rock pocket mice provide a useful system for studying the genetics of adaptation. Genetics seem to play a role in that their coat color typically matches the color of the rocks on which they live (Hoekstra and Nachman, 2003; Hoekstra, Drumm, and Nachman, 2004).

The main questions that this story brings to focus are: 1) is this coat color variation a consequence of natural selection; and 2) if there is variation in more than one area or region, are these caused by the same gene of not? This paper will explore coat coloration in pocket mice based on the work of evolutionary biologist Hopi Hoekstra. Authors have suggested that phenotypic variation is due to natural selection and that variation in multiple regions is caused by a few interacting genes.

Hoekstra received her B.A. in Integrative Biology from UC Berkeley. She then completed her Ph.D. in Zoology in 2000 as a Howard Hughes Predoctoral Fellow at the University of Washington. Hoekstra then moved to the University of Arizona as a NIH Postdoctoral Fellow where she studied the genetic basis of adaptive melanism in pocket mice. In 2003, she became an Assistant Professor at the University of California San Diego. Just recently, she moved to Harvard University, where she is the John L. Loeb Associate Professor of Biology in the Department of Organismic and Evolutionary Biology and the Curator of Mammals at the Museum of Comparative Zoology (Hoekstra home page). Pocket mice are the primary model organism for Hoekstra’s lab.

Pocket mice inhabit rocky areas and desert scrub at low elevations in the southwestern deserts of North America. Typically, they range from southern Utah through Arizona, New Mexico, and Texas (Hoekstra and Nachman, 2005). C. intermedius are nocturnal mammals and decrease activity from November through February. Young mice are born naked and typically attain their first coat at two to three weeks (Hoekstra and Nachman, 2005); the first coat is generally thinner and duller than the adult coats. Although there are no direct studies of pocket mice predators, it is well established that they are preyed upon by owls, snakes, and mammalian carnivores (Hoekstra and Nachman, 2005). Throughout most of their range, pocket mice have sandy dorsal coats with white tails, but the dorsum are banded, and the ventral hairs are light colored.

When I asked Hoekstra why they use wild rodents as their model organism in the lab in an email interview, these were the answers that she provided: “(1) they are closely related to model organisms like lab mice and rats, which have a plethora of genomic tools, (2) they can be brought into captivity and bred, (3) they can be easily caught in the wild with decent sample sizes, (4) there is a wealth of natural histories dating back to the early 1900’s describing geographic variation in Peromyscus, and (5) because they are wide-ranging across North America, there are many instances of local adaptation” (2009). Despite the fact that many populations have similar light-colored coats, many populations of rock pocket mice have been described as nearly black or melanic (Hoekstra and Nachman, 2005).

The different color landscapes, with ancient volcanic lava flows, created a patchwork of light, sandy habitats and dark lava habitats. The four lava flows studied in most Hoekstra studies include the Pinacate, Armendaris, Kenzin, and Carrizoza lava flows. The Pinacate lava flow is the oldest of the four, approximately 1,700,000 years old; whereas the Carrizoza flow is the youngest, only 1,000 years old (Hoekstra and Nachman, 2005). The Pinacate landscape is the most sampled lava bed because it is assumed to be the oldest; it is situated in northern Sonora, Mexico, and the adjacent Cabeza Prieta national Wildlife Refuge in southern Arizona (Hoekstra and Nachman, 2005). This lava flow has many rocky areas that are disjunct due to the accumulation of intervening deposits of sand (Nachman, Hoekstra, and D’Agostino, 2005). In this region, and in the other three sites, most of the mice captured on the dark rock (lava beds) are found to be melanic and most of the mice caught on the light rock are light-colored (Hoekstra and Nachman, 2005). Geographically proximate populations tend to be closely related and share morphological similarities, but they can vary significantly in coat color. Correlations between coat color and substrate can be demonstrated by quantifying light reflectance of dorsal hairs and the surrounding substrate (Hoekstra and Nachman, 2005).

Furthermore, there appears to be a correlation between the number of mice living on the flow in 2003, 225 mice were found on the Pinacate flow, whereas only 12 mice were found on the Carrizoza lava flow (Hoekstra and Nachman, 2005). This study suggests that more mice live on the older lava flows, whereas fewer mice live on more recent lava flows (Hoekstra and Nachman, 2005). Perhaps this is because mice have become better adapted to their environment over time and have thus been able to better survive in their habitats. Furthermore, the mice may not have adapted as well to the newer lava beds. Is coat color variation to match substrate an adaptation that rock pocket mice have evolved over time?
The first question that needs to be addressed in the story of these pocket mice is whether or not the coat color variation in the Pinacate rotor is due to natural selection. Natural selection, in the strict sense, is the process in which favorable heritable traits become more common in successive generations of a population. Furthermore, it is a process of adapting to the environment. Natural selection acts on the phenotype so that individuals with favorable phenotypes are more likely to survive and reproduce than those with less favorable phenotypes; this action occurs through mutations and changes in a species' genotype. Pocket mice are presumed to be driven by natural selection for crypsis, or camouflage, because their natural predators are visual hunters (Hoekstra, Hirschmann, Bundey, et al., 2006). Melanism is one form of concealing coloration from on looking predators; melanin is controlled through genetics (Hoekstra, Drumm, and Nachman, 2004). Natural selection on phenotypes leads to evolutionary change at the genetic level via mutation and the spread of favorable alleles.

Hoekstra and her lab did not conduct direct studies of relative survival of pocket mice with different coloration on different substrates. Instead, the introductions of most of her papers just cite the very close match of color on non-muscle tissue to the color of substrate and assume selection is motivated by pressure from owls. She assumes this through literature in which results of phenotypes from natural selection were apparent. Earlier studies by Dice and Blossom (1937; as cited by Hoekstra and Nachman, 2005) clearly demonstrated that owls discriminate between mice that do and do not match the color of their substrate (2005). Mismatched mice experience a higher risk of predation by owls and are therefore less likely to survive and reproduce. Thus, mice that match their substrate are less visible to predators and have a better chance for survival. Because owls presumably eat mismatched mice rather quickly, this leads to a difference in allele and phenotype frequency between light and dark habitats. Thus, owls appear to exert strong selection on coat color in pocket mice, and differences in coat color are an adaptation by pocket mice for crypsis (Nachman, Hoekstra, and D’Agostino, 2003). Adaptive differences in coat color between habitats imply that there must be a genetic difference between the phenotypes. What is responsible for the adaptive color polymorphism observed in C. intermedia?

Specific genes are now known to cause the coat color variation in rock pocket mice. In order to determine if these genes are related to the coat color variation in pocket mice, the Hoekstra lab has constructed a genetic linkage map for C. intermedia (Hoekstra and Nachman, 2005). The SNPs are then surveyed in the Pinacate population. These methods resulted in a strong correlation between substrate color and coat color for the dominant mutation. Thus, the rock pocket mice that are dark must be a result of a recessive mutation at the Agouti loci. The recessive mutation results in black phenotypes because Mc1r is the dominant allele (Hoekstra and Nachman, 2005). The opposite relationship is true with the Mc1r gene. The recessive mutation leads to light or yellow phenotypes, since phaeomelanin is produced, which is responsible for light coloration (Hoekstra and Nachman, 2003). The Agouti antagonist negates the action of Mc1r. Once full of melanin, eumelanosomes and phaeomelanosomes are secreted from the melanocyte as pigment granules (Hoekstra and Nachman, 2005). Thus, the interaction of these two genes plays a major role in determining the pigmentation patterns on coat hairs of pocket mice.

Mutations at the Agouti and Mc1r loci produce a range of phenotypes from dark to light color (Hoekstra and Nachman, 2005). These loci are fixed positions on a chromosome that are occupied by specific genes; they are the genetic underpinnings that contain the complex codes and pathways involved in pigment production. Dominant Agouti mutations result in increased Agouti expression and largely light phenotypes. On the other hand, the recessive mutation results in black phenotypes because Mc1r is the dominant allele (Hoekstra and Nachman, 2005). The opposite relationship is true with the Mc1r gene. The recessive mutation leads to light or pink phenotypes, since melanosomes are secreted from the melanocyte as pigment granules (Hoekstra and Nachman, 2005). The opposite relationship is true with the Mc1r gene. The recessive mutation leads to black phenotypes. Thus, the rock pocket mice in the Pinacate population are dark because the dominant mutation leads to black phenotypes. The rock pocket mice that are dark must be a result of a recessive mutation at the Agouti loci and a dominant mutation at the Mc1r loci (Hoekstra and Nachman, 2005). Deposition of pigment occurs during the hair growth cycle (Hoekstra and Nachman, 2005).

The Hoekstra lab has previously used a candidate-gene approach to identify the genes underlying color variation in the rock pocket mouse. The strategy behind this method is to develop single-nucleotide-polymorphism (SNP) markers for each candidate gene. A SNP is a single base difference in the sequence of a gene which alters the structure and function of the gene product (Hoekstra and Nachman, 2005). The SNPs are then surveyed in populations of light and dark mice. If a strong association between SNP variants and coat color phenotype was found, the lab sequenced the entire gene in light and dark individuals and tested for other markers. The Hoekstra lab used the SNP method in one particular population, the Pinacate population. These methods resulted in a strong correlation between substrate color and coat color for the dominant mutations in the Mc1r SNPs gene, but they showed no correlation with the Agouti SNPs in the Pinacate population (Hoekstra and Nachman, 2005). This finding led to the
characterization of the entire Mc1r gene in pocket mice. Four charge-changing amino acid polymorphisms in Mc1r are prevalent in beach mice populations (Nachman, 2003). The four mutations are at amino acid numbers 18, 109, 160, and 233 (Nachman, Hoekstra, and D’Agostino, 2003). Mice with one or two copies of the melanic allele are melanic, while mice without this allele are light; dark alleles are dominant over light alleles (Hoekstra and Nachman, 2005). This led to the question of whether or not similar melanic phenotypes arise independently in rock pocket populations on different lava flows and if these phenotypic changes occur through changes in the same or different genes and at the same or different mutations.

Melinic phenotypes are believed to evolve independently. In a 2003 study, the same four mutations in Mc1r seemed to be responsible for the adaptive melanism in the dark phenotype of Pinacate pocket mice (Nachman, Hoekstra, and D’Agostino, 2003). However, interestingly enough, the melanin Armendaris population showed no association with Mc1r mutations, indicating that adaptive dark color has evolved independently in this species through changes at different genes. The genes causing the melanin differentiation in the Armendaris population have yet to be identified. This is a big finding in the Hoekstra lab because they now know that phenotypes evolve independently and they can now look for different primary genes causing melanin coat colors besides Mc1r, if there are any.

Let’s add a twist to the story. Pocket mice are not the only mice to show color polymorphisms; old-field mice and beach mice show similar adaptations. The mainland subspecies, an old-field mouse, has a cryptic dark brown dorsal coat. The younger beach-dwelling subspecies, called the beach mouse, has a lighter coat produced by natural selection for camouflage on pale coastal sand dunes (Steiner, Weber, and Hoekstra, 2007). In beach mice and old-field mice, are coat color differences dependent on the same genes as pocket mice?

Beach mice comprise eight subspecies of the old-field mouse. The eight subspecies include five on the Gulf Coast and three (historically) on the Atlantic Coast (Steiner, et al., 2008). In a recent study (2007), Hoekstra and her lab found results indicating that coat color differences are dependent on the same genes as pocket mice. They used genome-wide linkage mapping in order to find the gene in which a mutation is located; in order to do this, they needed to use fine-scale SNPs analysis. Using genome-wide linkage mapping, they identified three regions associated with differences in pigmentation traits in beach mice and old-field mice (Steiner, Weber, and Hoekstra, 2007). Mc1r and its antagonist, Agouti, map two independent regions that together are responsible for most of the pigment differentiations between the subspecies.

Are these the only genes causing the phenotypes? In another recent study, Hoekstra analyzed mechanisms underlying convergent pigment pattern among subspecies of beach mouse inhabiting the Gulf and Atlantic coasts of Florida (Steiner, Rompler, Boettger, Schoneberg, and Hoekstra, 2009). After measuring color pattern in eight beach mouse subspecies, Steiner, et al. showed that three of the Gulf Coast subspecies are more phenotypically similar to an Atlantic coast subspecies than to their Gulf Coast neighbors (2009). However, light-colored beach mice do not form a monophyletic group, a group of organisms descended from a common ancestor (Steiner, Rompler, et al., 2009). Previous studies indicated that a mutation in Mc1r was the major contributor to pigment pattern in the Gulf Coast mice. However, despite their color similarities, the Mc1r allele was not found in the Atlantic coast mouse populations. Atlantic coast mice have high levels of Mc1r but lack unique alleles (Steiner, Rompler, et al., 2009). Different populations of pale mice appear to be pale because of differing genetic mechanisms. Mc1r and Agouti are together responsible for most, but not all, of coat color (Hoekstra and Nachman, 2003). The four mutations are at amino acid numbers 18, 109, 160, and 233 (Nachman, Hoekstra, and D’Agostino, 2003). Mice with one or two copies of the melanin allele are melanic, while mice without this allele are light; dark alleles are dominant over light alleles (Hoekstra and Nachman, 2005). This led to the question of whether or not similar melanic phenotypes arise independently in rock pocket populations on different lava flows and if these phenotypic changes occur through changes in the same or different genes and at the same or different mutations.

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References


