Melanism in Peromyscus Is Caused by Independent Mutations in Agouti

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Melanism in *Peromyscus* Is Caused by Independent Mutations in *Agouti*

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Abstract

Identifying the molecular basis of phenotypes that have evolved independently can provide insight into the ways genetic and developmental constraints influence the maintenance of phenotypic diversity. Melanistic (darkly pigmented) phenotypes in mammals provide a potent system in which to study the genetic basis of naturally occurring mutant phenotypes because melanism occurs in many mammals, and the mammalian pigmentation pathway is well understood. Spontaneous alleles of a few key pigmentation loci are known to cause melanism in domestic or laboratory populations of mammals, but in natural populations, mutations at one gene, the melanocortin-1 receptor (*Mc1r*), have been implicated in the vast majority of cases, possibly due to its minimal pleiotropic effects. To investigate whether mutations in this or other genes cause melanism in the wild, we investigated the genetic basis of melanism in the rodent genus *Peromyscus*, in which melanistic mice have been reported in several populations. We focused on two genes known to cause melanism in other taxa, *Mc1r* and its antagonist, the agouti signaling protein (*Agouti*). While variation in the *Mc1r* coding region does not correlate with melanism in any population, in a New Hampshire population, we find that a 125-kb deletion, which includes the upstream regulatory region and exons 1 and 2 of *Agouti*, results in a loss of *Agouti* expression and is perfectly associated with melanistic color. In a second population from Alaska, we find that a premature stop codon in exon 3 of *Agouti* is associated with a similar melanistic phenotype. These results show that melanism has evolved independently in these populations through mutations in the same gene, and suggest that melanism produced by mutations in genes other than *Mc1r* may be more common than previously thought.


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Introduction

From complex patterns, like the stripes of a tiger, to the simple changes in the presence/absence of pigment, as in arctic hares, the diversity in mammalian pigmentation is vast [1]. But in addition to diversity among species, there is often appreciable variation in pigmentation within species. Because members of the same species that differ in their pigmentation phenotype can be crossed, this within-species variation is amenable to traditional genetic analyses. In addition, the molecular genetic factors that regulate mammalian pigmentation are relatively well known [reviewed in 2–4], thus enabling the genetic bases of these phenotypes to be explored. Furthermore, a nontrivial advantage to studying pigmentation traits is that variation is often easily detectable by eye. Mutant phenotypes that affect the coloration of the entire body are especially conspicuous and are easily recognized by both captive breeders and field biologists. One such phenotype is dark pigmentation or melanism. It is clear that melanism has evolved many times in wide variety of animal taxa [5].

The genes that can cause darkening of coat color have been studied most thoroughly in the laboratory mouse. Although experimentally induced mutations in over 25 genes can produce dark fur in lab mice [6], spontaneous coat-darkening mutations have been reported in only four genes: the *Agouti* signaling protein (*Agouti*), attractin (*Atm*), melanocortin-1 receptor (*Mc1r*), and mahogunin (*Mgrn*) [7–10]. The protein products of three of these genes, *Mc1r*, *Atm*, and *Atm*, interact at the surface of pigment-producing cells (melanocytes) and constitute the machinery responsible for “pigment type switching,” the ability of melanocytes to switch between the production of dark brown/black (eumelanin) and light yellow/red pigment (pheomelanin). *Mc1r* is a membrane-bound receptor that, when active, signals the melanocyte to produce eumelanin, whereas *Agouti* is a paracrine signaling protein that antagonizes *Mc1r*, causing the melanocyte to produce pheomelanin. Thus, mutations that cause either constitutive- or hyper-activation of *Mc1r* or loss-of-function of *Agouti* will result in a melanic phenotype. The functions of *Atm* and *Mgrn* are not as well understood, although *Atm* is thought to stabilize interactions between *Mc1r* and *Agouti* [11]. Here, we focus on *Mc1r* and *Agouti* because their interaction has been well characterized in the lab mouse and thus can be extended to the study of melanism in other taxa.

Melanic phenotypes have evolved both in nature and in captivity in a wide diversity of animals and in some cases their
Melanism in Peromyscus

The genetic basis has been identified. In captive vertebrates, spontaneous mutants of Agouti, Mc1r, Mgm, and Atn have all been found to cause melanism [e.g., 12,13,10,9]. In natural populations, however, mutations in Mc1r are most commonly associated with melanism [e.g., 12,14–16], although both Agouti and Atn are larger mutational targets. In addition, mutations in Agouti or Atn that reduce protein expression or activity lead to melanism; these knock-out mutations are certainly more likely to occur than the gain-of-function Mc1r mutations that cause melanism because there are more ways to “break” a gene than to “improve” a gene’s activity. Thus, it is unclear why Mc1r has repeatedly been shown to be associated with melanin in nature and a key question is: are melanism-inducing mutations in Agouti not found because they occur less often, or are they simply more difficult to detect?

To address this question, we studied melanism in the deer mouse, Peromyscus maniculatus (Figure 1). Melanism has been reported in several populations of Peromyscus; melanic individuals have been captured in a number of locations in North America, including New Hampshire [17], California [10], Michigan [P. Myers, pers. comm.], and Alaska [C. Conroy, pers. comm.]. Although it is unclear if these melanic phenotypes affect fitness, their repeated occurrence provides us with multiple comparisons of the same phenotype in the same genetic system (i.e. species).

Horner et al. [17] showed that, in mice from New Hampshire, melanism is caused by a recessive allele at a single locus. The authors suggested the locus might be Agouti, based on its similarity to the nonagouti phenotype in Mus. Here we uncover the molecular variation that causes melanism in P. maniculatus from New Hampshire and show that the Agouti gene is responsible. We also investigate the molecular basis of melanotic phenotypes from geographically distant populations of P. maniculatus and find that melanism has independently arisen at least three times and by different mutations in the same gene, Agouti, in two of those cases.

Results

Melanism caused by a single, recessive locus

The inheritance of the melanin phenotype in the New Hampshire strain of P. maniculatus was previously investigated by Horner et al. [17]. We confirmed their results with two crosses that clearly demonstrate that a single autosomal recessive allele is responsible for the melanin phenotype (Table S1).

Large deletion in Agouti associated with melanism

To determine whether a mutation(s) in the Agouti locus is associated with melanism, we genotyped the 49 offspring of an A’/a × A’/a cross. We found a perfect association between successful amplification of exon 2 and phenotype: we always produced an exon 2 product of the expected size in wild type individuals (A’/a, N = 34) but never in melanic (a/a, N = 15) individuals. In addition, while we amplified all the Agouti exons (untranslated 1A, 1A’, 1B, 1C and translated 2–4) in all wild type offspring, we were able to amplify only exons 3 and 4 from melanistic mice. By contrast, we did not find any amino acid differences between wild type and melanic individuals in the entire Mc1r coding region. These results strongly suggest, first, that melanism is caused by variation at the Agouti locus and second, that a large deletion in Agouti may be responsible for the melanic phenotype.

Large deletion in Agouti associated with melanism

To determine, if there was a deletion in the a’ allele and if so, its size, we used genome-walking PCR to sequence upstream (5′) of exon 3. We found that sequence identity between the wild type BAC sequence and the melanic Agouti allele extends about 1.3 kb 5′ of exon 3. Thereafter, the melanic Agouti allele sequence is identical to the sequence 125 kb upstream in the wild type BAC (Figure 2). Thus, melanic P. maniculatus are homozygous for an allele with a large 125 kb deletion (A’2125kb), which eliminates the main regulatory region, the noncoding exons 1A, 1A’, 1B, 1C, and coding exon 2.

Figure 1. Pigmentation phenotypes of P. maniculatus. (A) Typical wild type individual, dorsal hairs are banded (containing both phaeomelanin and eumelanin) and ventral hairs are white with a light grey base. This phenotype is dominant to the melanic phenotype. (B) Melanic individual with completely eumelanin hairs. These mice were captured in Hubbard Brook Experimental Forest, NH. doi:10.1371/journal.pone.0006435.g001
To test whether this 125 kb deletion affects the abundance of Agouti transcript, we measured Agouti mRNA in the skin of P4 pups. In animals heterozygous for the wild type and the \(a^{125kb}\) alleles, levels of Agouti expression were significantly higher than those of animals homozygous for \(a^{125kb}\) (Figure 3A). These data show that the \(a^{125kb}\) allele produces significantly less Agouti mRNA transcript and is thus likely the cause of melanism. \(Mc1r\) transcript levels, on the other hand, were not significantly different between melanic and wild type individuals (Figure 3B). In addition, we performed in situ hybridizations on 12.5 day-old embryos to determine whether Agouti is expressed in melanic embryos. At this stage, wild type embryos express Agouti in the whisker plate and in parts of the limbs (Figure 3C), an expression pattern similar to that seen in Mus [20]. We did not detect any Agouti expression in melanic embryos (Figure 3D).

### Molecular basis of melanism in Alaskan mice

To determine if the same gene and same mutation was responsible for melanism in other populations of \(P. maniculatus\), we sequenced both \(Mc1r\) and \(Agouti\) in melanic and wild type mice from an additional population. First, we sequenced \(Mc1r\) in melanic (\(N = 2\)) and non-melanic (\(N = 4\)) \(P. maniculatus\) from Alaska and found four amino acid polymorphisms segregating in the sample (Figure 4). None of these polymorphisms likely cause the melanotic phenotype for several reasons: (1) none of these mutations overlap with any previously described darkening mutations, (2) all four amino acids appear in other, non-melanic individuals from other populations of \(P. maniculatus\) (Figure 4), and (3) none of the polymorphisms correlate with the melanotic phenotype in this population.

In the same sample, we also sequenced the coding exons of \(Agouti\) and found one segregating amino acid polymorphism, a mutation at nucleotide position 193 (in exon 3) that results in a change from glutamine to a stop codon at amino acid position 65 (\(a^{Q65term}\)). This premature stop codon eliminates exon 4, which contains a cysteine-rich region that is integral to the function of the Agouti protein (Figure 4; [21,22]). Thus, this mutation very likely results in a non-functional protein. Individuals both homozygous and heterozygous for the \(a^{Q65term}\) allele had the wild type phenotype, consistent with the \(a^{Q65term}\) allele being recessive and its being a null allele. Though the small number of animals sampled does not allow us to rule out the involvement of other loci, these data strongly suggest that the \(a^{Q65term}\) allele is the cause of the melanotic phenotype in the Alaskan population.

Melanism also has been reported in a third population, \(P. m. gracilis\) from the upper peninsula of Michigan [P. Myers, pers. comm.]. We sequenced the complete coding regions of \(Agouti\) in a single melanic individual. The \(Agouti\) sequence possesses neither the \(a^{Q65term}\) nor the \(a^{125kb}\) mutation, nor does it contain any obvious melanism-causing mutations in \(Mc1r\), demonstrating a third independent origin of melanism in \(P. maniculatus\).

### Discussion

The results of our laboratory crosses confirmed that melanism in New Hampshire \(P. maniculatus\) is caused by a single, recessive allele. In laboratory mice, dominant melanism is usually caused by alleles of \(Mc1r\), while recessive melanism is usually caused by alleles of \(Agouti\). Consistent with this dominance hierarchy, we found that melanism in \(P. maniculatus\) is perfectly correlated with the presence of an allele (\(a^{125kb}\)) with a large deletion at the \(Agouti\) locus. When mice are homozygous for this allele, the abundance of \(Agouti\) transcript in the skin is significantly lower than that in individuals with a single copy of the wild type \(Agouti\) allele. This accords with the observation that the deleted region contains the 5’ untranslated regions that are important for temporal and spatial regulation of \(Agouti\) and probably any associated cis-regulatory information. The deletion also encompasses exon 2, which contains the start of the \(Agouti\) protein (amino acids 1–54). Together, this evidence strongly suggests that the \(a^{125kb}\) allele causes melanism in \(P. maniculatus\) from New Hampshire.

Sequencing of \(Agouti\) and \(Mc1r\) coding regions in melanic individuals from other geographic locations shows that melanism arose independently at least three times in \(P. maniculatus\). Melanic individuals from Shrubby Island, AK are homozygous for an allele (\(a^{Q65term}\) of \(Agouti\)) that contains a premature stop codon in exon 3. This mutation is predicted to result in a non-functional protein. Although we cannot rule out contributions of linked variation to the melanotic phenotypes possessed by mice from New Hampshire and Alaska, the likely effects of the \(A125kb\) and \(Q65term\) mutations and the conservation of the site of deletion in these species make it unlikely that they arose separately in these populations.

![Figure 2. Schematic and VISTA alignment of the Mc1r and Agouti loci in Mus, Rattus, and Peromyscus.](image-url)

- Dark blocks represent coding sequences; light blocks represent untranslated exons. \(Mc1r\) consists of a single exon that spans approximately 1.5 kb similar to its Mus ortholog. The \(Agouti\) locus spans over 100 kb. Grey arrows indicate a duplication present in all three taxa; brackets indicate the inversion of the duplicated region in \(P. maniculatus\). Asterisks mark the location of a conserved region that is necessary for \(Agouti\) expression (Y. Chen and G. S. Barsh, pers. comm.). The red line and red arrowhead mark the locations of the \(a^{125kb}\) deletion and the \(a^{Q65term}\) premature stop codon, respectively. The conservation plot was generated by aligning \(Peromyscus\) BAC sequence and sequence from the \(Rattus\) genome using LAGAN [75] and plotting conservation with mVISTA [76].

Typically, dominant mutations in \(Mc1r\) and \(Agouti\) result in a non-functional protein. Individuals both homozygous and heterozygous for the \(a^{125kb}\) allele have the wild type phenotype, consistent with the \(a^{Q65term}\) allele being recessive and its being a null allele. Though the small number of animals sampled does not allow us to rule out the involvement of other loci, these data strongly suggest that the \(a^{Q65term}\) allele is the cause of the melanotic phenotype in the Alaskan population.

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Figure 3. Agouti and Mc1r expression in wild type and melanic mice. (A, B) Relative expression of Agouti and Mc1r transcripts in dorsal skin of P4 P. maniculatus was measured by quantitative RT-PCR. Expression level of the target gene is standardized with that of β-actin. We compared relative expression levels of each gene with Student’s t-test (two-tailed, unequal variance). For each phenotype class, N = 5. (A) Agouti expression is significantly higher in the dorsal skin of wild type mice than in melanic mice; expression level in melanic mice is not significantly different from zero. (B) Mc1r expression in wild type and melanic mice does not significantly differ. Bars indicate standard error. (C,D) Lateral views of whole-mount in situ hybridizations for Agouti in E12.5 embryos. (C) Wild type embryos express Agouti in the whisker plate and the limbs (arrows). (D) Agouti expression is not detected in aD125 kb homozygote embryos.
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mutations and the known effects of null Agouti alleles in other taxa, it is very likely that these mutations represent the causative variation underlying these melanic phenotypes. The melanic individual from Michigan possesses neither the $a_{D125kb}$ allele nor the $a_{Q65term}$ allele; melanism in this population must be caused either by variation at another locus or possibly by unexamined variation at the Agouti or Mc1r loci.

This study presents two cases in which a specific molecular variant at the Agouti locus appears to cause melanism in a natural population. Mc1r mutants represent the vast majority of cases of melanism in natural populations of mammals, despite many occurrences of melanic Agouti mutants in captive and domestic stocks (Table 1). There are a number of possible explanations for this discrepancy.

One possible explanation involves dominance. Haldane [23] suggested that, when natural selection acts on new (i.e., rare) beneficial mutations, adaptation will be biased toward fixing dominant alleles, which are immediately visible to selection (but see [24]). Thus, we expect that when melanism is adaptive, we may see a prevalence of melanic Mc1r mutants. On the other hand, if melanism is deleterious and is being held at mutation-
Melanism in *Peromyscus*

selection equilibrium, we might expect melanism caused by mutations in *Agouti* if they are recessive. Thus, depending on environmental conditions, expectations regarding the fixation probabilities of *Mc1r* versus *Agouti* alleles are different. In *Peromyscus*, the melanic alleles in both populations described in this study were found at low frequencies – 3–7% assuming Hardy-Weinberg equilibrium ([17]; data not shown) – and there is no obvious association between melanism and environmental conditions as observed in other species (e.g., pocket mice; [25]), suggesting these alleles may not be adaptive. Thus, if melanic phenotypes are often fixed from new dominant mutations rather than standing genetic variation, this may explain the prevalence of melanism caused by *Mc1r*.

Second, if mutations in *Agouti* have greater negative pleiotropic effects than mutations in *Mc1r*, then we would expect to see more evolution in the latter. Having fewer negative pleiotropic consequences of mutations at a locus translates to less evolutionary constraint (or higher net selection coefficients). While deleterious effects may be tolerated when organisms are raised in captivity, they could have important fitness consequences in nature.

Whether differing amounts of pleiotropy of mutations at these loci affects the evolution of melanism is difficult to say, because mutations in both *Agouti* and *Mc1r* may affect traits other than pigmentation. Mutations in *Mc1r*, for example, have recently been discovered to have effects in the nervous system [26]. Pleiotropy is especially well documented in *Agouti*: ectopic expression of *Agouti* in *Mus* can result in obesity and lethality [27,28] and null mutants in *Rattus* and *Peromyscus* exhibit behavioral differences [29,30]. But pleiotropic consequences may be mitigated by the precise type and location of mutations. It has been predicted that for any given

### Table 1. Spontaneous alleles causing melanic phenotypes in mammals and birds.

<table>
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<tr>
<th>gene</th>
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<td>F118S</td>
<td>[59]</td>
</tr>
<tr>
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<td>a</td>
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<td>11 kb insertion in intron 1</td>
<td>[7]</td>
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<td>166 bp deletion of entire exon 2</td>
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<td>5 kb insertion in intron 11</td>
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<td>5 kb insertion in intron 12</td>
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<td>8 kb insertion in intron 2</td>
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<td>E</td>
<td>black plumage</td>
<td>E92K</td>
<td>[68,69]</td>
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<td>E*</td>
<td>dark brown coat</td>
<td>L96P</td>
<td>[9]</td>
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<td>dark brown coat</td>
<td>E92K</td>
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<td>M73K, D119N*</td>
<td>[70,71]</td>
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<td>black coat until 8 weeks</td>
<td>S69L</td>
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<tr>
<td></td>
<td>w</td>
<td><em>Panthera onca</em></td>
<td>MC1R-A15</td>
<td>dark plumage</td>
<td>R230H</td>
<td>[14]</td>
</tr>
<tr>
<td></td>
<td>w</td>
<td><em>Stercorarius paraticus</em></td>
<td>dark</td>
<td>dark plumage</td>
<td>V85M and H207R</td>
<td>[74]</td>
</tr>
<tr>
<td></td>
<td>w</td>
<td><em>Sula sula</em></td>
<td>dark</td>
<td>dark plumage</td>
<td>V85M and H207R</td>
<td>[74]</td>
</tr>
</tbody>
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* indicates mutations in complete linkage disequilibrium.

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gene, mutations in the cis-regulatory elements may minimize antagonist pleiotropic effects relative to those in coding regions because such mutations can alter the time or place of gene expression in some tissues while preserving gene function in others [31–33]. Our data provide examples of mutations that are associated with morphological diversity: in one case, a premature stop codon, and in a second, a large deletion of both regulatory and exonic DNA. Thus, our data show, despite potential pleiotropic effects, both cis-regulatory and coding mutations in a highly pleiotropic gene, Agouti, cause a visible melanotic phenotype that segregates in natural populations. Alternatively, it is possible that the melanic alleles in this study do generate negative pleiotropic effects that prevent them from increasing in frequency.

The third possibility is that a bias exists toward detecting mutations in the small Mc1r locus versus the larger, more complex Agouti locus. In fact, one would expect that there are more possible mutations that can cause a null Agouti allele than a constitutively active Mc1r allele. Many cases of melanism that have not yet been assigned a precise mutational cause (e.g., some populations of pocket mice [34]; pocket gophers [35]; leaf warblers [36]) may be caused by variation at Agouti, or indeed other loci.

Understanding the genetic basis of phenotypes that have arisen independently underpins studies of convergence by natural selection. While the fitness consequences of the melanic phenotypes in this study are unknown, studies of pigmentation may be uniquely positioned to identify convergence and to uncover its molecular basis because pigmentation traits are easily recognizable and many of the genes involved in producing pigments are well characterized. As the number of cases of convergence on a particular phenotype increases, so does our understanding of the constraints limiting the ways that phenotypes can evolve. In some cases, like stomach lysozyme [37,38], pelvic reduction in sticklebacks [39,40], or cycloidenic resistance in a number of insect taxa (reviewed in [41]), evolution appears to be tightly constrained, and the same gene is the repeated target of natural selection. In other cases, such as pigmentation, many different genetic mechanisms can produce the same phenotype (beach mice [42,43]; pocket mice [34]; Drosophila [44]; cavefish [45,46]; Heliconius [47]). However, in these cases and others, it seems that a handful of proteins at key regulatory points in the pigmentation pathway are major targets of evolution change (e.g., Mc1r/Agouti in vertebrates; ebony/yellow in Drosophila; DFR in flowering plants [48]). Thus, natural selection may repeatedly target either the same key points in a genetic pathway or even the same genes to produce the most beneficial phenotype while minimizing deleterious pleiotropy. Future work on additional phenotypes in additional taxa will shed light on the myriad ways that evolution can generate morphological diversity.

Materials and Methods

Ethics statement

Experiments were approved by the Harvard University Institutional Animal Care and Use Committee and were conducted in accordance with National Institutes of Health regulations governing the humane treatment of vertebrate animals.

Animal samples

For this study, we first focused on mice from a wild-derived captive strain of melanic Peromyscus maintained at the Peromyscus Genetic Stock Center (Columbia, South Carolina). These melanic animals (P. maniculatus gracilis) are derived from mice captured in 1977 at the Hubbard Brook Experimental Forest in New Hampshire [17]. Second, to study the genetic basis of other melanic phenotypes, we obtained tissue samples of melanic mice from natural history collections originally captured in two additional populations in Alaska (P. m. keeni) and Michigan (P. m. gracilis).

Genetic Crosses

To determine the genetic basis of melanism in P. maniculatus from New Hampshire, we conducted two types of genetic crosses. First, to confirm dominance, we set up four mating pairs of wild type P. maniculatus baivdi and melanic P. m. gracils [17]. Second, for the single-locus test, we established three mating pairs and backcrossed mice that were heterozygous for the melanic allele to the wild type. We then scored the phenotypes of the resulting offspring by eye.

Tissue Samples

We acquired tissue samples from two additional populations of P. maniculatus that harbor melanic individuals. First, we received tissue samples from mice (P. m. keeni) inhabiting Shrubbery Island in southeastern Alaska (University of Alaska Museum of the North, accession numbers UAM20875, 20876, 20878, 20880, 20892), although the status of P. m. keeni as a subspecies of P. maniculatus [49] or its sister species, P. keeni, [50] is unresolved. We also acquired a tissue sample of a single melanic individual of P. m. gracils from Macinac County, Michigan (University of Michigan Museum of Zoology). Tissue samples from another melanic population (P. m. gambeli) in California [18] were not available.

PCR amplification and sequencing

We extracted genomic DNA from liver using the DNeasy kit (Qiagen). Primers and PCR conditions used to amplify the complete Agouti coding exons are shown in Table S2; these amplification primers were also used in the sequencing reactions. Primers to amplify the Mc1r coding region were used as previously described [51]. We used ABI3730xl and 3130xl sequencers (Applied Biosystems, Foster City, CA) and aligned all sequences in SEQUENCER (Gene Codes, Ann Arbor, MI). When a deletion was identified, we used genome-walking to identify the breakpoint (GenomeWalker Universal kit; Clontech, Mountain View, CA); primers are shown in Table S3. Once we identified the precise deletion breakpoint, we designed primers across the deletion to genotype individuals; these primers are listed in Table S2.

BAC sequencing

To examine the Mc1r and Agouti loci in Peromyscus, we screened an available BAC library for P. m. rufus. For the Agouti locus, we captured the entire described regulatory region [52] by using two probes representing untranslated exon 1A/1A' and the last coding region, exon 4, which span approximately 100 kb in Mus. A 160 kb BAC containing Mc1r and a 180 kb BAC containing Agouti were then shotgun sequenced by Agencourt (Beverly, MA) until sequences from each BAC could be assembled into a single contig for each locus and all gaps were filled.

Real time quantitative PCR

To quantify Mc1r and Agouti transcript levels in wild type and melanic mice from New Hampshire, we used quantitative real-time PCR to detect Mc1r and Agouti mRNA in the skin of 4-day-old (Pb) pups, a time when Agouti expression is high [52]. First, we extracted total RNA from dorsal skin that had been frozen in liquid nitrogen with an RNeasy kit (Qiagen). Next, we generated
cDNA pools by reverse transcribing from ~1ug total RNA with Superscript II reverse transcriptase and poly-dT20 primer. Finally, we measured transcript abundances with TaqMan custom probe based on exon-4 sequence (Applied Biosystems, Foster City, CA) as previously described [53] on a Mastercycler Realplex2 (Eppendorf North America, New York, NY). We compared expression of the target transcript to that of β-actin by calculating qCT in which ΔCT is the difference between the target and β-actin CTs for a given sample. We assayed expression level for each individual in duplicate.

In situ hybridization

We generated a cDNA pool from Peromyscus embryonic skin at E13, and amplified the entire coding region of Agouti (exons 2 to 4). An Agouti anti-sense riboprobe was obtained by RNA synthesis reaction and used to perform in situ hybridization on wild type and melanin embryos at E12.5 as previously described [54].

Supporting Information

Table S1  Melanism is caused by a single autosomal recessive allele in P. maniculatus. We found complete reversion of the melanin phenotype in the New Hampshire strain of P. maniculatus consistent with previous observations [17]. Offspring resulting from crosses between homozygous wild type mice (A+/A+) and homozygous melanin mice (a+/a+) were all phenotypically indistinguishable from wild type (N = 64), confirming that the allele(s) causing the melanin phenotype is recessive to the wild type allele. In a second experiment, offspring that were heterozygous for the melanin allele (A+/a−; although phenotypically wild type) – were intercrossed, resulting in 49 offspring, of which 34 (69%) were the wild type phenotype, 15 (31%) were melanin, and none had an intermediate phenotype. The ratio of phenotypes is not significantly different from 3:1 (\( \chi^2 = 0.02, 1 \text{ d.f.}, p > 0.5 \)), confirming that a recessive allele at a single locus is responsible for the melanin phenotype in this strain of P. maniculatus. Subsequent genotyping of these offspring revealed a ratio of homozygous wild type:heterozygous:melanised melanin ratio not significantly different from 1:2:1 (\( \chi^2 = 0.38, 2 \text{ d.f.}, p > 0.6 \)).

Found at: doi:10.1371/journal.pone.0006435.s001 (0.04 MB DOC)

Table S2  Standard PCR primer sequences and conditions. Found at: doi:10.1371/journal.pone.0006435.s002 (0.03 MB DOC)

Table S3  Genome walking PCR primer sequences. Found at: doi:10.1371/journal.pone.0006435.s003 (0.03 MB DOC)

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Author Contributions

Conceived and designed the experiments: EK MCM HEH. Performed the experiments: EK MCM CDW. Analyzed the data: EK MCM HEH. Contributed reagents/materials/analysis tools: CDW HEH. Wrote the paper: EK HEH.

References


