

MOLECULAR GENETICS OF COLOR MUTATIONS IN ROCK POCKET MICE.

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Introduction

THE ROCK POCKET MOUSE

The rock pocket mouse, *Chaetodipus intermedius*, is a small, nocturnal animal found in the deserts of the southwestern United States. Because most rock pocket mice have a sandy, light-colored coat, they are able to blend in with the light color of the desert rocks and sand that they live on. But populations of primarily dark-colored rock pocket mice have been found living in areas where the ground is covered in a dark rock called basalt, which was caused by geologic lava flows thousands of years ago. Scientists have collected data from a population of primarily dark-colored mice living in an area of basalt in Arizona's Pinacate lava flow, as well as from a nearby light-colored population. Researchers analyzed the data from these two populations to search for the genetic mutation responsible for the dark coat color. Through their analyses, they discovered a mutation in the *Mc1r* gene that is involved in coat-color determination.

THE MC1R GENE

The coat color of rock pocket mice is primarily determined by two pigments: eumelanin, which is dark colored, and pheomelanin, which is light colored. The synthesis of these pigments is controlled by the products of several genes, including the *Mc1r* gene. This gene encodes a protein called melanocortin 1 receptor (MC1R). This receptor is found embedded in the membrane of melanocytes, which are cells specialized for pigment production. The melanocytes of wild-type (nonmutant) mice produce more pheomelanin than eumelanin. The result is a sandy-colored mouse. The mutated version of the *Mc1r* gene, however, triggers melanocytes to increase the production of eumelanin, resulting in the dark coat-color phenotype.

GENE MUTATION

A gene mutation is any change in the DNA sequence of a gene. Gene mutations can change the structure of the resulting protein. A change in protein structure can change, negate, or have no effect on function. There are several types of mutations, and several results that mutations can have on the amino acid sequences of proteins.

| Types of Mutation | Description |
|-------------------|--|
| Substitution | The replacement of one nucleotide of DNA for another. Mutations that affect a single nucleotide are called point mutations |
| Insertion | The addition of one or more nucleotides to the DNA gene sequence. The insertion can result in frameshift mutations |
| Deletion | The loss of one or more nucleotides from the DNA gene sequence. The deletion can result in frameshift mutations |

| Results of Mutation | Description |
|---------------------|---|
| Silent | This mutation does not cause a change in the amino acid sequence of the protein; therefore, there is no change in the resulting protein |
| Missense | This mutation causes an amino acid in the sequence to be changed to another amino acid. This type of mutation causes a change in the primary structure of the protein (the linear sequence of amino acids), which typically results in a change in the three-dimensional conformation of the protein. |
| Nonsense | This mutation causes the protein to be truncated (cut short) due to the incorporation of a "stop" signal into the DNA sequence. This results in translation being stopped before the amino acid sequence of the protein is completed. |

Procedure

- Using the DNA nucleotide sequence in the tables determine the complementary messenger RNA (mRNA) sequence for the portion of the *Mc1r* gene provided. The numbers above some of the columns indicate amino acid positions in the protein sequence. (Note: You are only transcribing a small portion of the DNA sequence for this protein. The actual gene contains 951 base pairs.)
- Using the mRNA sequence determined in Step 2, determine the resulting amino acid sequence of the MC1R protein. You may use the genetic code chart provided in your textbook. (Note: This is only a portion of the 317 amino acids in the entire protein. The numbers above some of the columns in the tables indicate amino acid positions in the protein sequence.)
- There are five mutations in the dark-color *Mc1r* mutant gene. Compare the DNA sequence of the wild-type *Mc1r* gene with the DNA sequence of the mutant *Mc1r* gene. Indicate the locations of the five mutations by circling the five single DNA nucleotides that are mutated in the mutant *Mc1r* gene table.
- From the introduction, determine whether each of these mutations is a silent, missense, or nonsense mutation.
 - Using the mutant *Mc1r* gene data, shade in the columns (including DNA, mRNA, and amino acid) in the mutant table that contain a silent mutation. Use a **blue** colored pencil to do this.
 - Likewise, use a **red** colored pencil to shade in the columns that contain a missense mutation.
 - Shade any columns that contain nonsense mutations by using a **green** colored pencil.
- Answer the questions following the gene tables.

Gene Tables: Copy into you Notebook and complete

WILD-TYPE MC1R GENE (LIGHT-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 015 | | | | | | | | | 024 |
| DNA | TTG | AGG | TGG | GCG | TGT | CCG | CAA | GGA | GTG | GAG |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

MUTANT MC1R GENE (DARK-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 015 | | | | | | | | | 024 |
| DNA | TTG | AGG | TGG | ACG | TGT | CCG | CAA | GGA | GTG | GAG |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

WILD-TYPE MC1R GENE (LIGHT-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 105 | | | | | | | | | 114 |
| DNA | CGG | GAC | CGG | TGG | GCC | CAC | TGA | CAC | CAT | GTC |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

MUTANT MC1R GENE (DARK-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 105 | | | | | | | | | 114 |
| DNA | CGG | GAC | CGG | TGG | ACC | CAC | TGA | CAC | CAT | GTC |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

WILD-TYPE MC1R GENE (LIGHT-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 154 | | | | | | | | | 163 |
| DNA | TCA | TAA | CAC | TGT | GAC | GGG | GCC | CGA | GCC | ACC |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

MUTANT MC1R GENE (DARK-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 154 | | | | | | | | | 163 |
| DNA | TCA | TAA | CAC | TGT | GAC | GGG | ACC | CGA | GCC | ACC |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

WILD-TYPE MC1R GENE (LIGHT-COLORED COAT PHENOTYPE)

| | | | | | |
|------------|-----|-----|-----|-----|-----|
| | 208 | | | | 212 |
| DNA | CAC | GTG | TAC | GAA | CGT |
| mRNA | | | | | |
| Amino Acid | | | | | |

MUTANT MC1R GENE (DARK-COLORED COAT PHENOTYPE)

| | | | | | |
|------------|-----|-----|-----|-----|-----|
| | 208 | | | | 212 |
| DNA | CAC | GTG | TAC | GAG | CGT |
| mRNA | | | | | |
| Amino Acid | | | | | |

WILD-TYPE MC1R GENE (LIGHT-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 230 | | | | | | | | | 239 |
| DNA | GAA | CAG | GTG | GTT | CCA | AAG | GCT | GAG | TTT | CCG |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

MUTANT MC1R GENE (DARK-COLORED COAT PHENOTYPE)

| | | | | | | | | | | |
|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 230 | | | | | | | | | 239 |
| DNA | GAA | CAG | GTG | GTG | CCA | AAG | GCT | GAG | TTT | CCG |
| mRNA | | | | | | | | | | |
| Amino Acid | | | | | | | | | | |

| | | | | | |
|------------------------|---|--------------------------|----------------------------|------------------------------------|--|
| Middle Base 5' Base | U | C | A | G | Middle Base 3' Base |
| U | Phe Phe Leu Leu | Ser Ser Ser Ser | Tyr Tyr Stop Stop | Cys Cys *Sec *Stop Trp | U C *A G |
| C | Leu Leu Leu Leu | Pro Pro Pro Pro | His His Gln Gln | Arg Arg Arg Arg | U C A G |
| A | Ile Ile Ile ▲ Met Initiator | Thr Thr Thr Thr | Asn Asn Lys Lys | Ser Ser Arg Arg | U C A G |
| G | Val Val Val Val | Ala Ala Ala Ala | Asp Asp Glu Glu | Gly Gly Gly Gly | U C A G |

Conclusion Questions

- Using the amino acid numbers provided above the first and last column of each table, list the locations of the five amino acids that contain a mutation. _____
- Of the five mutations you identified in the Mc1r gene, how many are the following: ___ substitutions ___ insertions ___ deletions
- Of the five mutations you identified in the Mc1r gene, how many are the following: ___ silent ___ missense ___ nonsense
- Which four amino acid locations (see Question 1 above) contain the missense mutations? _____, _____, _____, _____
- Explain the link between DNA sequence and protein structure and function.
- Using the information on the Mc1r gene in the introduction and your knowledge of proteins, develop a hypothesis to explain how the change in MC1R protein function might directly affect a rock pocket mouse's coat color. Be specific and consider both the light-colored and dark-colored phenotypes.
- Explain why the mutation at amino acid location 211 is not as significant as the other four mutations.
- Mutations are a source of genetic variation. In the film, Dr. Sean Carroll says that mutations occur randomly. What does this mean?
- It is a common misconception that "all mutations are bad." Use the example of rock pocket mice to explain why this statement is not true. In your answer, explain how the dark coat-color mutation can be an advantage to some mice and a disadvantage to others.
- Use your understanding of evolution and the information in the film to explain how the dark-colored mutation came to be so common in some populations of rock pocket mice. Be specific.

