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The bear necessities: A genetic panel for bear identification

Featured scientist: Isabella Livingston (she/her) from North Carolina State University Written with Kate Price

Research Background:

Baby black bear, Murray.

North Carolina is home to many black bears. As human development expands into bear habitats, conflicts between people and bears are becoming more common. In these situations, identifying individual bears and understanding their origins is essential. This ensures that wildlife officials can correctly manage aggressive or relocated bears. It also allows for better tracking of bear populations and their movements across the state, helping to inform long-term conservation approaches.

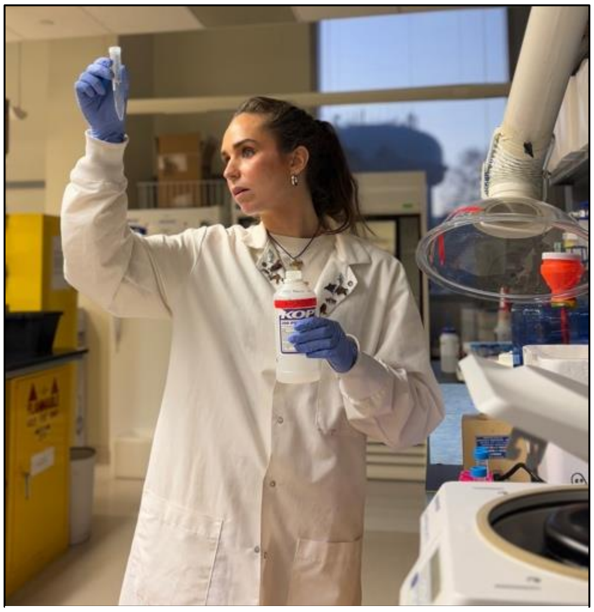
Though each individual bear has its own **genotype**, or unique genetic makeup, individuals within the same population often share more DNA with each other than with members of other populations. A group of scientists started comparing the DNA of black bears in California and identified 11 unique regions, called **loci,** in the DNA of bears from different populations. This set of loci that the scientists can use to assign individual black bears to different populations is called **Ursaplex.**

Each loci have **microsatellites**, which are repetitive sequences of nucleotide bases that vary between individuals or populations. Different versions of the microsatellite loci are called **alleles.** By examining these patterns in a bear's genotype, scientists can identify bears at an individual level and tell which population they are from.

Isabella is a wildlife geneticist who studies how we can use genetic tools to conserve wild animal populations. She has always been passionate about animals and conservation. Isabella, along with other scientists, wants to test whether or not the Ursaplex panel could work for black bears in North Carolina.

North Carolina bears are split into three different **management groups** based on where they are found: **Mountain, Piedmont, and Coastal**. Isabella wanted to know whether black bears show genetic differences based on which management group they live in. If so, she wanted to see if any of the microsatellites in the Ursaplex panel could be used to identify which management group a bear is from.

Isabella obtained blood or saliva samples for 350 black bears from collaborators at the Wildlife Resource Commission, the state agency for wildlife management. The samples came from bears in the Mountain and Coastal management groups. The Piedmont bear population is significantly smaller and elusive, so samples from Piedmont bears were not available. She extracted the DNA from the samples and found the genetic sequence at each of the 11 loci in Ursaplex. Isabella looked at the number of nucleotide base repeats in each bear's genetic sequence and used the data to identify any patterns based on where the bear was from. Each of the 11 loci included are bi-allelic, meaning each bear will have two copies of the locus (one from their mom and one from their dad).



Isabella examining a sample in the lab.

Recently, Isabella received a blood sample from a new baby bear, Murray, who was rescued by wildlife managers. This baby bear was alone when he was found, so we don't know where in the state he came from. He was found in the Eastern part of the state, so Isabella thought that his parents were likely both Coastal management group bears.

Scientific Questions: Where did Murray come from? Were his parents from the same management group, or different ones?

What is the hypothesis? Find the hypothesis in the Research Background and underline it. A hypothesis is a proposed explanation for an observation, which can then be tested with experimentation or other types of studies.

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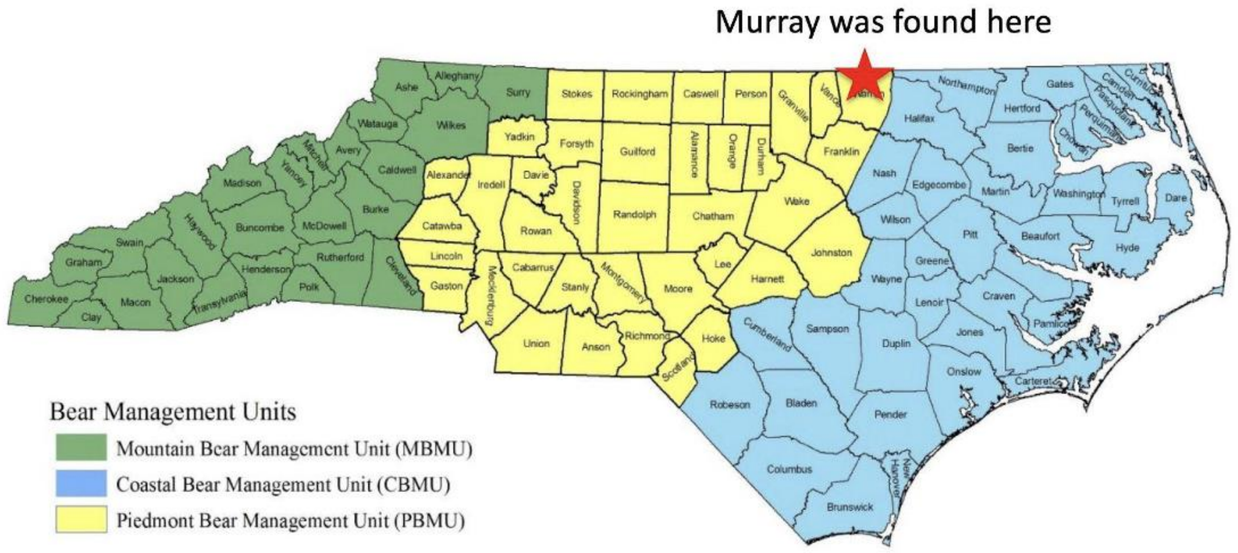
Scientific Data:

Use the map and tables below to answer the scientific question: Using the list of alleles that are unique for each North Carolina black bear management (Table 1), determine the location the baby bear is likely from. Use the table of alleles for potential parents and compare it to Murray to find out who its parents were (Table 2).



Map of North Carolina black bear management groups. The star shows where Murray was found.

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Locus	Mountain Private Alleles	Coastal Private Alleles
1	8	13,14
2	none	8
3	1,2,3,4,9,13,17,33	5,6,7,15,18,20,22,24, 26,27,29,31,32
4	5,10,11	none
5	11	8
6	none	none
7	8,10,12,14, 20	2,5,7,9
8	none	none
9	none	2
10	7	2,3
11	11	4,6

Table 1. Private alleles, or alleles that are specific to a population, for the Coastal and Mountain bear populations. Compare the alleles in this table to the alleles of individual bears to determine which population they came from.

	Potential Parents													
	Male 1		Male 2		Male 3		Female 1		Female 2		Female 3		Murray	
Locus	Private Alleles													
1	9	13	12	8	13	14	10	8	12	12	13	14	13	12
2	10	12	9	10	11	8	10	11	9	10	8	9	9	8
3	18	26	2	2	24	26	33	2	17	2	5	26	2	26
4	1	6	10	5	4	3	11	5	3	10	3	3	3	5
5	6	8	11	11	8	9	11	6	4	5	8	4	11	8
6	6	7	10	10	6	6	9	8	10	9	7	9	7	10
7	2	5	12	14	7	16	8	8	19	20	7	7	12	7
8	22	18	17	20	21	19	19	21	18	18	21	18	21	20
9	2	11	11	11	2	1	6	6	8	5	2	2	2	11
10	2	4	7	7	2	3	5	6	7	7	4	3	7	4
11	4	6	11	9	4	4	11	11	9	11	4	6	6	9
Coastal or Mountain														

Table 2. The alleles of potential parents and baby Murray. Note there are two sets per individual, because each bear has two chromosomes, like humans. This means there are two copies of each locus in an individual bear's DNA.

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Complete the table below: Pulling from Table 1 and 2, use a check mark (✓) in each cell to denote when a parent bear shares an allele with Murray at each locus. The bears that have check marks in all cells are the parents.

Bear ID	Locus 1	Locus 2	Locus 3	Locus 4	Locus 5	Locus 6	Locus 7	Locus 8	Locus 9	Locus 10	Locus 11	# shared with Murray
M1												
M2												
M3												
F1												
F2												
F3												

What data will you use to answer the question?

Independent variable(s): ____

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Dependent variable(s): ____

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Interpret the data:

Make a claim that answers the scientific questions - Where did Murray come from? Were his parents from the same management group, or from different ones?

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What evidence was used to write your claim? Reference specific parts of the tables or map.

Explain your reasoning and why the evidence supports your claim. Connect the data back to what you learned about how we can use genetic sequences to identify which population an individual is from through private alleles.

Did the data support Isabella’s hypothesis? Use evidence to explain why or why not. If you feel the data are inconclusive, explain why.

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Your next steps as a scientist: Science is an ongoing process. What new question(s) should be investigated to build on Isabella's research? How do your questions build on the research that has already been done?