**How Can Population Sizes Of Grizzly Bears Be Estimated?**

**I. Introduction**

You will be exploring a DNA fingerprinting technology that wildlife management biologists use to identify animals without ever touching them. Grizzly bears (*Ursus arctos*) once roamed most of the North American continent. Habitat destruction and direct conflicts with humans have reduced their range in the lower 48 states to estimates of less than 1,000 grizzly bears south of the Canadian border. Many questions remain on how to best ensure the long-term survival of this species.

The success of bear conservation efforts cannot be evaluated without reliable information on population size and trends. Until recently, population studies in grizzly bear habitats were conducted with radiotelemetry. This method requires bears to be sedated an d collared with a radio transmitter, causing stress in the animals as well as potential danger to the biologists who handle the bears. The methods also require frequent overhead airplane or helicopter flights to monitor the bears. It is now possible to gather bear population data more efficiently through less invasive conservation genetics methods.

For example, DNA extracted from bear hair samples that are systematically collected from hair traps can be used to identify an individual, its species, and gender without interacting directly with the bear. Each DNA fingerprint consists of a unique pattern of bands made visible in a gel through laboratory techniques. To estimate the number, **N**, of bears in an area, a so-called mark and recapture method can be used.

At first, a number of bear hair samples are collected, **T**, and the bears these samples came from are identified through DNA fingerprinting technology. These bears are now tagged and marked. Two weeks later, another set of bear hair samples, **S1**, of bear hair is collected in the same area, and the new samples are analyzed. The number, **St1**, of tagged or previously identified bears in this second sample, is also counted.

**N** is the unknown total number of bears in this area. The proportion of identified or tagged bears in the **total population** should be approximately equal to the proportion of identified bears (**St1**) in the sample (**S1**).

Therefore : **T/N = St1/S1**

Since **T**, **S1**, and **St1** are known, **N** can be estimated by solving the equation :

**N = (T x S1) / St1**

When the next set of bear hair samples, **S2**, is collected, the bears identified in the previous bear hair samples have to be added to the initial number, **T**, of tagged or identified bears, which is equal to [**T + (S1-St1)**], to obtain the total number of bears that are now tagged or identified.

Therefore : **T + (S1-St1) / N = St2/S2**

By taking these successive sets of hair samples from their hair traps, it is possible to obtain a better estimate of the total bear population in the area.

These are the assumptions for this experiment.

1. All bears are equally likely to leave hair samples in the traps. A common exception occurs when some of the previously identified animals hide, then the estimate tends to be too large. Sometimes, some “trap-happy” animals are more likely to return to the hair traps than others. In this case, the estimate for **N** tends to be too small.

2. During the period of the study, the bear population had no additions or deletions, i.e. no changes in the number of animals. Deaths of identified bears tend to make the estimate too large.

**II. Procedure**

1. Start the activity by going to the following website :

<http://glencoe.mheducation.com/sites/dl/free/0078802849/383918/BL_29.html> .

2. In the Grizzly Bear Hair Trap Map, a number of hair traps have been placed in the area in

which the bear population is to be estimated. Bears visiting this area may leave hair samples

on the barbed wire hair traps. Select the “**Trapping Trip 1**” button to obtain samples of the

bear.

3. Use the pipette to drag and drop the **DNA samples** into the wells of the electrophoresis unit.

Add migration dye to each well by clicking on the “**Add Dye**” button. Next, click the

“**Power On/Off**” button to turn on the power. When the migration dye has reached the end of

the gel, the electrophoresis run is complete.

4. Drag and drop the gel columns to the Viewing Box so they lie side by side for better

comparison. Each gel piece represents the DNA fingerprint of an individual bear. To identify

individual DNA fragments, a number has been placed above each gel for easier comparison

with other gels.

5. View the DNA bands and note how many bears were “trapped” in the first “field trip (hair

sample size)”. All of these bears are now marked (total number of identified bears in the

population). Record the numbers in the Data Table.

6. Another bear sample was collected “two weeks after the initial sample”. Click the ‘**Trapping**

**Trip 2**” button to obtain additional bear hair samples from the traps in the same area. Use the

same technique as for the sample one.

7. At the end of the electrophoresis run drag and drop the gel columns to the Viewing Box.

Compare the “fingerprints” from the new samples to the ones that are already in the viewing

tray.

8. Next, analyze the data. Record the sample size (number of hair samples **(S)** collected in this

trapping field), and note how many bears in the field are now fingerprinted or ”marked **(T)**”,

(remember to add the number of bears identified in this sample to the previous number **T** of

tagged bears). Record the number of “recaptured” bears (repeats). Click the **Table/Graph**

button to record data.

9. Repeat the sequence of “trapping field trips”, DNA fingerprinting, and data recording for the

additional two trapping trips. Select the trapping trips in sequential order. Samples collected

during these trapping trips are at intervals of “two weeks”. This process happens for a total of

8 weeks.

10. Refer to the recorded data and estimate the total population of bears in the study area.

Record this data in the Estimated Total Number of Bears (N) column of the Data Table.

11. Read the Laboratory Handbook to understand the technology of bear hair DNA

fingerprinting in more detail.

**III. Data**

1. Record your data in the table.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Hair Trapping**  **Field Trips** | **Hair Samples**  **(S)** | **Total Number**  **Of Identified**  **Bears (T)** | **Repeats**  **(St)** | **Estimated**  **Total Number**  **Of Bears (N)** |
| 1st |  |  |  |  |
| 2nd |  |  |  |  |
| 3rd |  |  |  |  |
| 4th |  |  |  |  |

**IV. Analysis & Conclusions**

1. DNA fingerprinting identifies individual bears and also allows for determining the gender of

the bear. What information does it not provide that might be useful for deciding on

conservation efforts?

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2. Bear hair may also be collected from trees that the bears rub themselves on against. In a

study using DNA fingerprinting of hair collected from rub trees, it was found that the

population in the area contained more male bears than female bears. Explain this outcome.

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3. What other problems might DNA fingerprinting of bear hair solve?

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4. The police arrested three suspects and obtained DNA fingerprints from each individual. What

does the investigator need to establish whether one to determine which of the three might be

the culprit in the crime? Explain your answer.

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5. How could DNA fingerprinting technology is used to establish that a highway cutting

through grizzly bear habitat stops the bears from moving from one side to the other?

Explain your answer.

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6. Monarch butterfly populations are found east and west of the Rocky Mountains. How could

DNA fingerprinting technology be used to establish that they constitute one breeding

population or two separate breeding populations? Explain you answer.

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7. Describe the advantages and disadvantages of radiotelemetry and DNA fingerprinting

methods for obtaining wildlife population data.

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