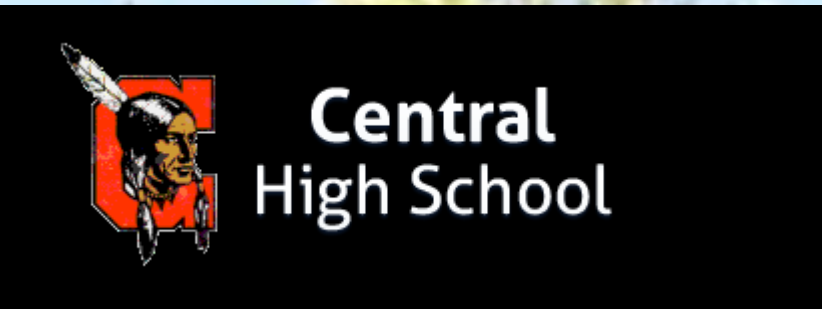


The Genetic Structure of Two Aspen Groves in the Laramie Range

Dorothy Tuthill¹, Kim Parfitt², AP biology students of Cheyenne Central High School

¹ Berry Biodiversity Conservation Center, University of Wyoming, ²Central High School, Cheyenne, Wyoming



Aerial view of the study site, showing location of each of the samples.

HYPOTHESES

We investigated the genetic structure of two, adjacent aspen groves located along Middle Crow Creek to determine if these groves represented clones, and if so, if they were remnants of the same clone. We hypothesized that: 1) All trees within each grove would be genetically identical to each other, and 2) The two groves would be genetically different.



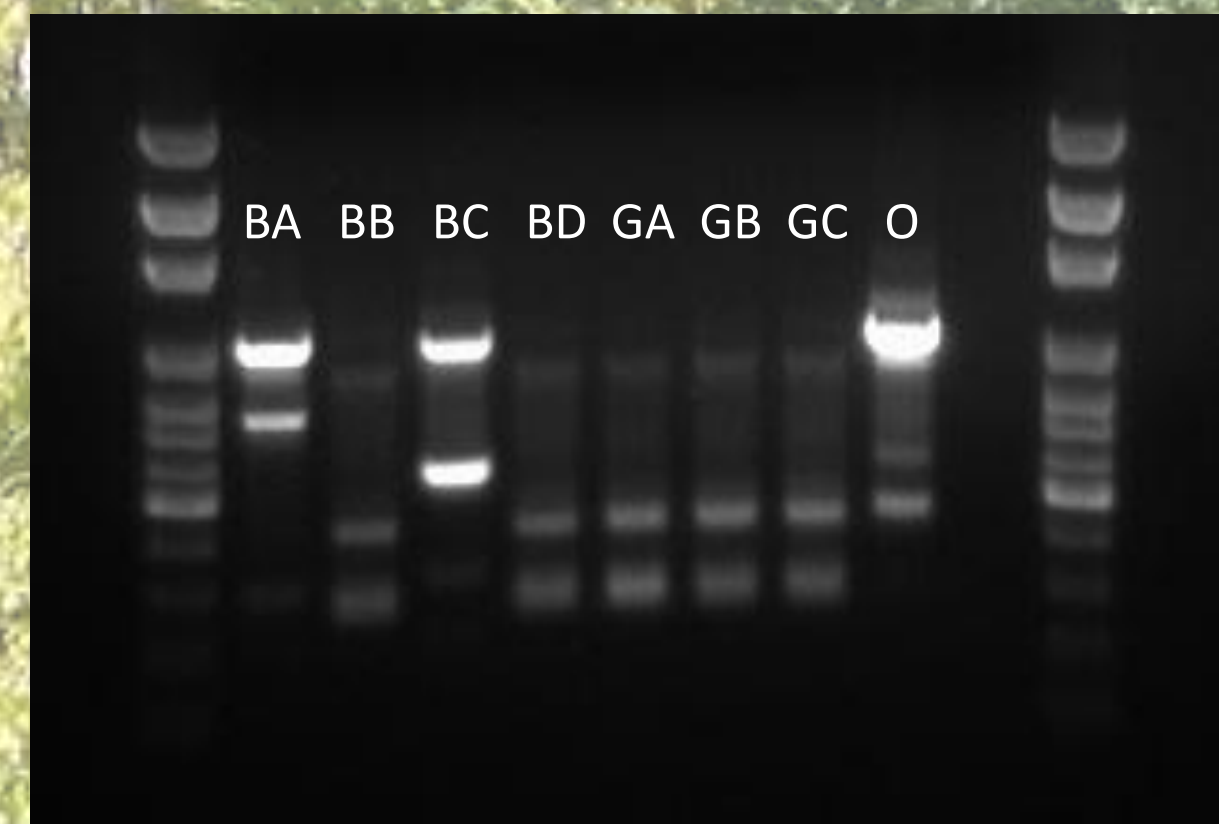
METHODS continued

DNA extraction from the leaves was done at the Berry Center (UW campus) by grinding the leaves with liquid N₂, then following DNeasy kit procedures. PCR and gel electrophoresis were done at Central High. To determine if samples were genetically identical, visual comparisons were made between the samples.

METHODS

Our study site (at lower right and above) was located at Blair Picnic Area, in the Pole Mountain Unit of the Medicine Bow National Forest. The larger of the two aspen groves, named Bertha (B) is located directly south of, and adjacent to, the picnic ground. The smaller grove (Grandmother's grove, G) is southeast of Bertha, separated by approximately 13 m of open space. Both groves are located on the east side of Middle Crow Creek, and are bounded to the west by wet meadow and to the east by sagebrush and grass covered hills.

Leaf samples were collected to represent the two groves and an outlier (O). Each sample consisted of two healthy-looking, green leaves. Four samples were made from Bertha (BA-BD), and three from Grandmother's Grove (GA-GC). The outlier sample (O) was collected approximately 100m NW of the nearest edge of Bertha, and separated from Bertha by a road and a meadow.



This figure shows DNA fingerprints using one primer. You can see that BA, BC, and O are unlike the other five samples.



CONCLUSIONS (from student reports)

We found that neither hypothesis was correct.

The first hypothesis is partially correct, yet it is incorrect as well. Bertha was not composed entirely of clones because samples BA and BC were consistently different from the rest of the samples. Grandmother grove, however, was similar throughout the data. The second hypothesis is also rejected to some degree because the samples BB and BD were almost identical to the ones collected from Grandmother grove. In some ways the groves are genetically different because the samples BA and BC were slightly different throughout the trials.

Perhaps at one time they were combined into one large grove. There are large parts of each grove that are genetically identical, but smaller parts that are different. Those smaller parts that are different have a different DNA. Our class came to the conclusion that the small patches that BA and BC were in came from seeds, perhaps from the trees in the larger groves, but because they were not reproduced asexually they are not genetically identical.