# AFLP Comparative Analysis of Andropogon gerardii with GeneMarker® & GeneMapper® Software Packages

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In tallgrass prairie ecosystems, the dominant C4 grass, *Andropogon gerardii,* determines community structure and levels of ecosystem function (Smith and Knapp 2003). *A. gerardii* is clonal and mostly reproduces vegetatively through buds produced on belowground rhizomes (McKendrick et al. 1975). Thus, intra-specific diversity is a function of its clone size; areas with large clones will be less diverse than areas with many smaller clones. Despite the importance of understanding the diversity of this ecologically important species, few studies have tried to determine the size of clones and finer-scale patterns of diversity. Preliminary data suggests that clones are often smaller than 2 $m^2$. I am using AFLP analysis to determine the clone size and fine-scale diversity of *A. gerardii* populations at Konza Prairie in Kansas. AFLP analysis is a technique that can be used to detect differences among genotypes (Vos et al. 1995) and is powerful enough to detect differences between siblings and clones (Douhovnikoff and Dodd 2003**).** Information obtained from this study can be used to determine the appropriate sampling scale for future studies examining the diversity of *A. gerardii* affects ecosystem processes.

AFLP data was from a 3730 48-Capillary Electrophoresis DNA Analyzer (Applied Biosystems). To compare AFLP analysis softwares, GeneMapper (v3.7, Applied Biosystems) and GeneMarker (v1.6 Softgenetics LCC) were compared. The AFLP data used in the comparison were 60 multi-plexed samples, using three EcoR1 labeled primers 6Fam, NED, and Vic, and one unlabeled MSE primer. Liz-600 (GeneScan) was the size standard used.

Using GeneMapper, the analysis time took 2 minutes and 44 seconds. 13 samples failed the analysis; the size standard was inaccurately called and a further 8 samples needed to be further checked because of size standard related problems. Using GeneMarker the analysis took 17.96 seconds and all samples were included in the analysis, because the size standard was accurately called for all the samples. Of the 60 samples, the lowest **size calibration quality score** was 92. In creating the bins, GeneMapper automatically deleted alleles that were not polymorphic, while GeneMarker creates bins for all alleles whether or not they are polymorphic. After the software has chosen bins, I have found it necessary to go through and personally double check the bins. Picking polymorphic alleles is easier in GeneMarker, as one can pick bins in a trace-overlay setting. GeneMapper does have a trace-overlay view, however, one is not able to bin in that view.

Due to the faster processing speed and higher accuracy of size standard calling, GeneMarker was used to analyze our ALFP data.

**Analysis Recap - 60 lanes AFLP data**

| | Analysis Time | # Sized Correctly | % Failed Analysis | % Requiring Size Call Adjustment |
|---|---|---|---|---|
| GeneMapper v 3.7 | 2 min 44sec | 39 | 21.7 | 13.3 |
| GeneMarker v 1.6 | 17.96 sec | 60 | 0 | 0 |

**References:**

Douhovnikoff V, Dodd RS. 2003. *Theoretical Applied Genetics* 106: 1307-1315.
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Vos P, Hogers R, Bleeker M, Reijans M, van de Lee T, Hornes M, Frijters A, Pot J, Peleman J, Kuiper M, Zabeau M. 1995. *Nucleic Acids Research* 23: 4407-4414.