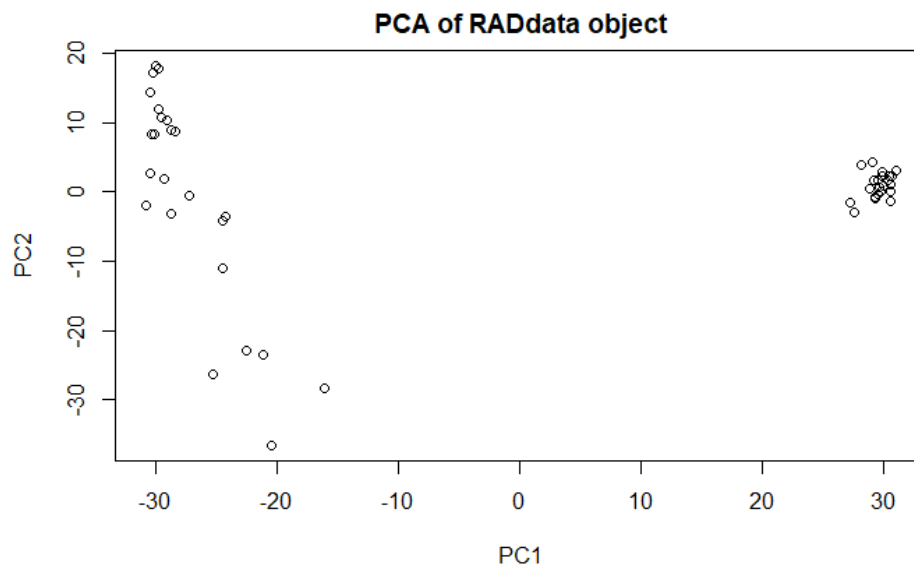


Identification of CUF101 Allele Frequency & Population Structure from Different Seed Sources

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Alfalfa cv CUF101 is very non dormant cultivar (Fall dormancy score; FD= 9) and the highly adapted alfalfa variety in low desert valley of California and Arizona which developed by collaboration of University of California, Davis, the US Department of Agriculture, and California farmers. The first released of this cultivar was in 1976. (<https://fsp.ucdavis.edu/seed-catalog/alfalfa-varieties/cuf-101>) In this study, CUF101 seed from the 45 different seed lot were germinated on petri dish at room temperature for seven days, after that seedling plant tissue were collected for DNA extraction and The DNA samples were used to generate GBS library with PstI restriction enzyme. Tassel5GBSv2Pipeline (Glaubitz et al., 2014) was used for SNP discovery and polyRAD package in R (Clark and Sacks, 2019) was used and Genotype calling, the 34,843 high confident SNP data were used to determine population structure and allele frequency by using package polyRAD in R. Generally, the population structure of this study can be separated into three population structure groups from difference CUF101 seed lots. There is a set of markers that could be used as the specific loci for alfalfa cv CUF101 t and could be used for future CUF 101 study. The result from this study can be used to identify loci specific to alfalfa cv CUF101 from the different seed sources.

Figure 1. The first two principal component analysis (PCA) of alfalfa cv CUF101 indicates population structure form difference CUF101 seed sources



References

Clark LV, Lipka AE, and Sacks EJ (2019) Improvements to Genotype Calling in Polyploids Using the polyRAD R Package. Plant and Animal Genome Conference XXVII, January 12-16, San Diego, California, USA. doi:10.13140/RG.2.2.18358.75847

Glaubitz, J. C., Casstevens, T. M., Lu, F., Harriman, J., Elshire, R. J., Sun, Q., and Buckler, E. S. (2014); TASSEL-GBS: a high capacity genotyping by sequencing analysis pipeline. PloS one, 9(2), e90346.

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