

Identifying Potential Nesting of Fiber Quality Alleles within the Population Structure of Obsolete U.S. Cotton Cultivars

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Fiber Quality in Upland Cotton

- ▶ Cotton (G. hirsutum) 95% of global cotton fiber production
 - ▶ US largest exporter of cotton
 - ▶ Texas largest export commodity
 - ▶ 1.6 Billion Dollars to Texas economy (Texasagriculture.gov, 2016)
- Improving fiber quality is important
 - listed as an important priority producers want from science (Hake 2016)
 - ► Allow for use in more efficient textile technologies
 - Produce better products
 - Obtain a premium for farmers

Fiber Quality in Upland Cotton

- ► High Volume Instrumentation (HVI) was not widely implemented into breeding programs until the 1980s and 90s.
 - ▶ 100 years of selections not using these technologies
 - ► Many sources of superior fiber quality alleles likely overlooked
- ► Advanced Fiber Information System (AFIS) was developed in the 1990s (cost limits use/acceptance)

Genetic Diversity of Cotton

- ► Most cotton cultivars in the United States can be traced back to an original 1806 introduction from Mexico (Smith and Cothren 1999)
- ► Many genetic studies corroborate a narrow genetic diversity (Paterson 2009 and references therein)
- ► Low genetic diversity could allow for tapping into standing genetic variation of obsolete cultivars without much yield drag (Tyagi et al. 2014)
- ► Can we tap into alleles that may have been overlooked from the USDA Obsolete US Cultivar Collection using genomic selection?
 - ▶ What role does population structure play with fiber quality?
 - ▶ Lui et al. 2015 (PlOS one), Wientjes et al. 2013 (Genetics), exc.

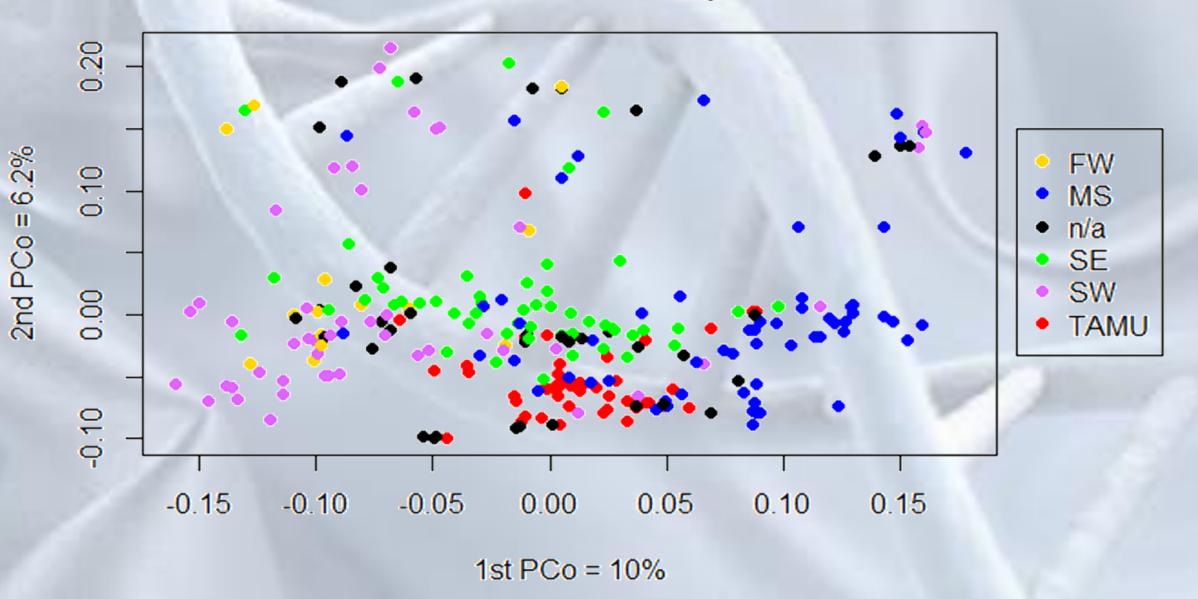
What We are Working With

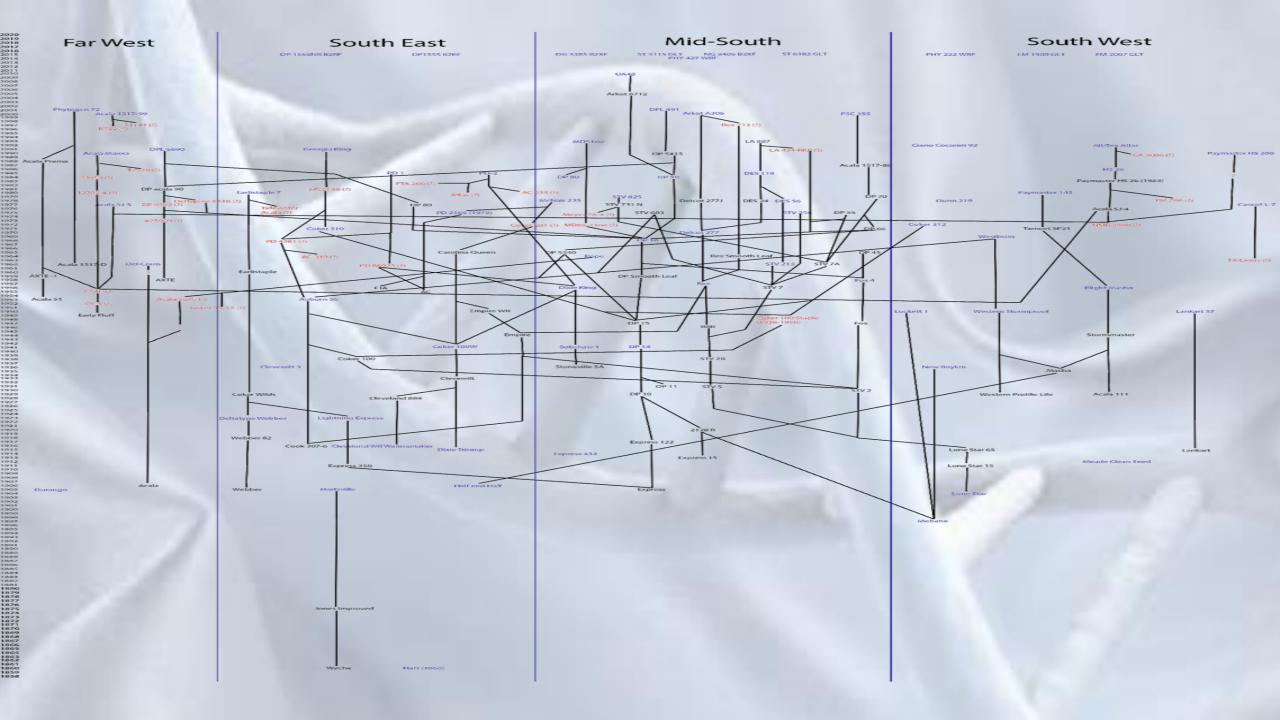
- Genotype information on 258 obsolete US cotton Cultivars
 - Selected based on SSR diversity analysis of collection
 - ► Hinze et al. 2015 (TAG)
 - ► Genotyped using 63K SNP array
 - ► Hulse-Kemp et al. 2015 (G3)
 - ► Approximately 24,000 high confidence SNPs
- ▶ Phenotype data on sub-sample of 128 cultivars
 - ▶ Planted in 2016 using RCBD with 3 replications in 2 locations
 - ► HVI & AFIS
 - ► Waiting on spin data

US Cotton Growing Regions



2 Dimensional PCoA Colored by Location

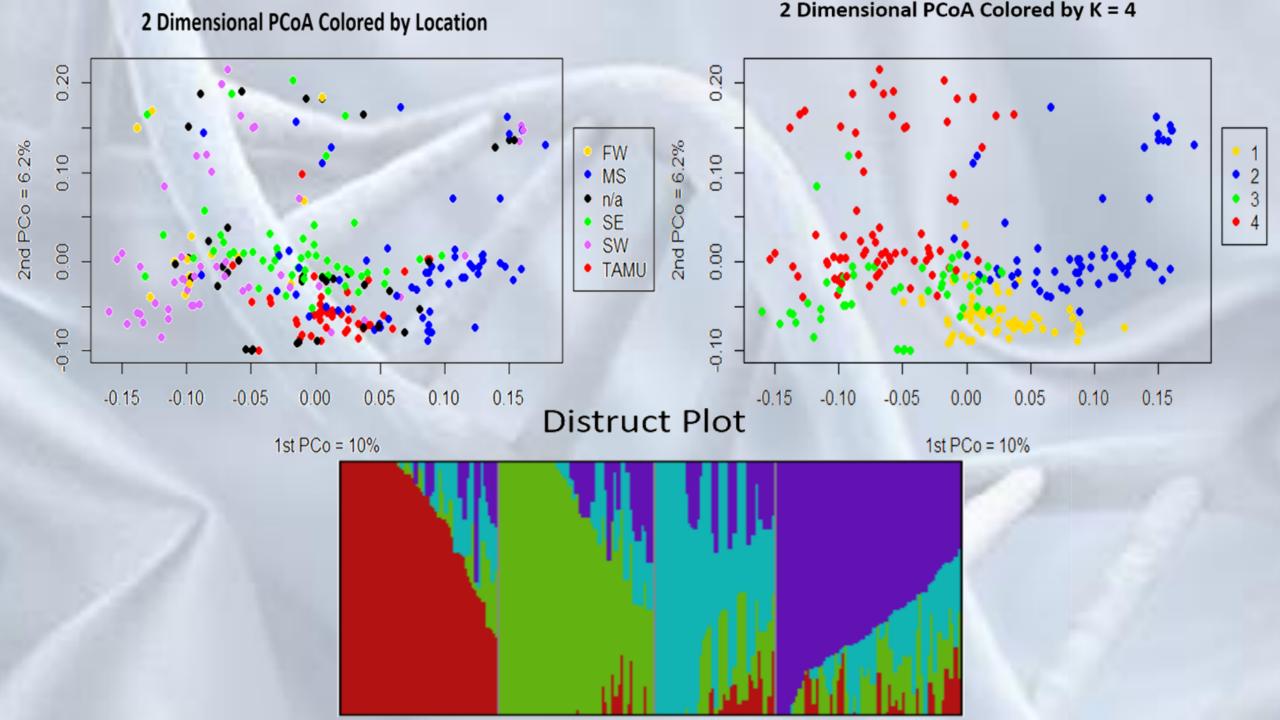




Quantifying Population Structure

fastStructure

- ▶ Raj et al. 2014 (Genetics)
- ► K=1 through K=10
 - ► Not clear at distinguishing the best model
- ▶ Combined with PCoA to see what makes the most sense



What Markers Contribute the Most to Population Structure

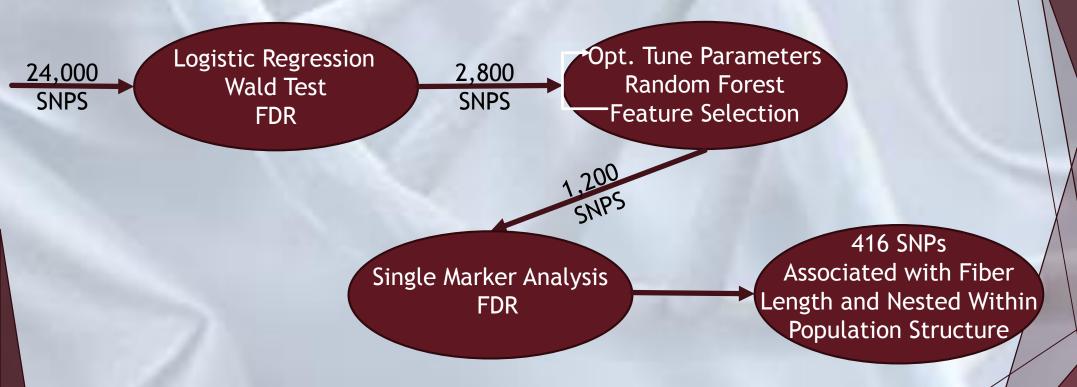


Prediction Error Comparison for Full and Reduced Random Forest Model

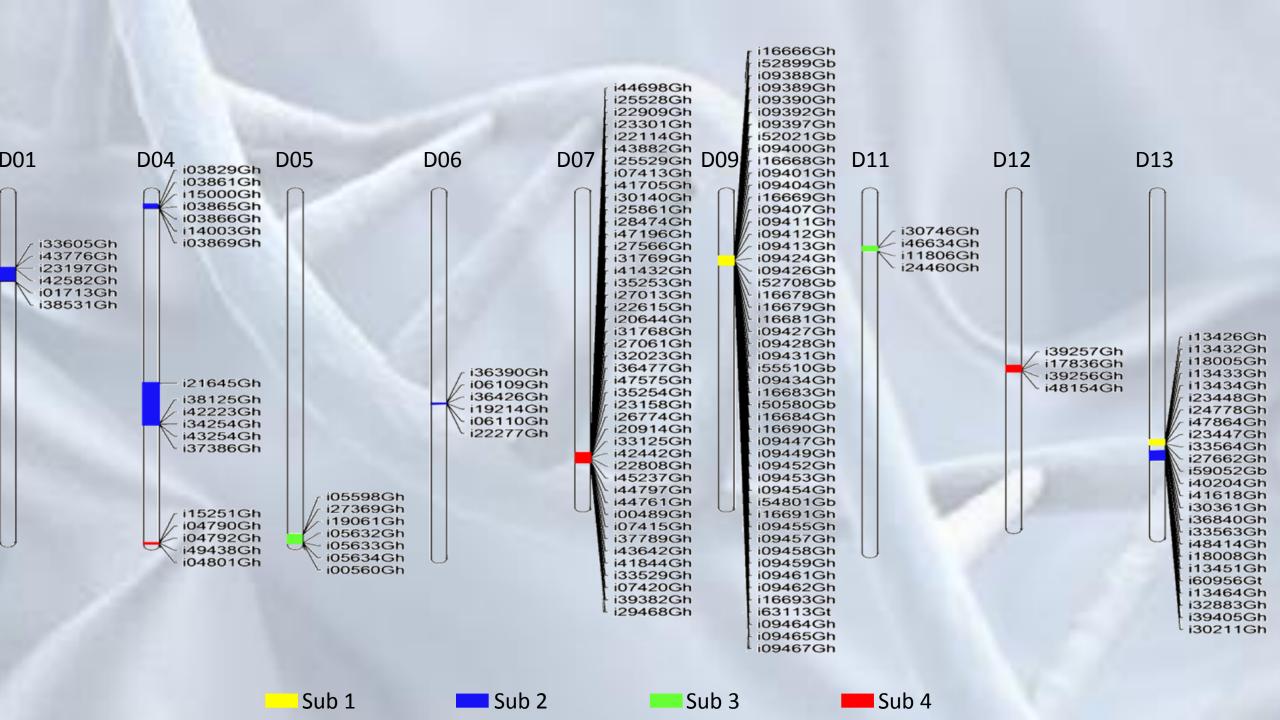
Model	1 st Quartile	2 nd Quartile	Median	Mean	3 rd Quartile	4 th Quartile
Full	0.07364	0.09302	0.1008	0.09767	0.1037	0.1124
Reduced	0.0814	0.09012	0.0969	0.09574	0.09981	0.1085

▶ 10 Replications of K = 10 Folds Cross Validation

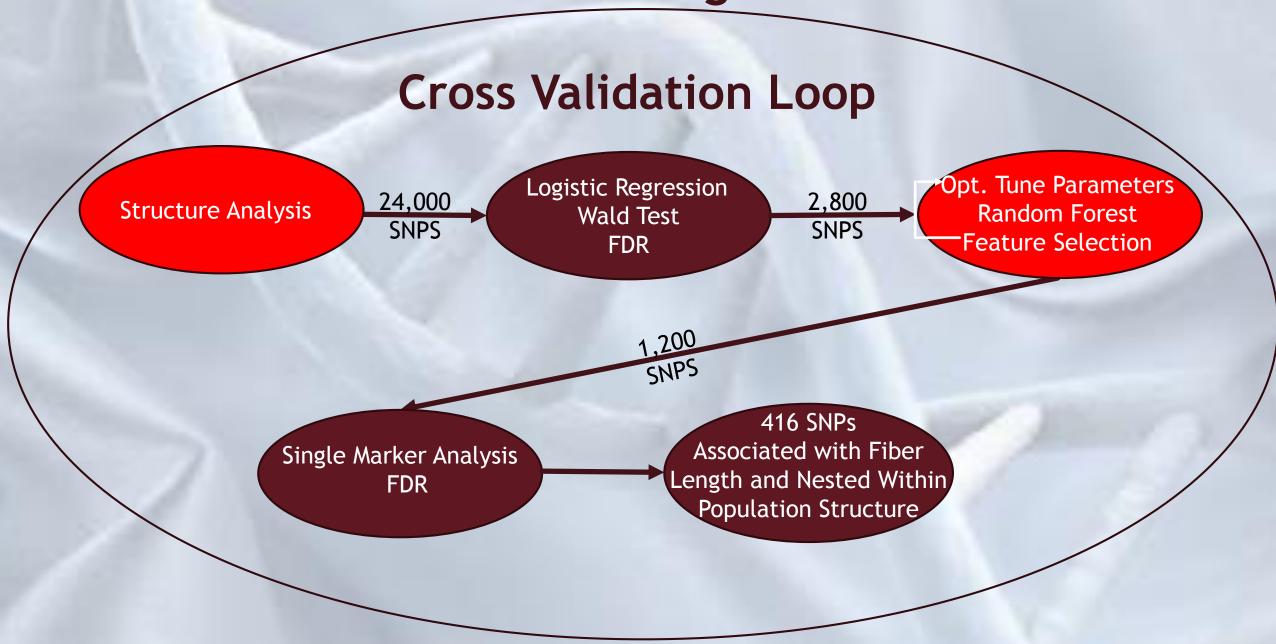
What Markers Contribute the Most to Population Structure







Potential Problem of Overfitting



Summary

- ► This analysis does appear to Identify nesting fiber quality alleles in population structure.
- ► This information could prove useful in developing training populations for genomic selection, developing GWAS population, and in general breeding decision making.
- **▶** Potential Problem of Overfitting

Thanks

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COTTON INCORPORATED

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