

Acknowledgements

- Cotton Incorporated



COTTON INCORPORATED

- Technicians and part-time workers

Why do we need to characterize diversity?

- Diversity is what gives plants the ability to adapt to changing environments
- Efficient conservation depends on our understanding of the available diversity
- Efficient utilization by breeders depends on knowledge of the extent, nature, and structure of available diversity

How do we characterize diversity?

- Morphological methods
- Molecular methods

Morphological characterization

Dr. James Frelichowski, curator



For molecular characterization, we are primarily using Simple Sequence Repeats (SSRs)

Use available DNA markers

Work with collaborators to develop new markers

Work with collaborators to perform molecular analyses

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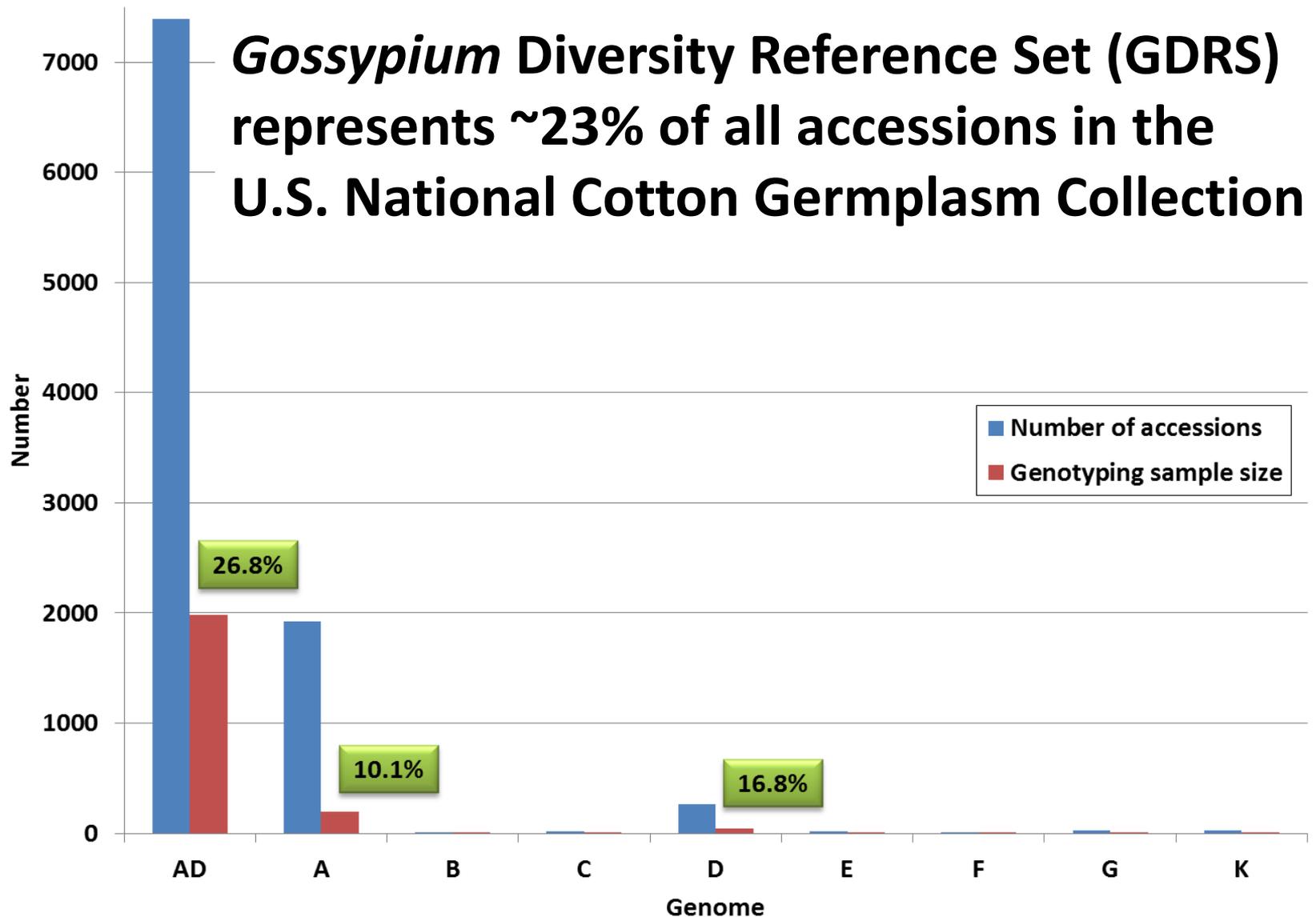
Development of a core set of SSR markers for the characterization of *Gossypium* germplasm

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Lori L. Hinze · Richard G. Percy · Jinfa Zhang · Peng Chee ·
Brian E. Scheffler · Don C. Jones

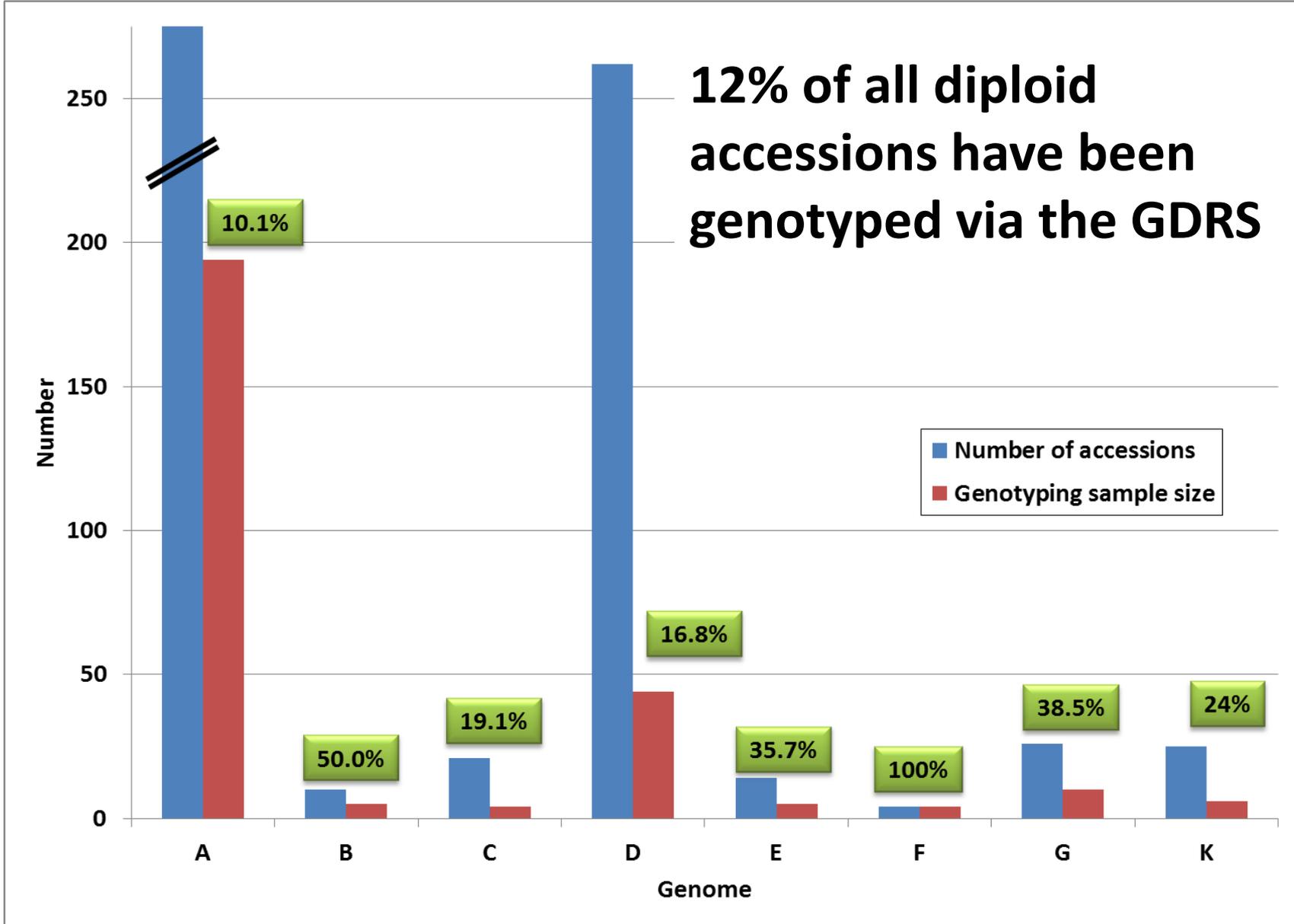
***Gossypium* Diversity Reference Set (GDRS) represents range of variation in U.S. NCGC**

Genome Group	Number of Species	Number of Accessions
-----Tetraploids-----		
AD	6	1,982
-----Diploids-----		
A	2	194
B	1	5
C	2	4
D	10	44
E	3	5
F	1	4
G	3	10
K	6	6
Overall	34 species	2,254 accessions

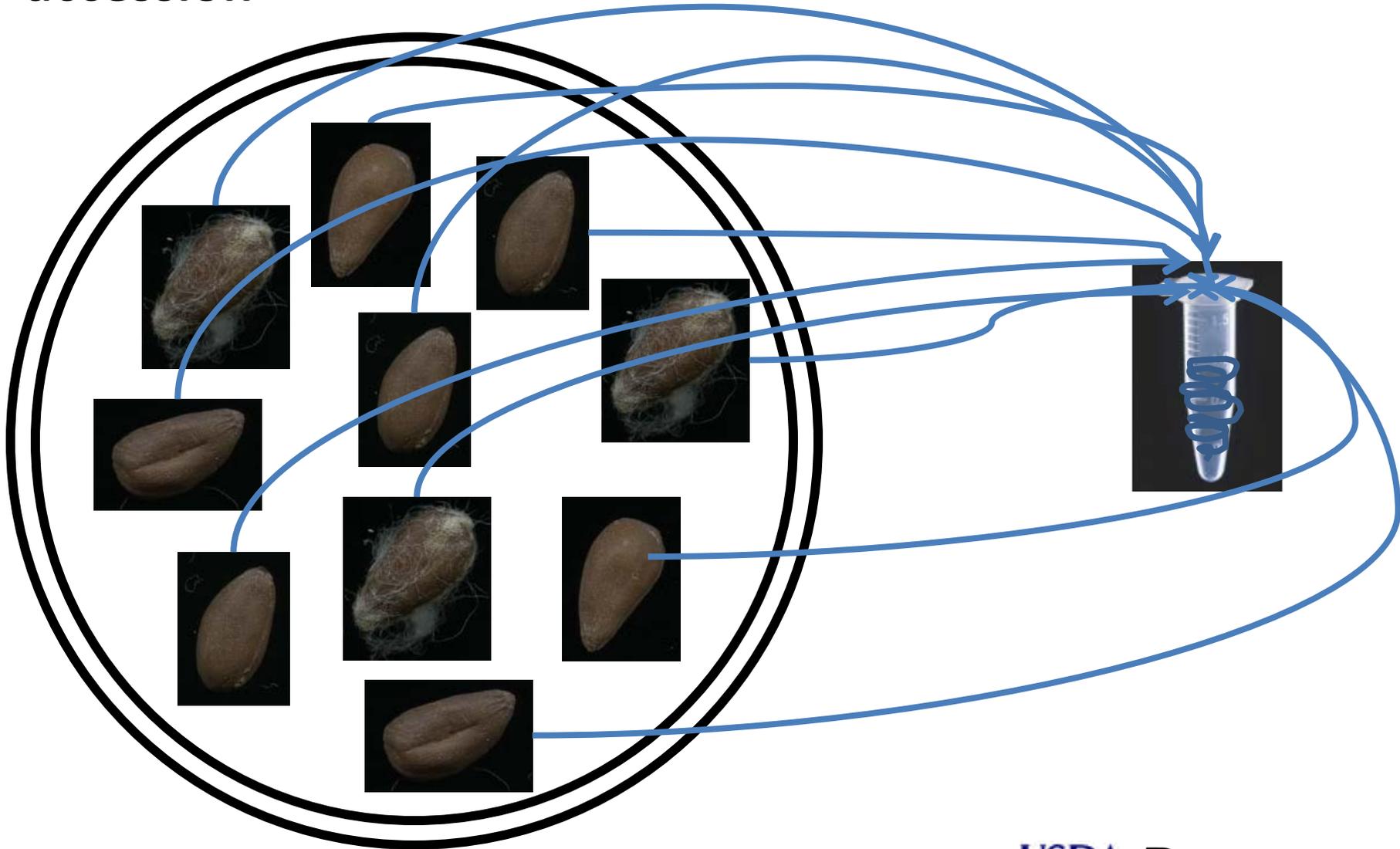
Gossypium Diversity Reference Set (GDRS) represents ~23% of all accessions in the U.S. National Cotton Germplasm Collection



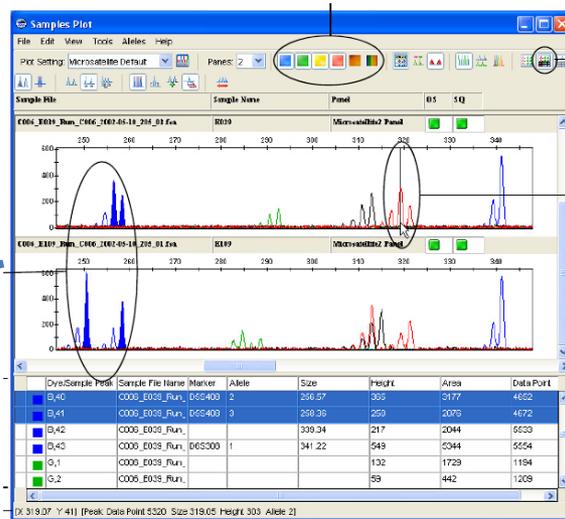
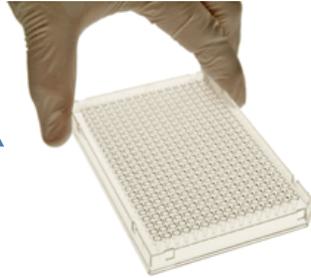
12% of all diploid accessions have been genotyped via the GDRS



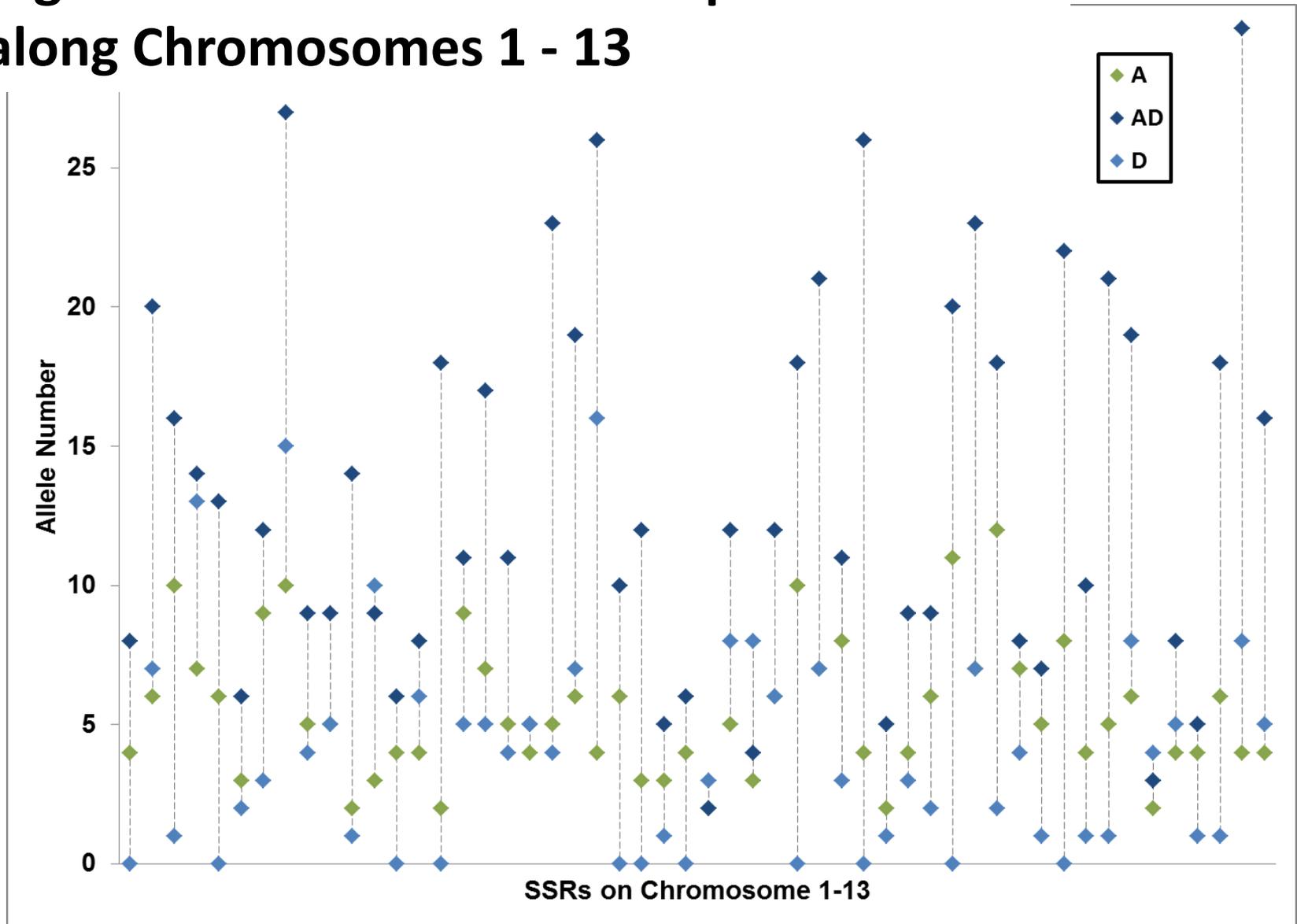
We extracted DNA from 10 seeds representing each accession



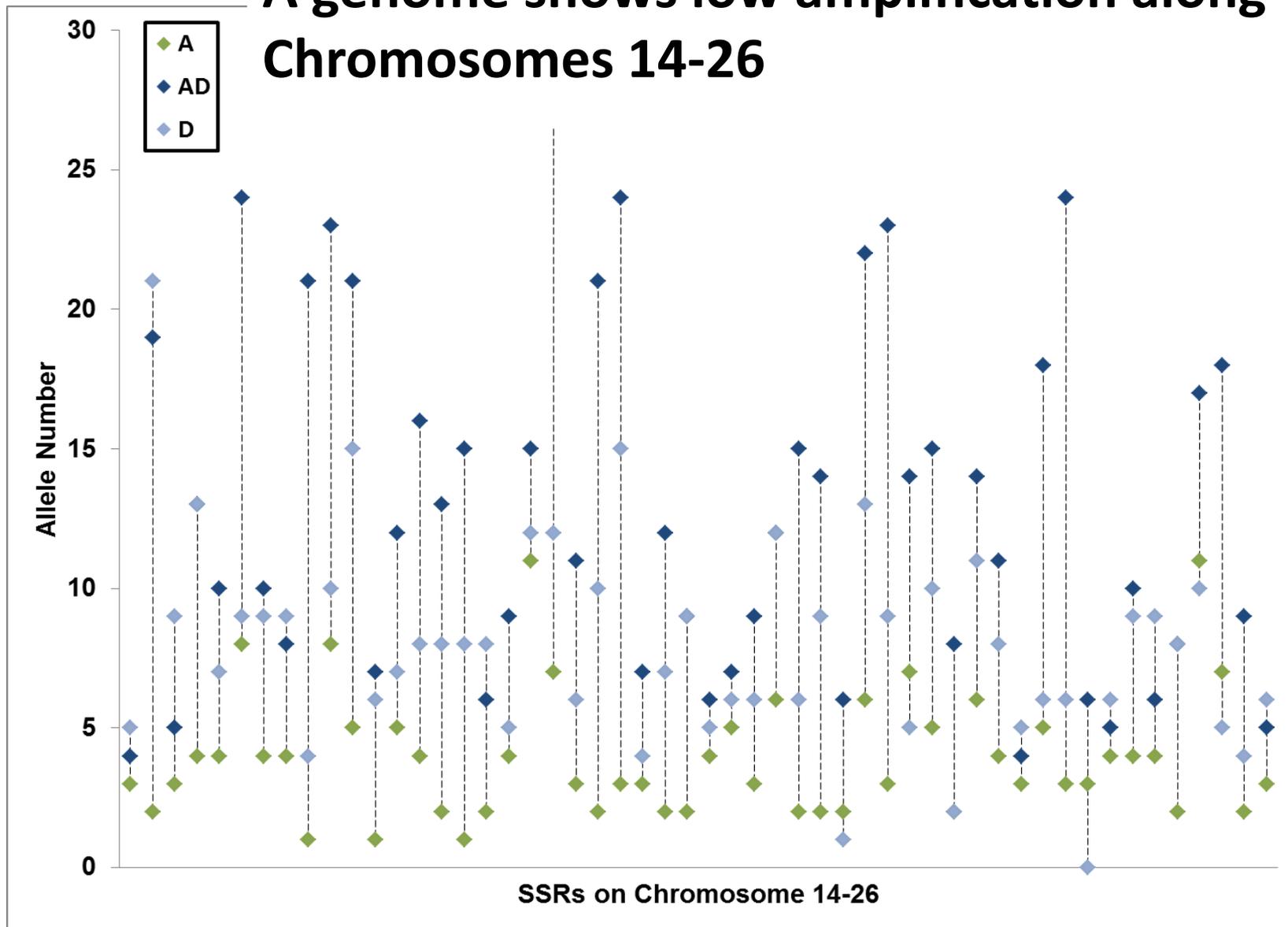
USDA Mid-South Area Genomics Laboratory genotyped accessions prior to fragment analysis



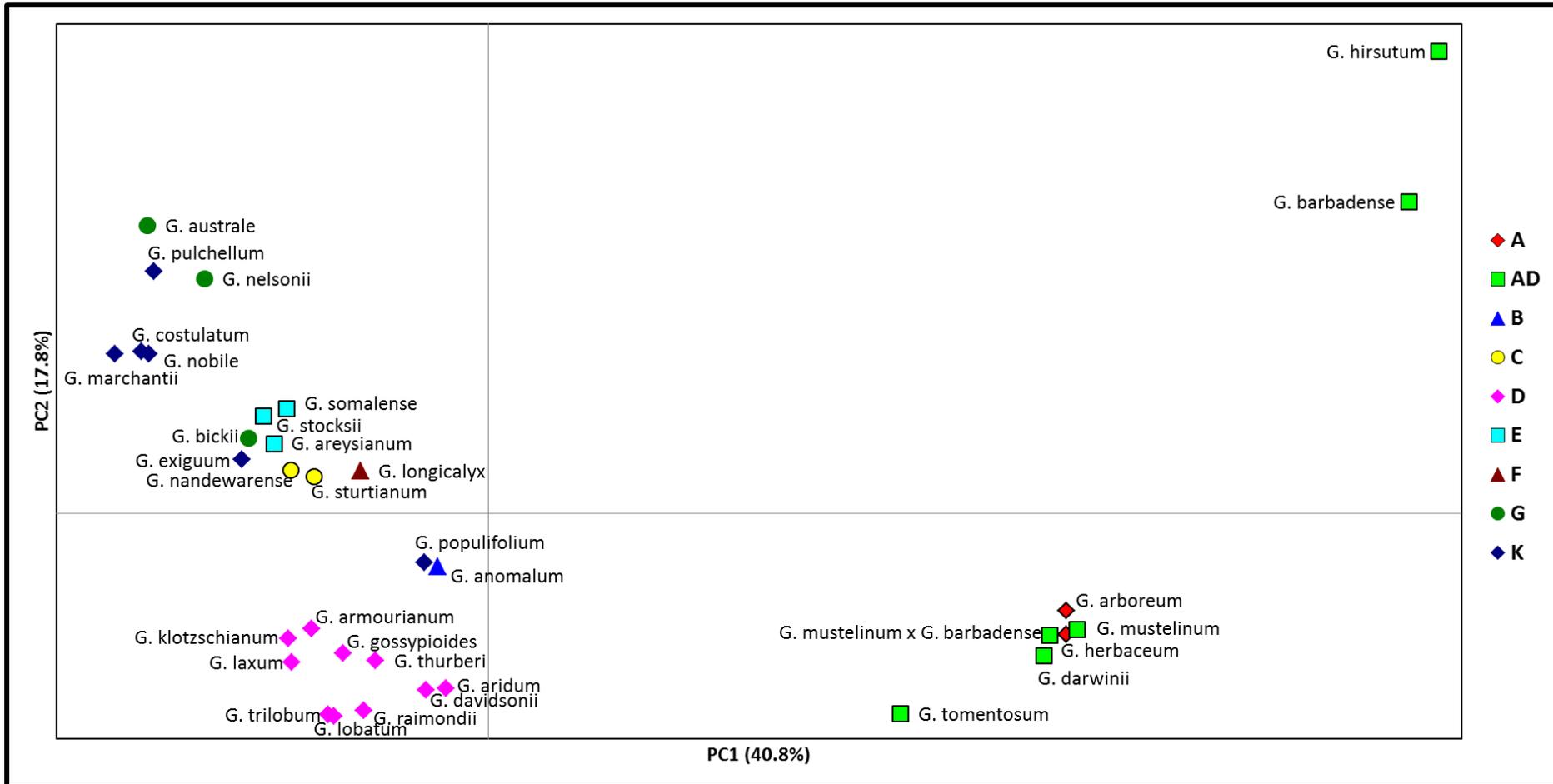
D genome shows minimal amplification along Chromosomes 1 - 13



A genome shows low amplification along Chromosomes 14-26

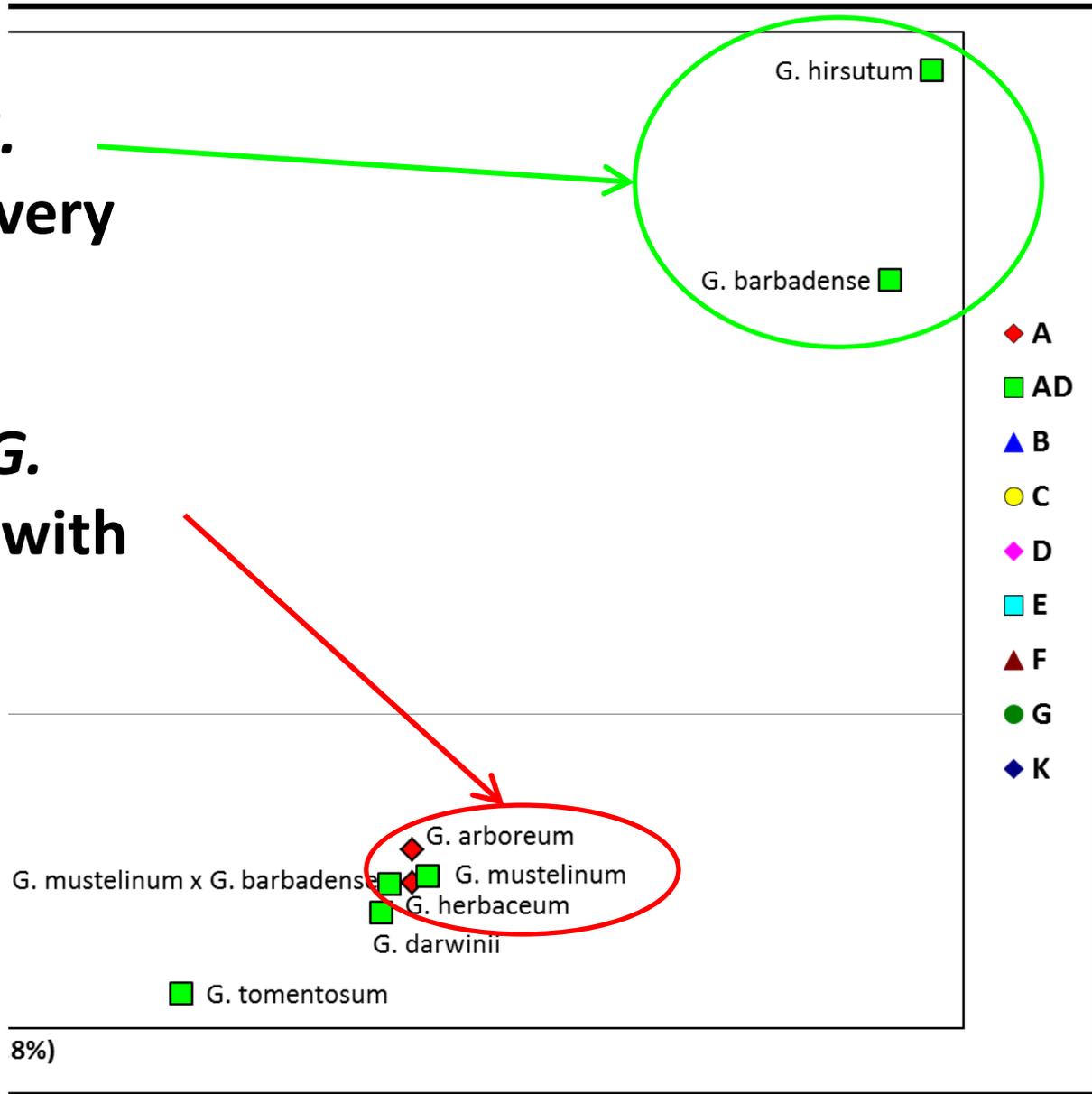


Our work shows that tetraploid species and A-genome diploids are separate from remaining diploids

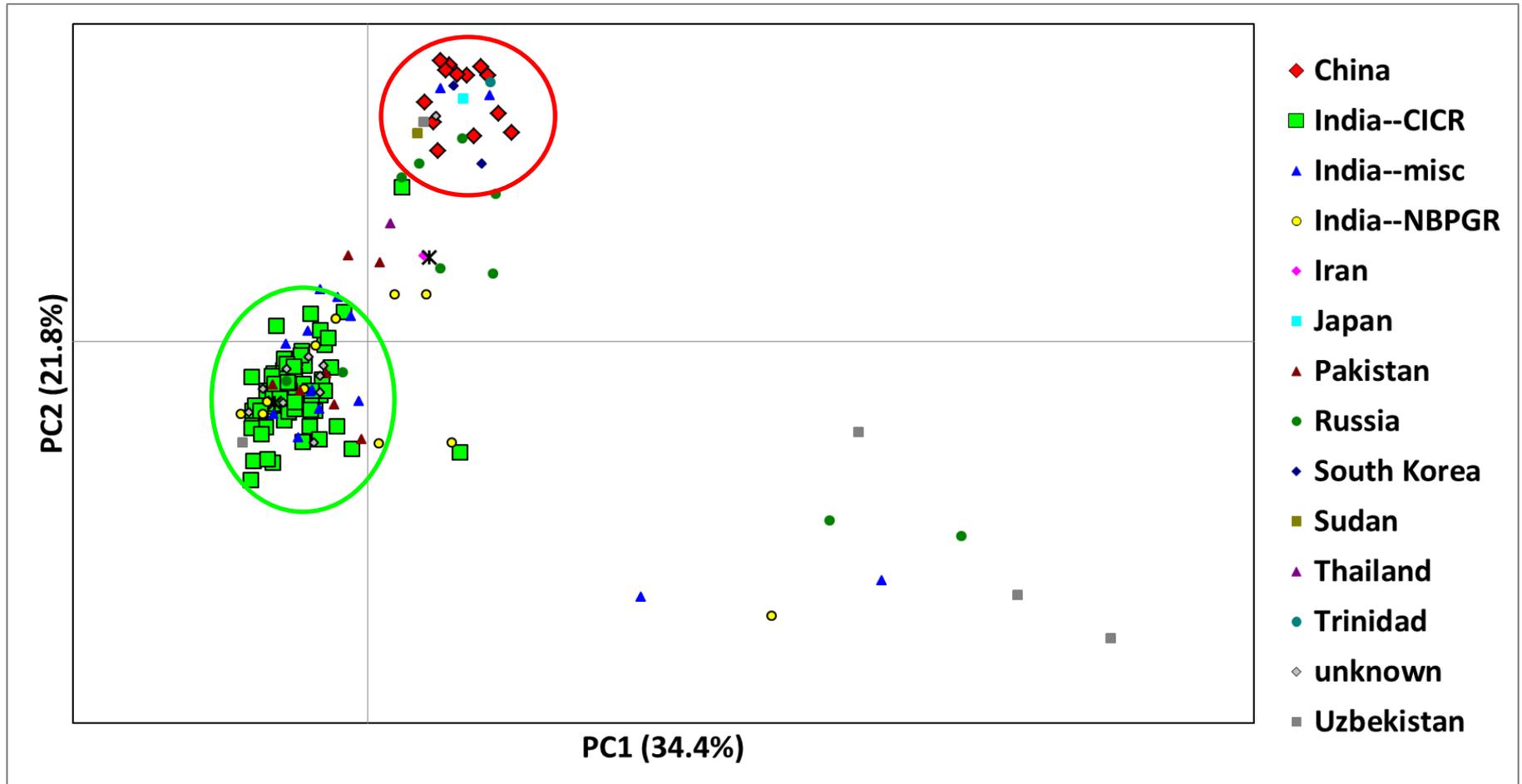


***G. hirsutum* and *G. barbadense* are a very distinct cluster**

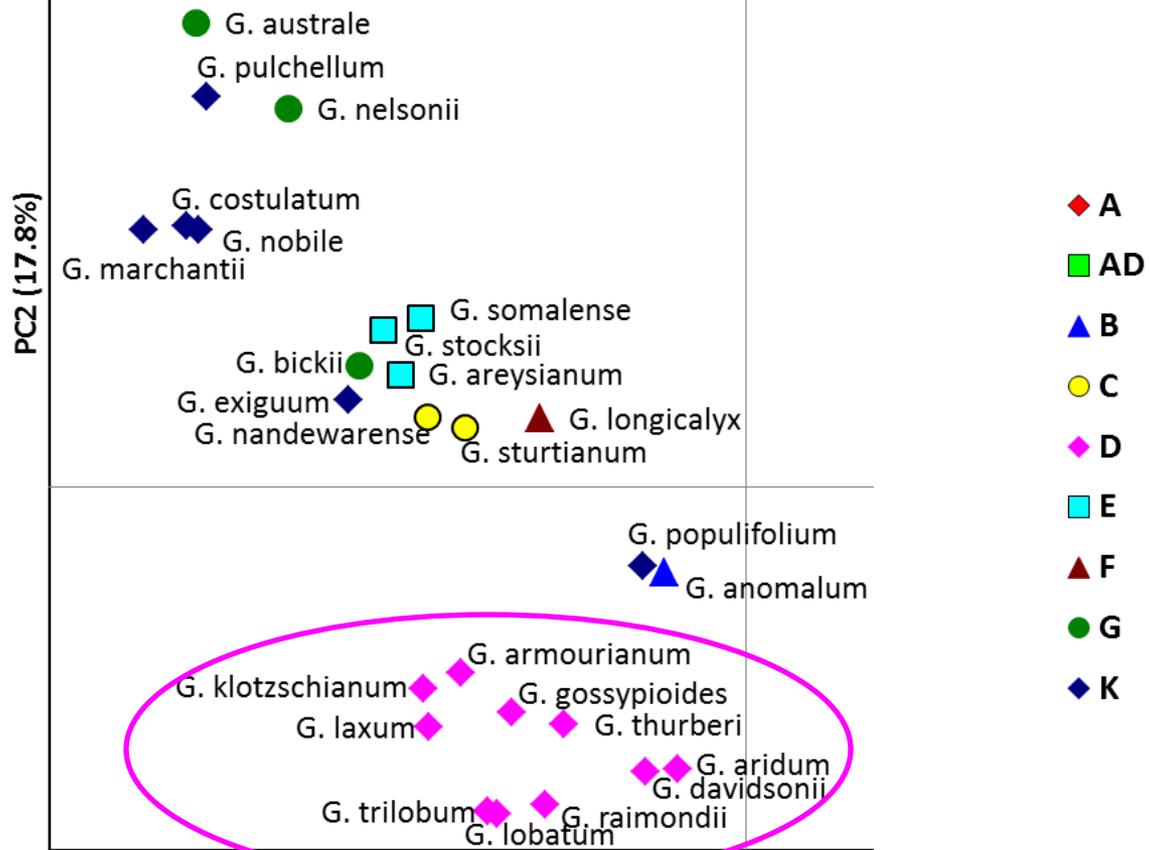
***G. arboreum* and *G. herbaceum* group with non-cultivated tetraploids**



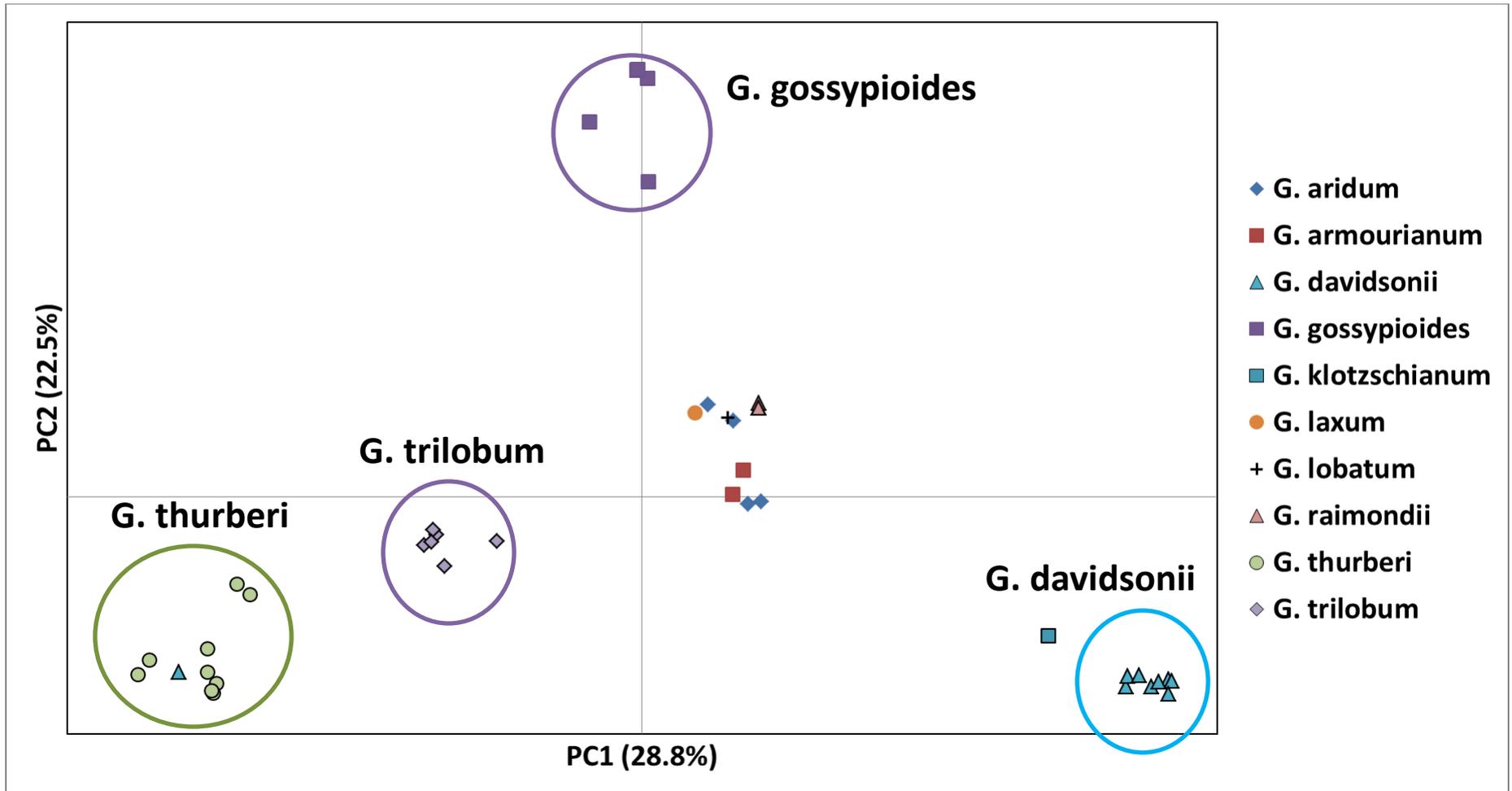
Within *G. arboreum* diploids, accessions from China and India appear to form separate clusters



PCA separated 10 D-genome species from other diploids



D genome diploid species form separate clusters



Ongoing Research

- Identify diversity reference sets/core collections for species diversity and traits of interest
- Identify relationships between marker diversity and phenotype
- Identify useful alleles/accessions for breeding programs



In summary, the GDRS is a useful framework to understand the molecular makeup of U.S. NCGC

- Tetraploids show greatest amplification
- Diploid species show low variation with this core set of SSRs
- Need to identify additional SSRs prior to genotyping diploids

Questions?

