



Recent highlights in crop improvement research:

Sorghum (and pearl millet)





New tools for sorghum



- Sorghum genome sequenced
 - 8X sequence available; initial assembly essentially complete; analysis well underway
 - Genes largely confined to chromosome ends
 - Synteny appears to hold very well across the rice and sorghum genomes

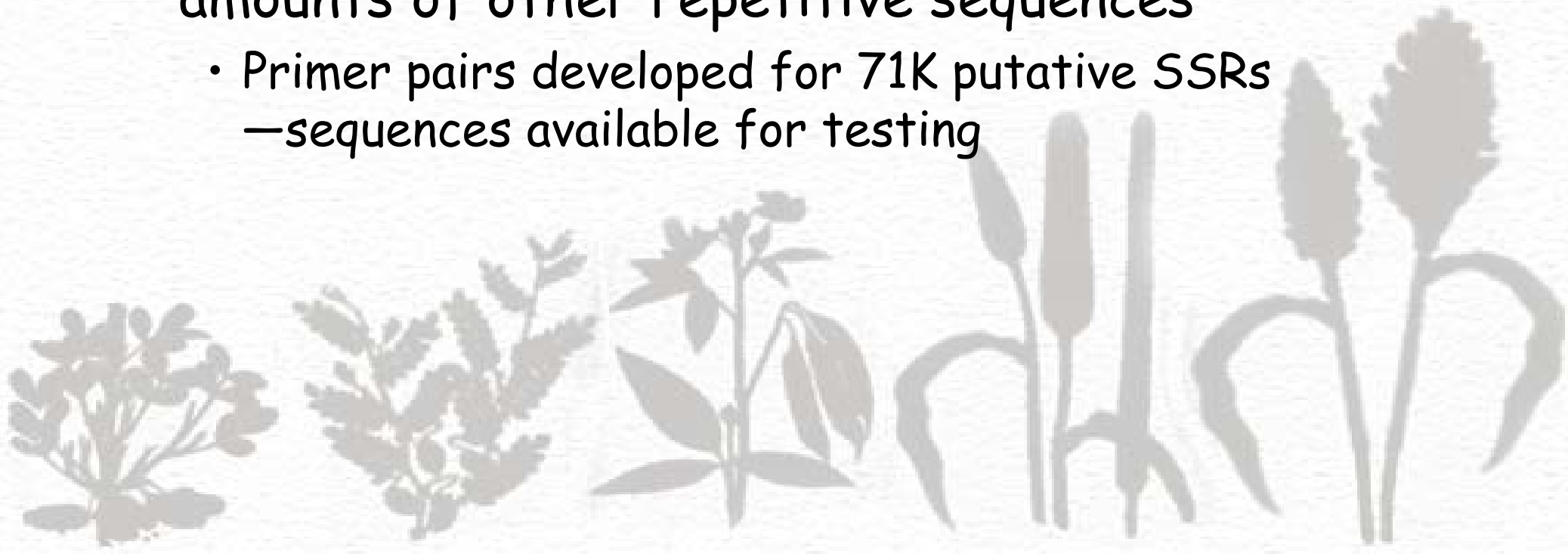




New tools for sorghum



- Sorghum genome sequenced (continued)
 - Major difference of sorghum genome compared to that of rice is 4X more heterochromatin in centromeric regions and modest increase in amounts of other repetitive sequences
 - Primer pairs developed for 71K putative SSRs
 - sequences available for testing

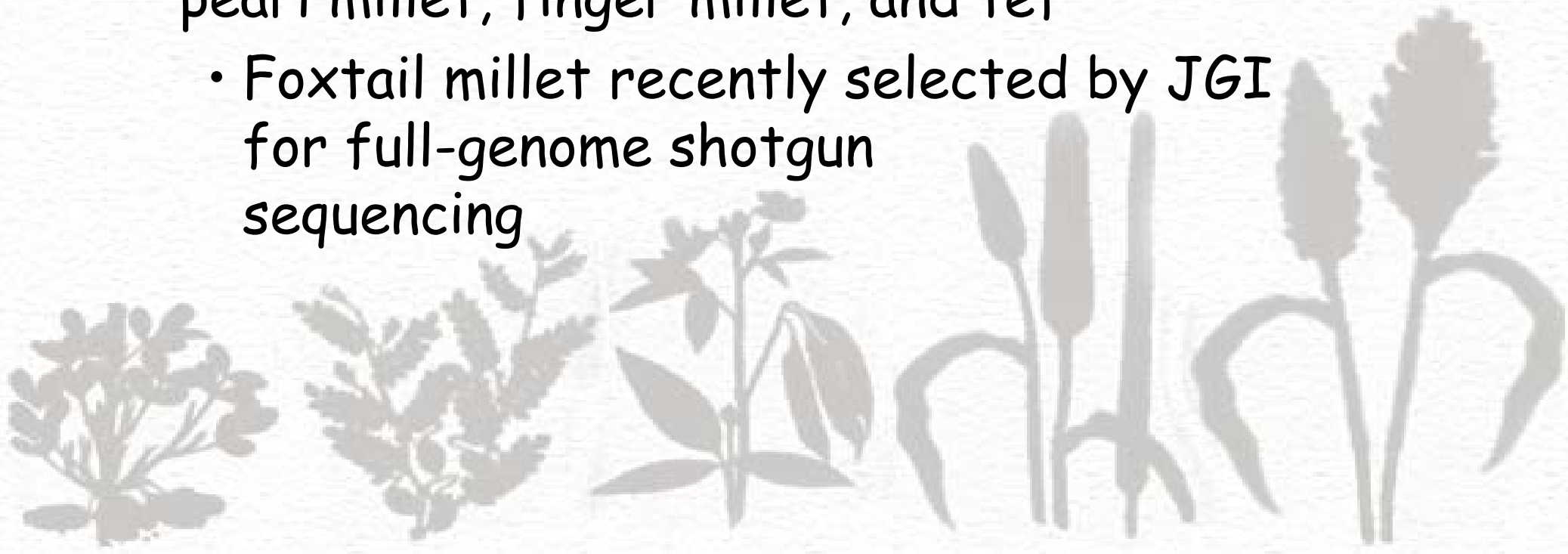




New tools for sorghum



- Sorghum genome sequenced (continued)
 - Comparisons with rice suggest that methyl-filtered libraries will be enough for genome sequencing of orphan cereal species such as pearl millet, finger millet, and tef
 - Foxtail millet recently selected by JGI for full-genome shotgun sequencing

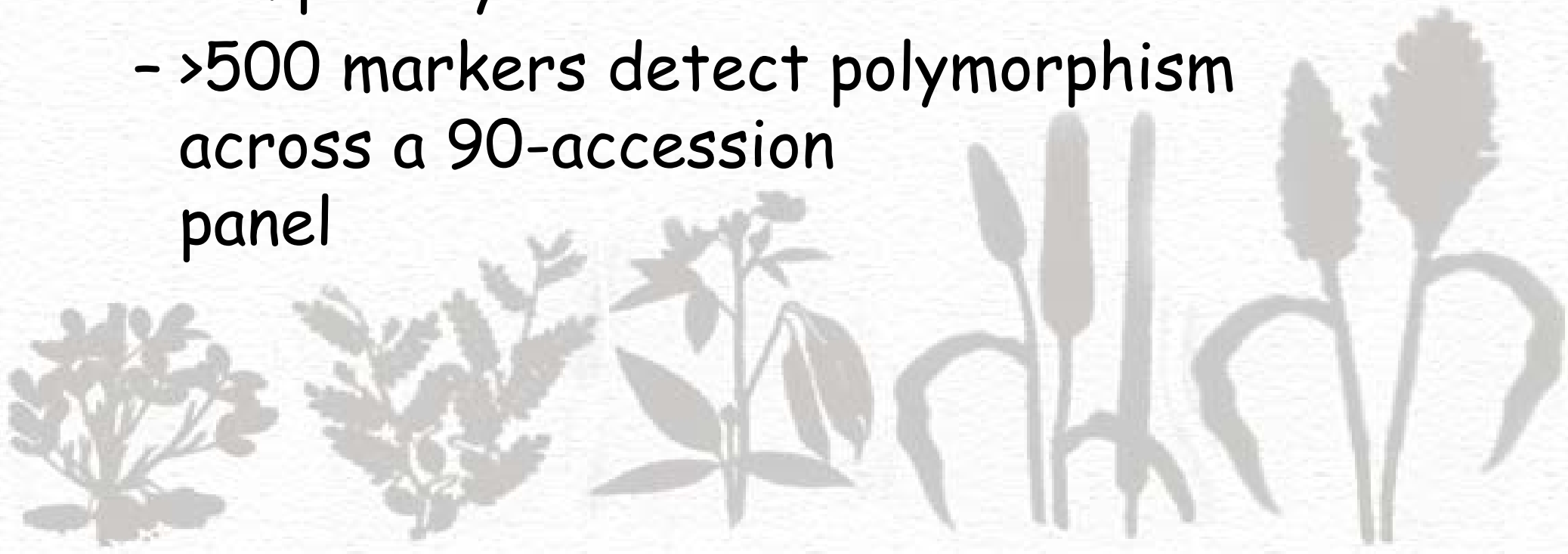




New tools for sorghum



- Sorghum DArT™ array (Mace et al., 2007; BMC Genomics, in review)
 - 12,000-clone array based on *PstI*+ *BanII* complexity reduction
 - >500 markers detect polymorphism across a 90-accession panel



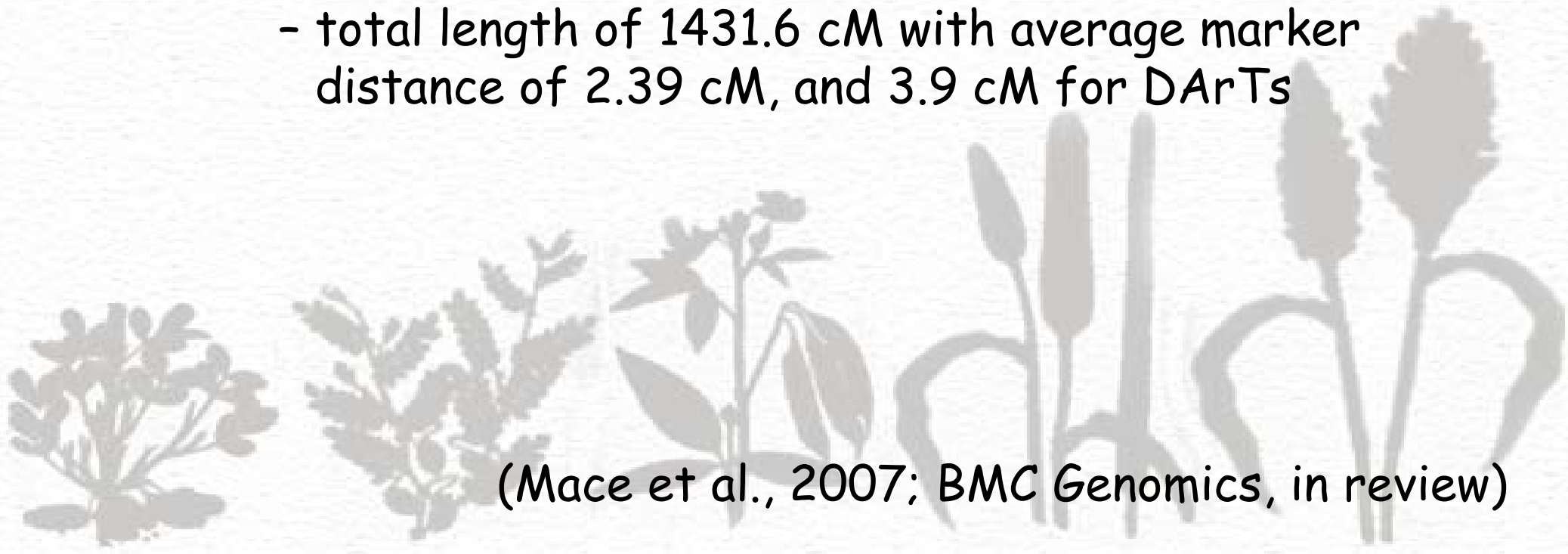


New tools for sorghum



- Sorghum DArT™ array (continued)
 - integrated map based on DArT and other markers confirms Mendelian segregation
 - 596 total markers mapped in R 931945-2-2 x IS 8525
 - total length of 1431.6 cM with average marker distance of 2.39 cM, and 3.9 cM for DArTs

(Mace et al., 2007; BMC Genomics, in review)





New tools for sorghum



- Sorghum DArT™ array (continued)
 - CIRAD has adopted this technology, showing that results for diversity analysis largely agree with those based on RFLP and SSR markers
 - ICRISAT is in the process of adopting DArT technology





New tools for sorghum



- TILLING populations
 - BTx623-based population developed at Texas Tech University
 - same genetic background as available BACs and genome sequence
 - Second population developed at University of the Southern Cross





New tools for sorghum



- Small Illumina chip for sorghum
 - Developed in IGD at Cornell University
 - Circa 350 features
 - Use demonstrated in diversity analysis of panel of "converted" sorghums
 - Manuscript recently accepted in Crop Science





New tools for sorghum



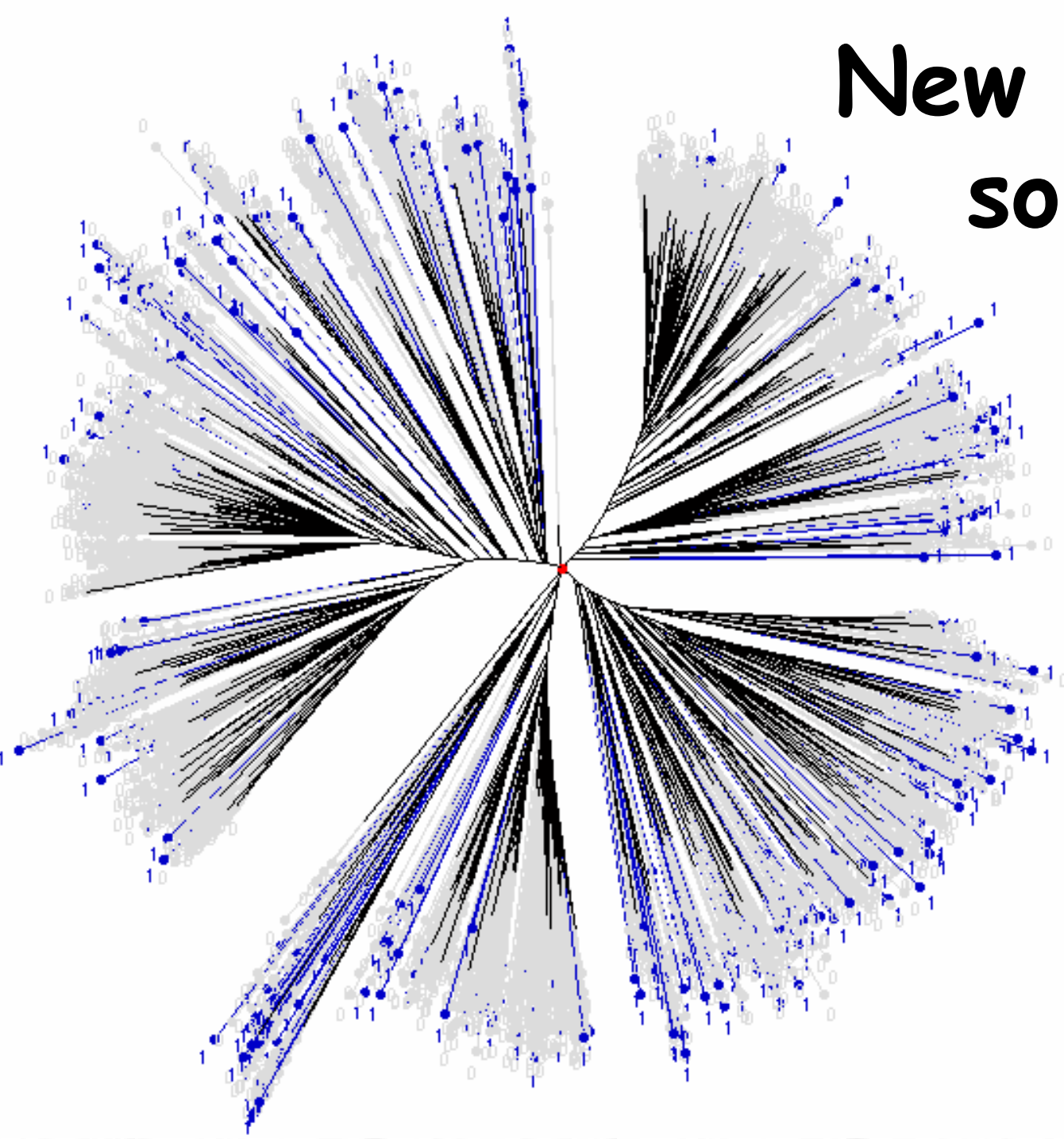
- 384-entry GCP sorghum reference set
 - selected from 3365 accessions based on amplification product diversity from 41 SSR primer pairs
 - represents wild and landrace variability available to sorghum breeders, as well as race x geographic origin
 - DNA currently available for 350 of 384
 - seed for 170 of 384



New tools for sorghum



- 384-entry GCP sorghum reference set





Ready to begin sorghum allele mining



- Suggested targets:
 - Genes underlying stay-green QTLs associated with
 - improved terminal drought tolerance
 - better stover feed value, and,
 - increased sweet sorghum productivity
 - Alt_{SB} for aluminum tolerance (underway in GCP)
 - Brown midrib genes associated with
 - lignin biosynthesis
 - Forage/stover digestibility, and,
 - ease of juice extraction





New tools for pearl millet



- TILLING population
 - P 1449-2-based population being developed at ICRISAT
- Additional genomic SSRs under development
 - >500 sequenced clones from an enriched library show promise





Marker-assisted backcrossing during 2006/07



- Sorghum
 - *Striga* resistance
 - Stay-green component of terminal drought tolerance
 - Shoot fly resistance
 - Aluminum tolerance
- Pearl millet
 - Downy mildew resistance
 - Terminal drought tolerance
 - Stover yield & quality





Marker-assisted breeding products

- Pearl millet in India
 - Downy mildew resistance
 - “HHB 67 Improved” is now being adopted by farmers & the seed industry in India
 - Seed of new hybrid for 50,000 ha in 2007
 - DM increasing on original “HHB 67
 - Expect 250,000 ha coverage by “HHB 67 Improved” in Rajasthan and Haryana during 2008 rainy season





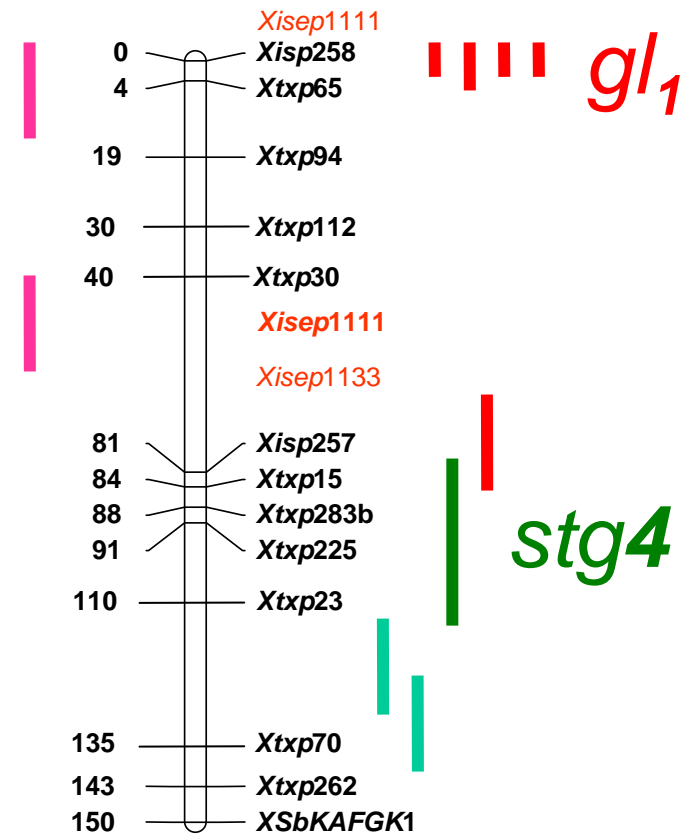
Markers still a constraint



- While QTL mapping has identified flanking markers for several sorghum QTLs

- many of the markers are not polymorphic in elite genetic backgrounds,
- many of the mapped markers are not easy to use, and
- the SSR-based linkage maps have many large gaps.
- Therefore we clearly need more mapped markers, and are working to map more.

SBI-05





*Thanks for your
kind attention!*