

Quantitative Genomic Analysis of Leaf Architecture in Sorghum.

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BACKGROUND

The global population is expected to reach 8 billion by 2030, at the same time, the globally available arable land per capita is expected to reduce by close to 20% by 2030 (source FAO.org). This poses the challenge of how to increase our crop productivity per land size to ensure global food security. Breeders have approached this through the breeding of crop ideotypes, that is plants with model traits (short height, erect leaf angle and inflorescence morphology) known to influence photosynthesis, growth and grain production (Donald, 1968). Therefore, it is imperative to understand the genetic basis of these traits for genomic enabled breeding targeting crop improvement for increased yield. However, complex traits like these are difficult to map by QTL analysis techniques involving association mapping as they are limited in power to detect the genes underlying the complex traits due to confounding population structure, low-frequency alleles and allelic heterogeneity. Therefore to solve these problems, the newly developed NAM population offers a leverage and higher power by being able to manipulate allelic frequency and population structure to its advantage.

OBJECTIVE

The objective of this study is to:

- Understand the genetic architecture of leaf angle and leaf width in sorghum in terms of numbers of QTL underlying the traits, their effects and frequencies.

METHODOLOGY

- The NAM population was generated by a cross between a common parent (RTx430) and 10 diverse parents to generate 2500 recombinant inbred lines (F_7 and F_8).
- The NAM population was evaluated in two locations (semi-arid in Western Kansas and humid continental in Eastern Kansas) for two years.
- The RILs were phenotyped for leaf angle and pre-flag leaf width.
- Genome Wide Association Mapping and Joint Linkage Analysis were performed with ~100,000 markers using multi locus mixed model (Segura et al. 2012) and stepwise regression plugin in TASSEL 5.0 (Bradbury et al. 2007)
- Cross validation was performed using ridge regression-Best Linear Unbiased Prediction (rrBLUP) implemented in R (Endelman, 2011).

RESULTS

- Heritabilities of 0.67 and 0.14 were observed for leaf angle and pre-flag leaf width respectively.
- Only about 5 of the identified QTL (44 QTL) for both traits were large effect QTL while the rest were minor effect QTL.
- QTL were found to be associated with genes involved in auxin and ethylene biosynthesis and leaf developmental biology e.g. Lateral Organ Branching (LOB), Homeodomain Leucine Zipper (HD-ZIP), YUCCA 5 (Flavin Monooxygenase), Apetalla 2 (AP2).
- The two traits appear to be under the control of low to moderate frequency QTL
- Cross validation results showed a high correlation between observed and predicted trait values for leaf angle (0.70) while leaf width showed a lower prediction accuracy (0.33).

CONCLUSION

- Leaf architecture in sorghum appear to be characterized by a few major effect QTL and many low effect QTL signifying the quantitative nature of the traits.
- The use of the NAM population enabled the accurate estimation of the effects of the QTL and also facilitated the effective mapping of these traits.
- The genes found to be associated with QTL underlying leaf angle and leaf width will provide a pedestal for future works using molecular genetic approaches to characterize them.
- Cross validation prediction results and important QTL identified in this study elucidates the potentials of marker assisted selection and genomic selection for breeding programmes targeting leaf architecture traits for improved yield.

REFERENCES

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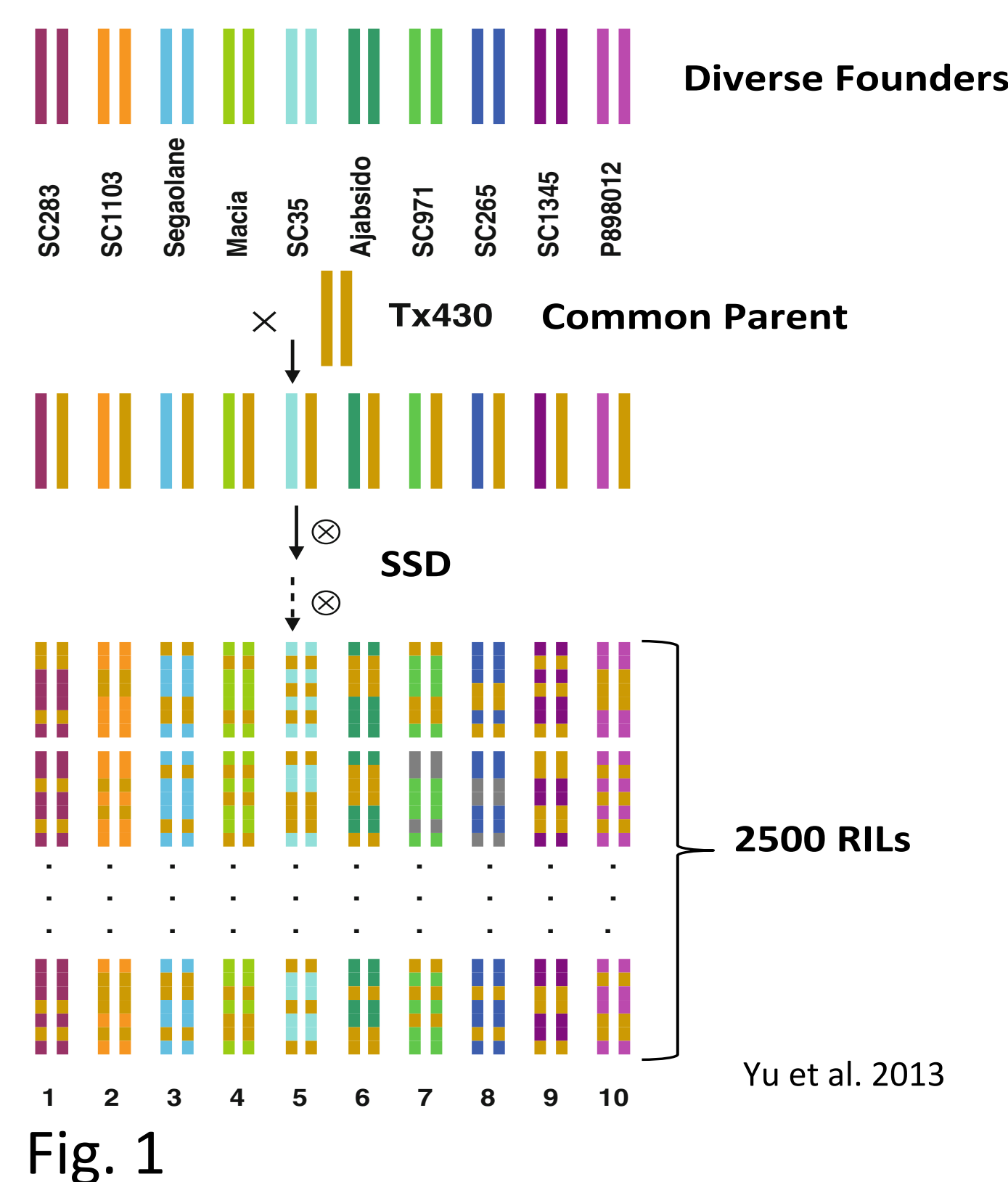


Fig. 1

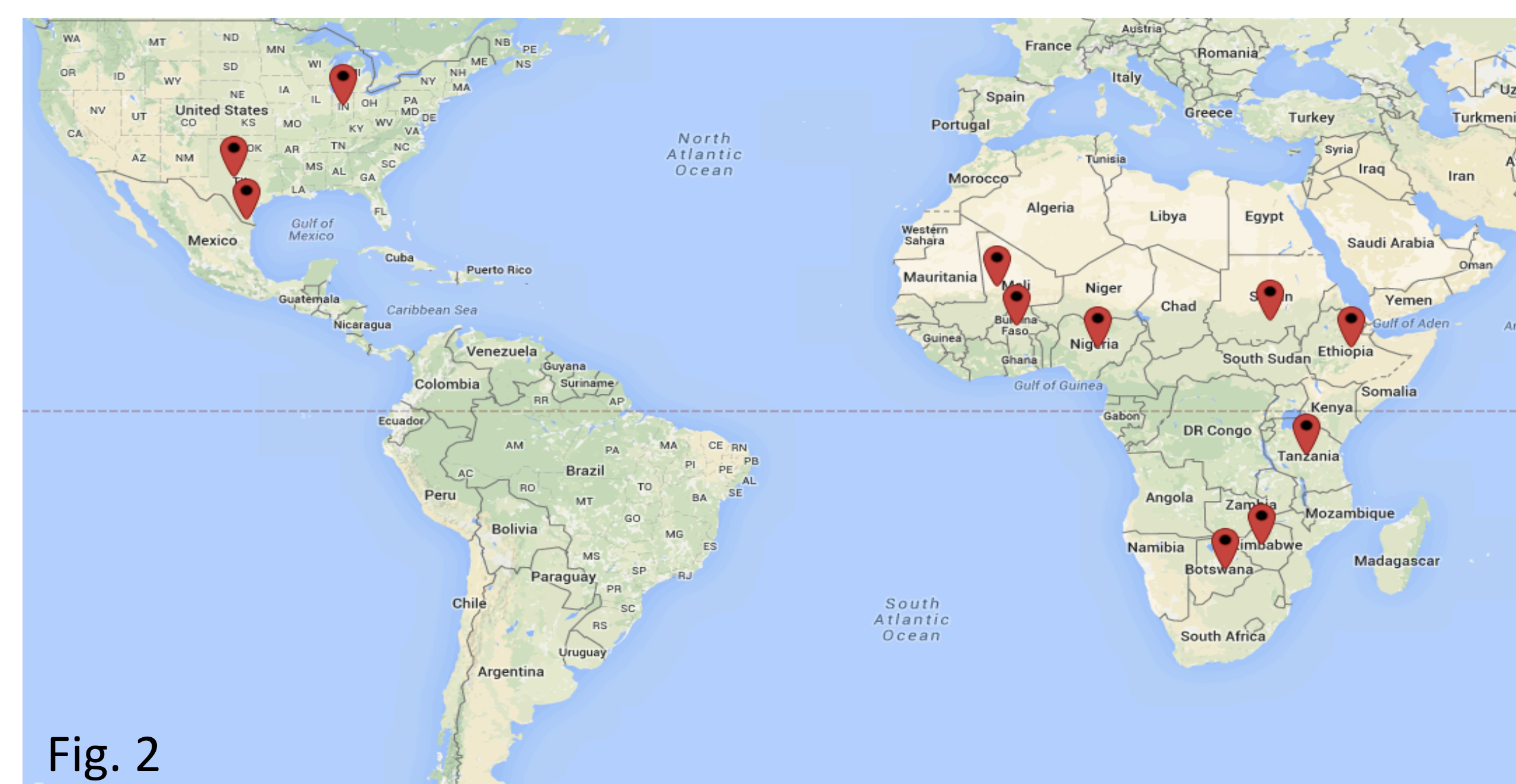
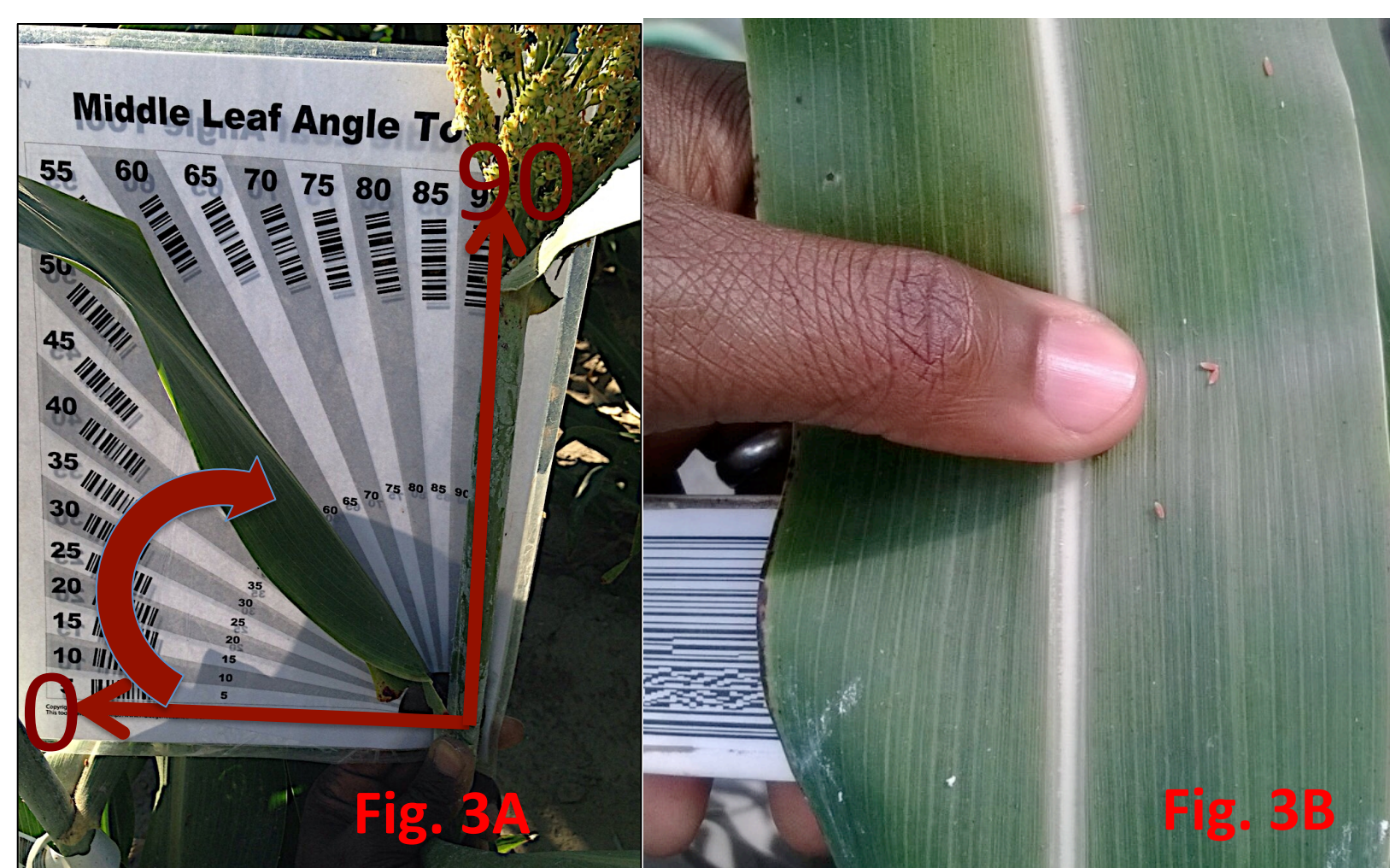


Fig. 2

Fig. 1: Schematic overview of Sorghum NAM design.

Fig. 2: Geographical origin of NAM founders



Fig. 3 Leaf angle measurement (A) leaf width measurement (B)

Fig. 4 NAM population field trial in (A) Manhattan (Humid Continental) and (B) in Hays (Semi Arid)

GWAS AND JOINT LINKAGE RESULTS

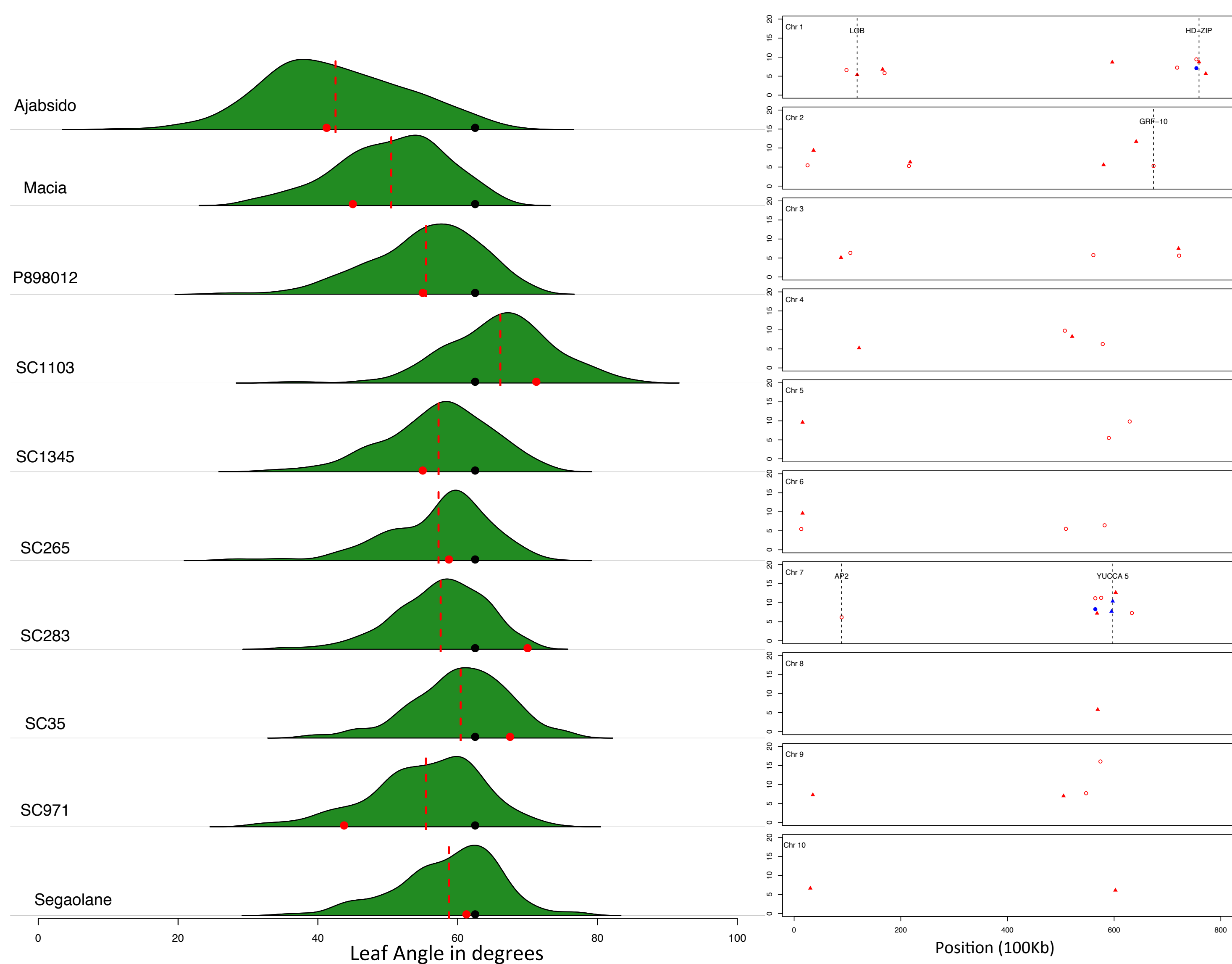


Fig. 5 Density plots showing phenotypic distribution for leaf angle across the 10 NAM families. Fig. 6 Plots showing the physical distance (100kb window) on the x-axis and -log of p-values on the y-axis. Triangles are QTL for leaf angle (red: joint linkage; blue: GWAS) and open and solid circles are QTL for pre-flag leaf width (red: joint linkage; blue: GWAS)

CROSS VALIDATION RESULTS

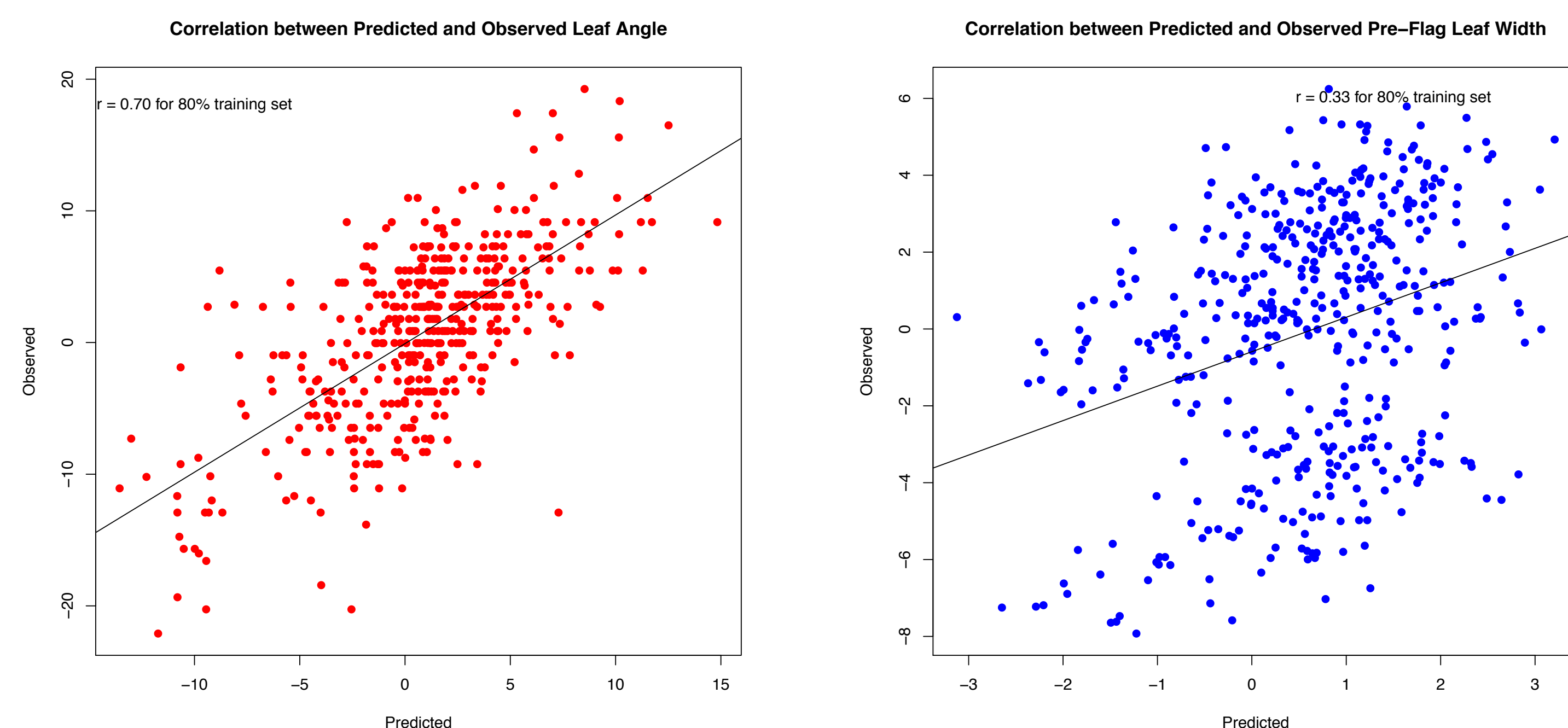


Fig. 8(A) Correlation between predicted and observed trait values for leaf angle. 8(B) Correlation between predicted and observed trait values for leaf width

Pre Flag Leaf Width QTL Effect

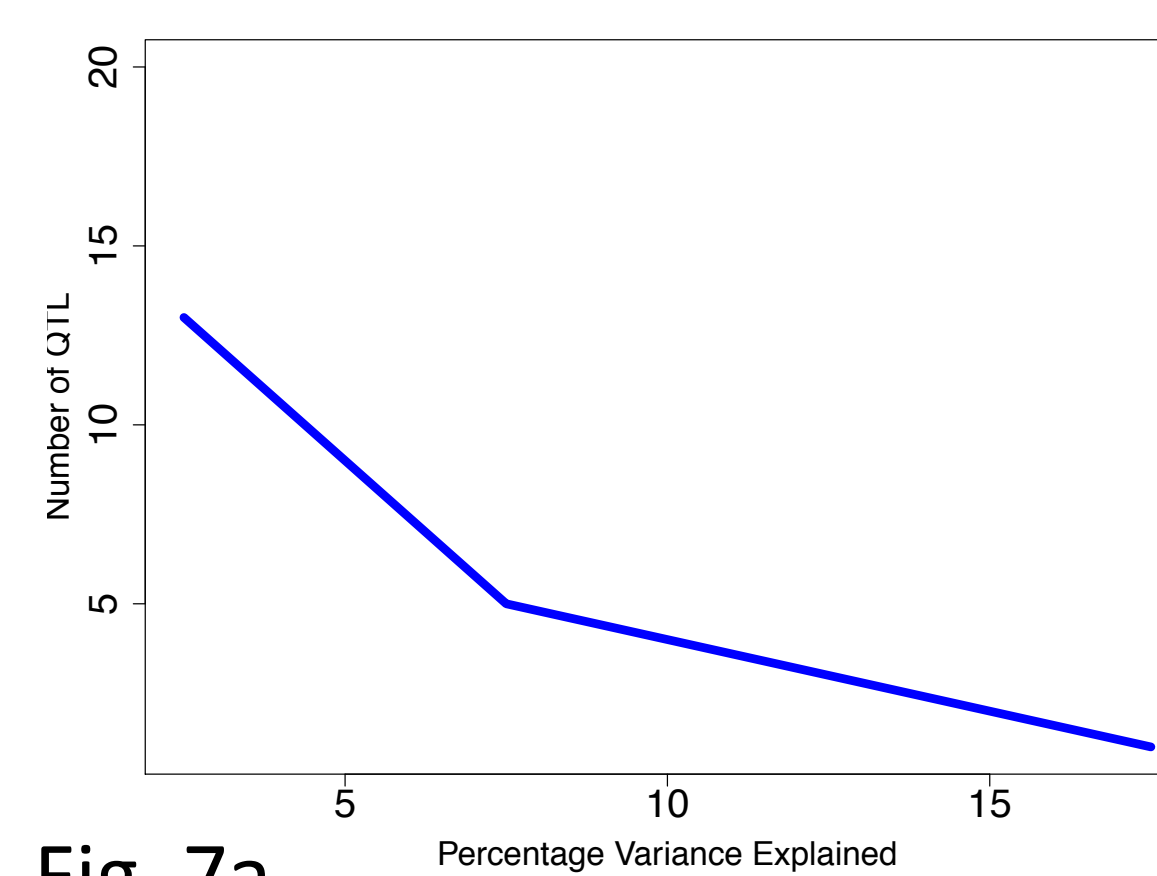


Fig. 7a

Leaf Angle QTL Effect

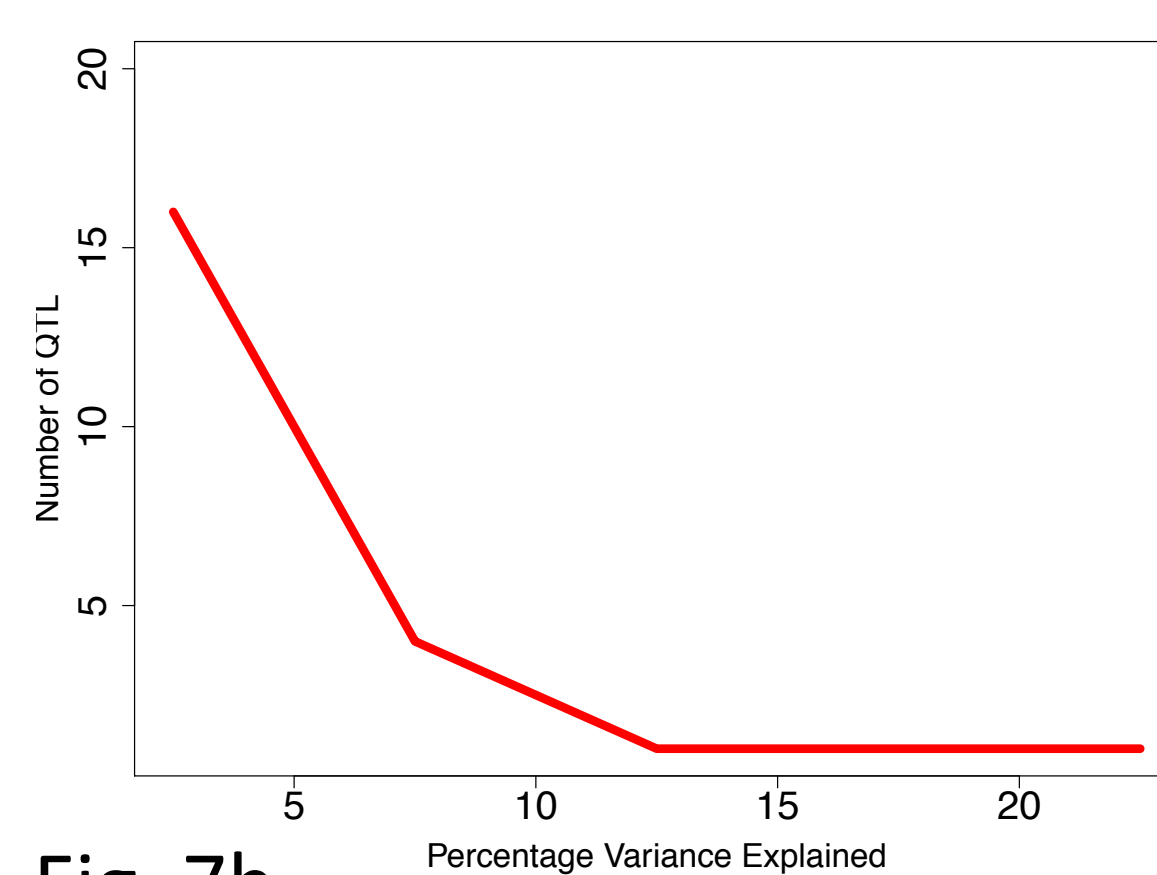


Fig. 7b

QTL Frequencies

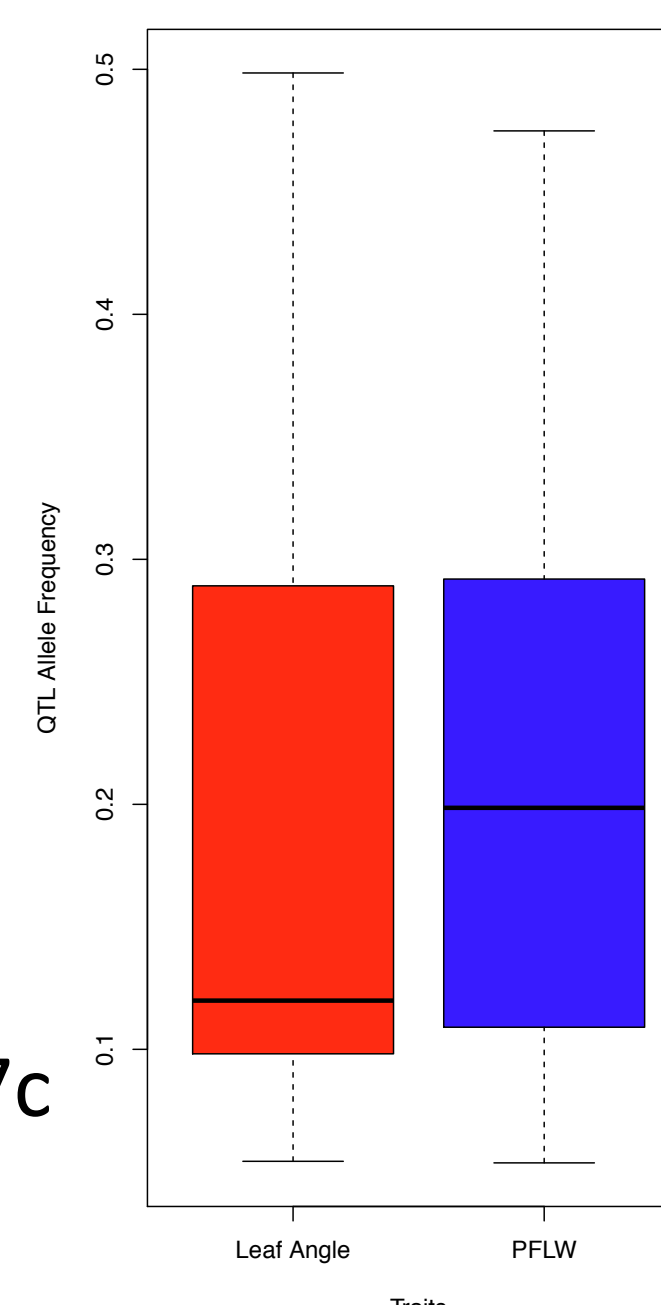


Fig. 7c

Fig. 7a,7b:Proportion of variance explained by QTL in pre flag leaf width and leaf angle. Fig. 7c: Distribution of QTL frequencies for pre flag leaf width and leaf angle