

The genetic control of tissue growth under water-limited conditions

Reduction in leaf expansion is one of the first responses to water deficit. It is assumed that the control of tissue development under water deficit contributes to traits such as early vigor, as well as maintenance of growth of reproductive organs, which may be important components of crop drought resistance. To reduce the effect of drought on yield, new approaches for bridging traditional breeding to molecular genetics are needed. To dissect the underlying mechanisms controlling tissue expansion under water-limited conditions, we used a multilevel approach combining whole plant modeling, quantitative genetics, and genomics.

The overall aim of this project is to identify QTL regions and candidate genes controlling tissue regulation, develop models to predict how different allelic combinations impact growth under different drought scenarios, and, ultimately, develop new phenotypic and genetic selection criteria for efficient breeding.

I. Quantitative genetics

The Vandana/Moroberekan backcross population was evaluated in the field under well-watered conditions (wet season screen) and vegetative-stage drought stress (dry season screen). QTL analysis was conducted on traits related to leaf morphogenesis and expansion measurements.

II. Modelling

The dynamics of leaf growth as affected by environmental variables was investigated in two accessions; Apo (drought-tolerant) and IR72 (drought-sensitive). For drought treatments, the dry-down method was used, which allowed soil moisture (fraction of transpirable soil water; FTSW) to be used as the stress covariable.

III. Transcript profiling

Changes in candidate genes related to cell elongation were investigated in Apo, IR64, IR72, IR71525-19-1-1, and Moroberekan. The dry-down method was used and the zone of leaf expansion sampled at FTSW 0.6, 0.4, and 0.1 in stressed pots. Controls were simultaneously sampled.

Results

Water deficit significantly reduced the rate of leaf production and total number of leaves across genotypes. Under drought stress, Vandana invested a significantly higher proportion of its above ground biomass in leaves than did Moroberekan. Within the BC population a large phenotypic variation for biomass partitioning was observed, ranging from 16% to 74% in leaves at 977 °C days. Significant variation was also noted in rate of leaf area production under stress (Fig1).

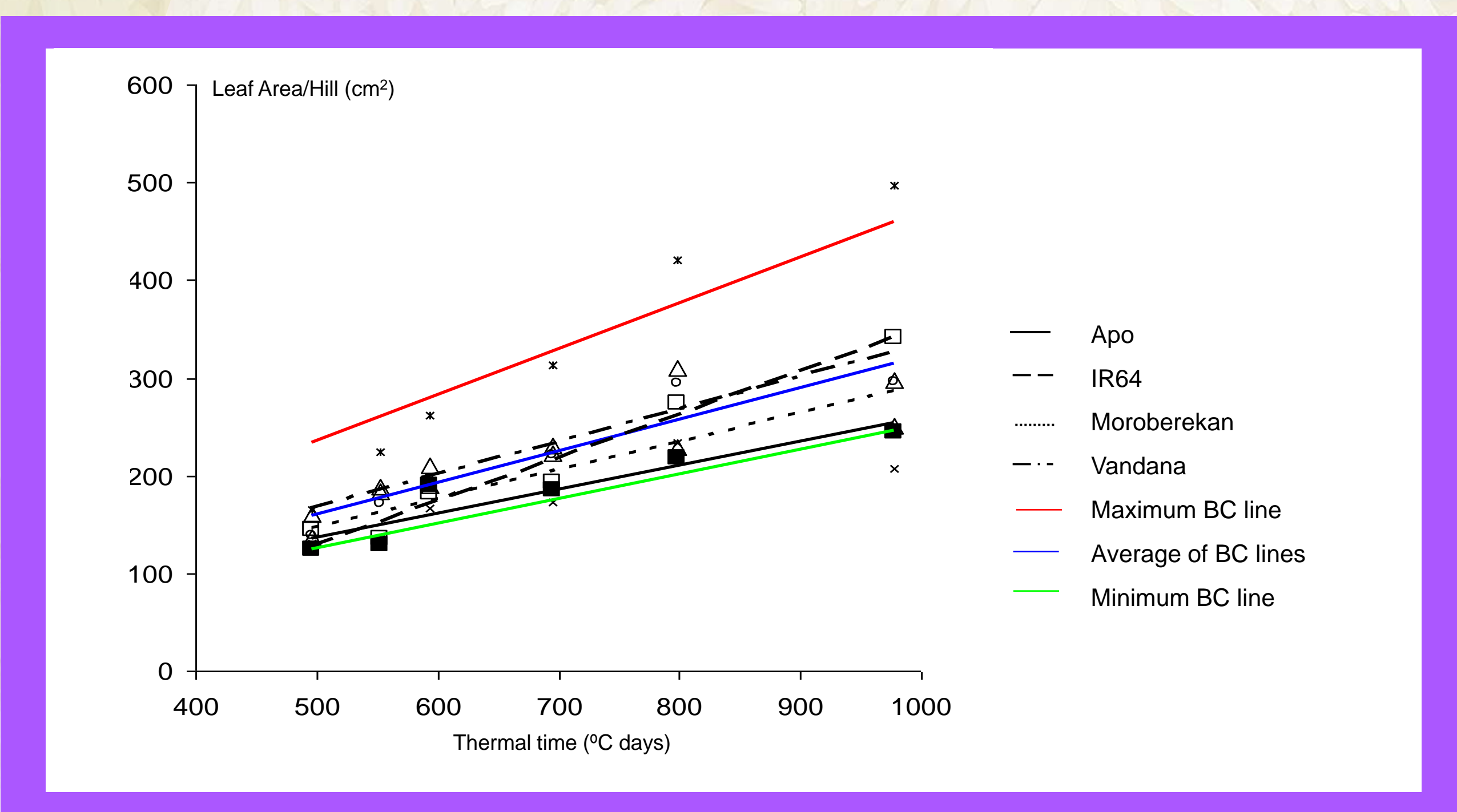


Fig 1. Leaf area development during drought stress in four accessions and average of the BC populations. The two BC lines with the highest and lowest increase in leaf area are also presented.

A total of 20 significant QTLs were identified for leaf elongation, leaf area, phenology, biomass partitioning, and accumulation. These were located in 14 regions (Fig 2). The Moroberekan allele contributed positively to 12 QTLs. Two regions (on chromosomes 2 and 4) had more than one QTL for growth under drought stress. Only one region was common for both shoot growth ability and shoot growth maintenance (chromosome 4, between markers *RM241* and *RM348*). However, under well watered conditions, the Vandana allele had a positive affect on growth, whilst under drought stress, the Moroberekan allele positively affected shoot growth.

Environmental factors strongly influenced elongation rate. Elongation consistently started to decrease at higher soil water content compared with transpiration (Fig 3). Significant genotypic variation in the FTSW threshold value, at which leaf elongation began to decrease was observed. Increasing VPD decreased leaf elongation rate; this difference was more pronounced under well watered conditions.

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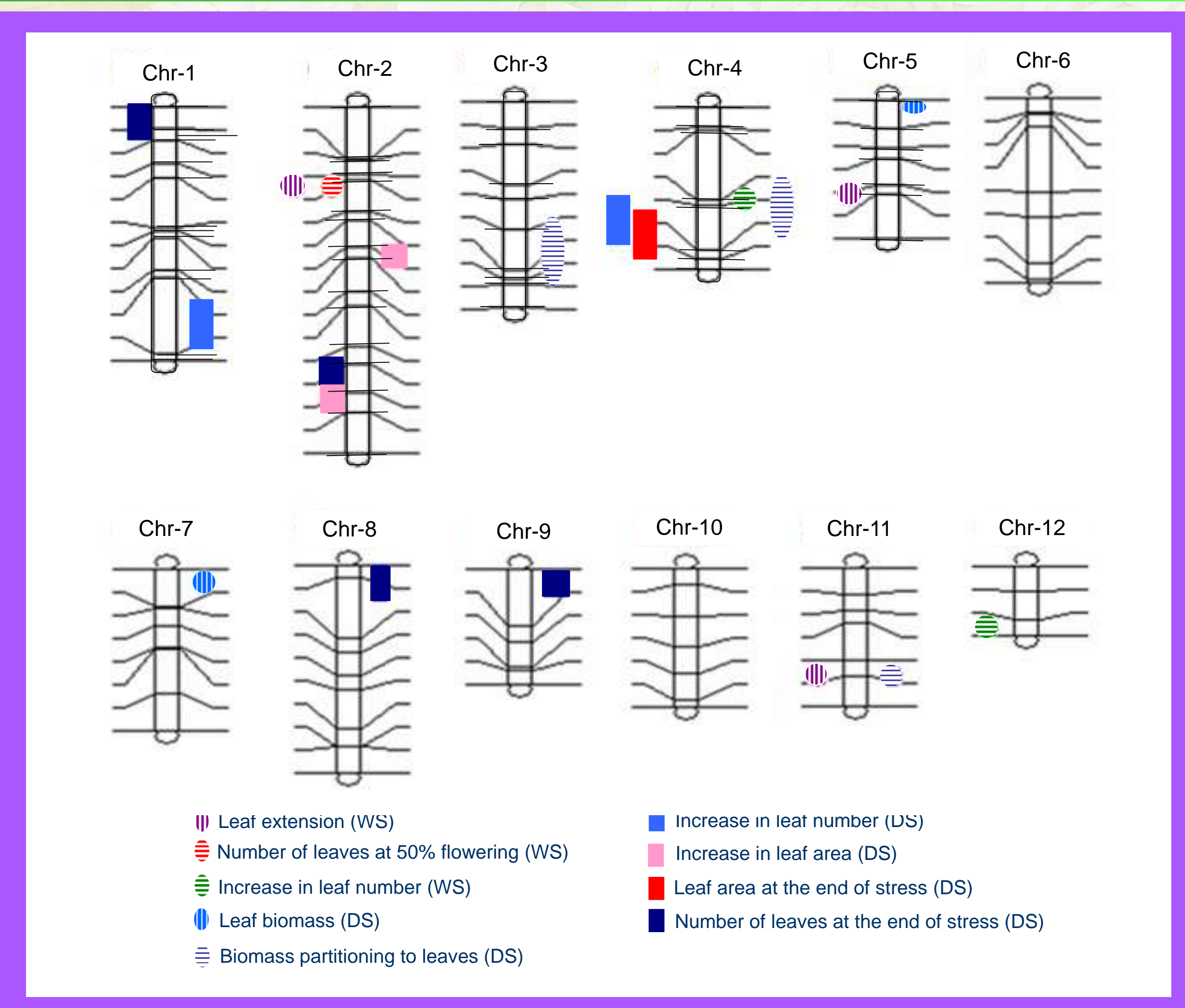


Fig 2. QTLs identified for leaf growth and development in the dry season (DS) and wet season (DS). Boxes and circles represent 1 LOD score. For boxes and circles on the left of the chromosome the Moroberekan allele increased the trait; on the right of the chromosome the Vandana allele increased the trait.

Leaf expansion was not restricted to one leaf per tiller, under drought stress, leaf expansion decreased at the same rate across tillers. Expansion was greater during the day than at night.

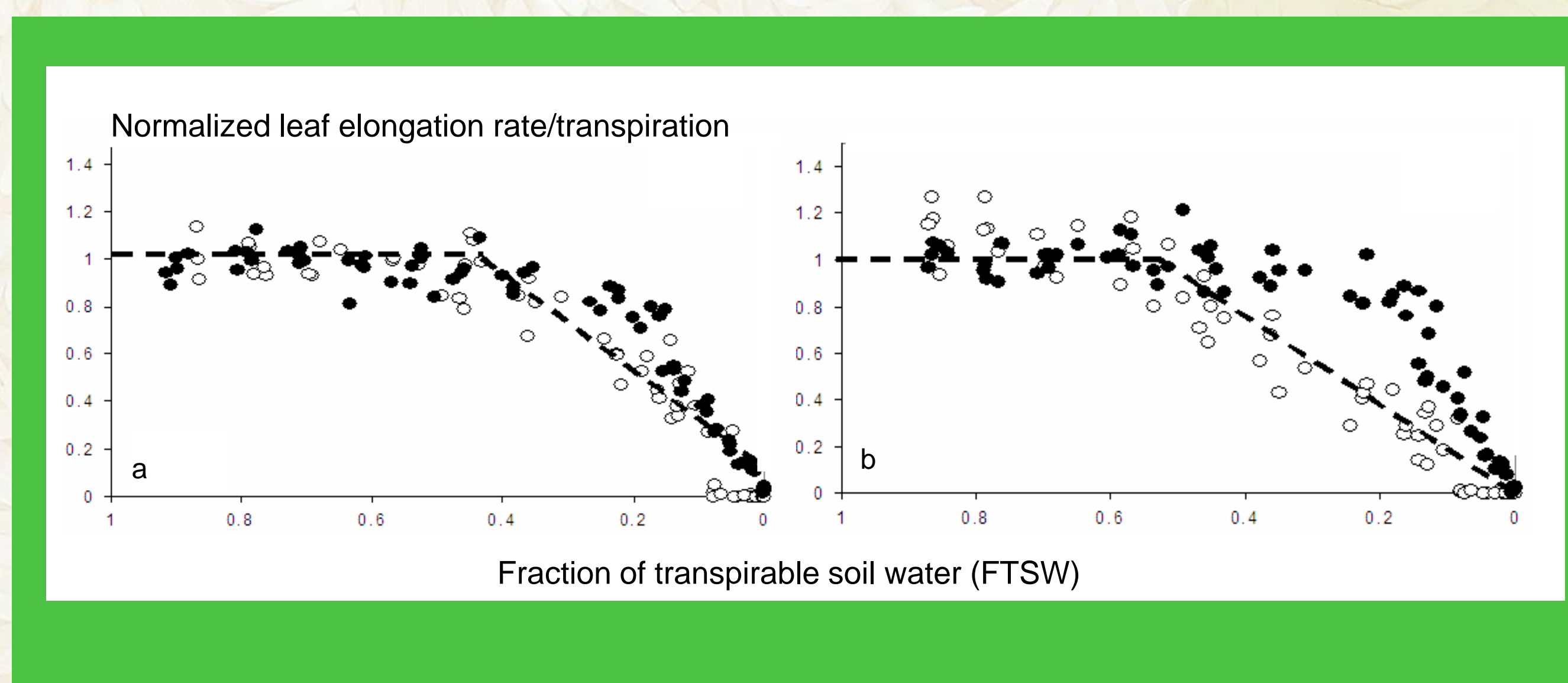


Fig 3. Comparative analysis of leaf elongation rate and transpiration responses to soil drying (FTSW) in a) Apo (drought-tolerant) and b) IR72 (drought-sensitive). The black circles represent normalized leaf elongation rate and white circles normalized transpiration.

Four expansins and five genes related to drought response were chosen from RT-PCR results for QPCR. Highly significant differences were observed in expression patterns of genes between the cultivars. There was a significant interaction of the level of stress intensity (FTSW). Many expansins had higher expression at FTSW 0.4, corresponding to when leaf elongation began to decline. *EXPA2* had the highest expression of the four expansins.

Conclusion

The mechanisms of tissue growth regulation under drought stress are being unraveled using quantitative genetics, modeling, and transcript profiling. Leaf elongation is strongly influenced by environmental factors, however, significant genotypic variation was identified. Two regions of the genome and candidate genes related to tissue growth maintenance under drought stress were identified and are currently being confirmed.

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