

Identification of orthologous regions associated with tissue growth under water-limited conditions

Plant recovery from early season drought is related to the amount of biomass retained during stress and biomass production after the end of stress. 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. To dissect the underlying mechanisms controlling tissue expansion under water-limited conditions, we used a multilevel approach combining quantitative genetics and genomics.

To identify orthologous genetic regions controlling tissue growth under water-limited conditions a series of QTL mapping and microarray gene expression studies were conducted in rice and maize. Results of differentially expressed genes from microarray experiments, QTLs and candidate genes related to growth in the different species are compared on consensus maps (within species) and then on synteny maps (between species), to identify common genetic regions between rice and maize.

Identification of QTLs associated with leaf growth

i) rice

The Vandana/Moroberekan backcross population was evaluated in the field over three seasons (2005-2007). Leaf expansion and morphogenesis were measured and QTL identified.

ii) maize

Leaf elongation rate of the 6th leaf was measured in the greenhouse on 200 RILs from a mapping population developed at CIMMYT in the sixth inbreeding level from the cross between 2 tropical maize inbred lines, Ac7645 and Ac7729/TZSRW (Welcker et al. 2006).

Comparison of rice QTL and gene expression data

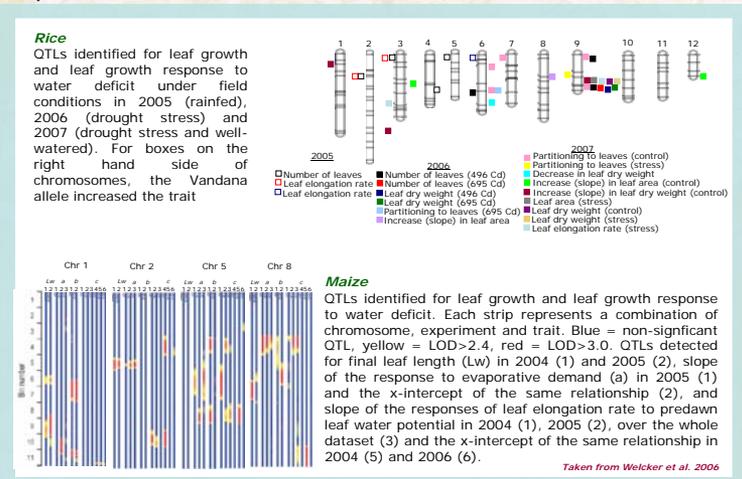
Microarray was performed on the 6th leaf of Vandana, Moroberekan and 2 backcross lines under well-watered and water-limited (FTSW 0.5) conditions. Differentially expressed gene (DEG) aggregates were computed from comparisons between the two water levels. QTL and DEG aggregates were plotted on the rice genome using TIGR (Osa1 release 5).

Identification of orthologous regions in maize and rice

QTL positions in the physical genome were inferred using coordinates of the corresponding markers onto the physical genome. Coordinates of rice SSR markers on the physical map were determined by searching the Gramene annotation of the TIGR rice genome ver5 (www.gramene.org/) for positions of well-durated markers or a similarity search using the BLAST-like Alignment Tool (BLAT, Kent 2002) against the full-length contigs of TIGR rice genome ver 5.0 (tile size = 6-8) with the published sequence or primers of SSR markers on Gramene. Coordinates of maize RFLP markers on the physical maps were determined by searching the Maize Genome Sequence (www.maizesequence.org) annotation of the draft sequence available for available annotation of the positions of the maize markers. Rice-maize genome synteny information was obtained from Gramene.

QTLs associated with leaf growth in rice and maize

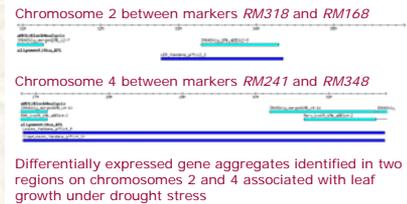
Many QTL were identified in rice and maize controlling leaf growth under water-limited and well-watered conditions. In each crop, several regions were detected across traits and/or experiments.



Rice and maize under experimental conditions

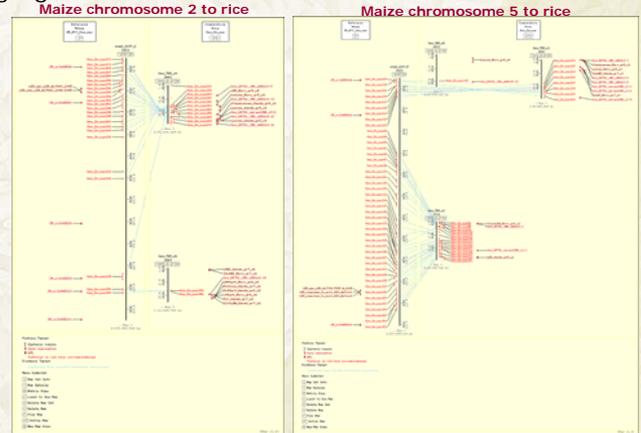
Differentially expressed gene aggregates in rice: colocalization with QTL associated with leaf growth

Several QTL regions associated with leaf growth under drought stress contained differentially expressed gene (DEG) aggregates, although this was not consistent across all genotypes.



Orthologous regions controlling tissue growth under water-limited conditions in rice and maize

The identification of syntenic regions between maize and rice is currently underway. In maize QTL identified on chromosomes 2 and 5 were also identified as QTL controlling leaf growth across experiments and containing DEG aggregates.



Conclusions and future perspectives

To identify a common genetic basis for tissue growth under water-limited conditions the mechanisms controlling leaf growth under water-deficit in rice and maize were dissected using QTL mapping and transcript profiling. Ongoing analysis of orthologous regions has identified several syntenic regions between rice and maize.

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