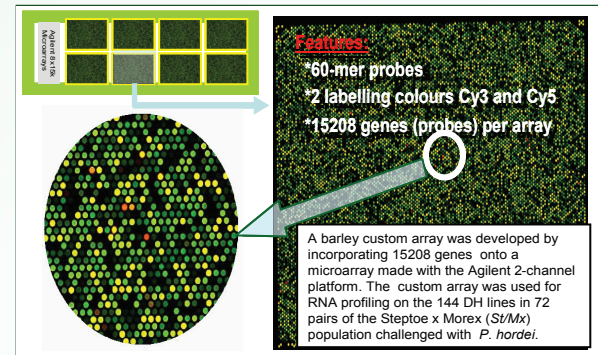


Transcript-Level Variation in Barley Seedling Leaves Challenged with *Puccinia hordei* and the Molecular Basis of Partial Resistance to Leaf Rust

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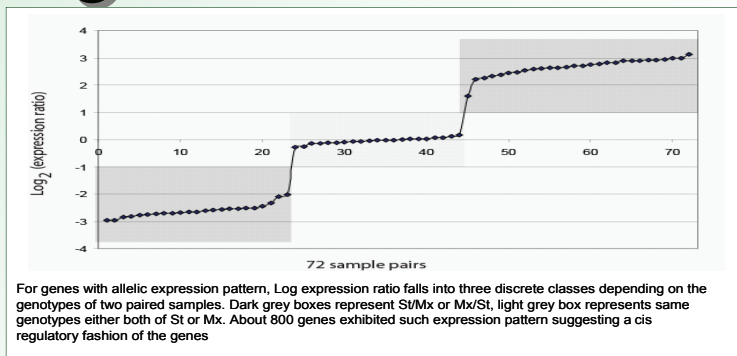
1 Microarray platform: 15k x 8 Barley 2 Agilent custom arrays



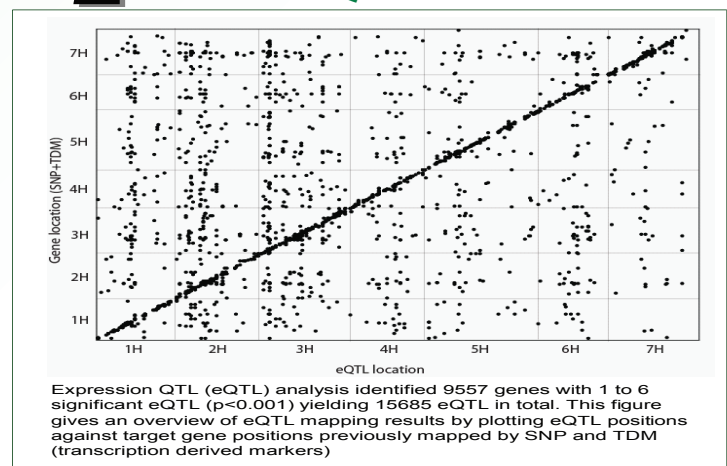
Introduction

In the present study, we employed an integrated strategy combining genetical genomics with genetic mapping to identify candidate genes for QTL previously identified for partial resistance to barley leaf rust. Genetical genomics is a novel strategy which uses transcript abundance as a surrogate phenotype (rust resistance) to map the genetic determinants for variation of gene expression, also known as expression QTL (eQTL) mapping. The advantage of the approach is that many thousands of surrogate phenotypes can be analyzed in a single experiment. eQTL mapping, when jointly analyzed with traditional phenotypic QTL analysis, offers considerable power to link observed transcript variation with phenotypic variation (leaf rust resistance). Co-localization of eQTL and phenotypic QTL can potentially help unravel the molecular basis of the observed phenotype and accelerate the identification of genes underlying partial resistance to leaf rust.

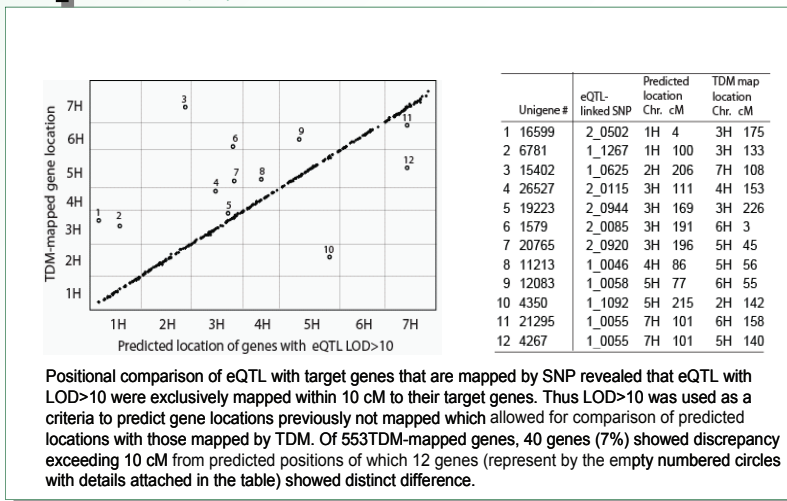
3 Allelic specific expression pattern



2 Overview of eQTL results



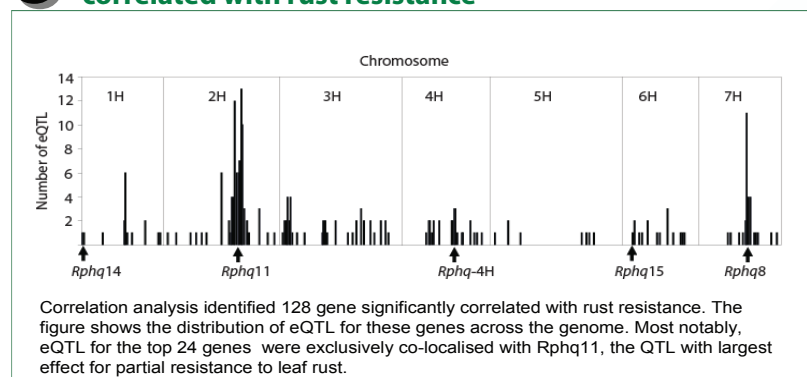
4 Gene locations are predictable on eQTL LOD scores and highly consistent with TDM



Conclusion remarks

By using strategy of genetical genomics in combination with resistance QTL mapping, a number of candidate genes have been identified. Further investigation such as genetic or comparative mapping of candidate genes with rice genome will further refined the candidate gene list. And in addition, ontology analysis of genes correlated with rust resistance and genes with eQTL co-localized with resistance QTL may point to master regulators and regulatory pathways underlying the partial resistance. Knowledge of the genes regulated by the master regulators may provide insight into the molecular and biochemical nature of the resistance, and help cloning the causal genes.

5 Distribution of eQTL for genes with expression correlated with rust resistance



6 Identification of candidate genes on regulatory fashion

Resistance QTL	eQTL	cis	trans	unknown
Rphq14 (1H)	1	1	0	0
Rphq11 (2H)	54	32	2	20
Rphq-4H (4H)	8	4	0	4
Rphq15 (6H)	4	3	1	0
Rphq8 (7H)	26	9	2	15
total	93	49	5	39

Regulatory fashion of eQTL co-localised with the resistance QTLs. Those of genes being cis-regulated are priority candidates, while genes with as yet unknown regulatory fashion are potential candidates for resistance to leaf rust

Acknowledgements

We are gratefully acknowledge the following people for their helpful discussions and assistance throughout the experiment: J. Morris, J. McNicol, L. Ramsay, D. Marshall, L. Milne, A. Gonzalez, Z. Kohutova, F. Meijer-Dekens, R. Agnoulm, F. Yeo.