A45   IDENTIFICATION OF QTLS FOR YIELD AND YIELD COMPONENTS IN RICE BASED ON GxE INTERACTION WITH AMMI MODEL

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Objectives :

The objective of the present study was to identify quantitative trait loci for yield and yield components showing genotypic main effects by AMMI analysis for further detailed research, such as map-based cloning or marker-assisted selection (MAS).
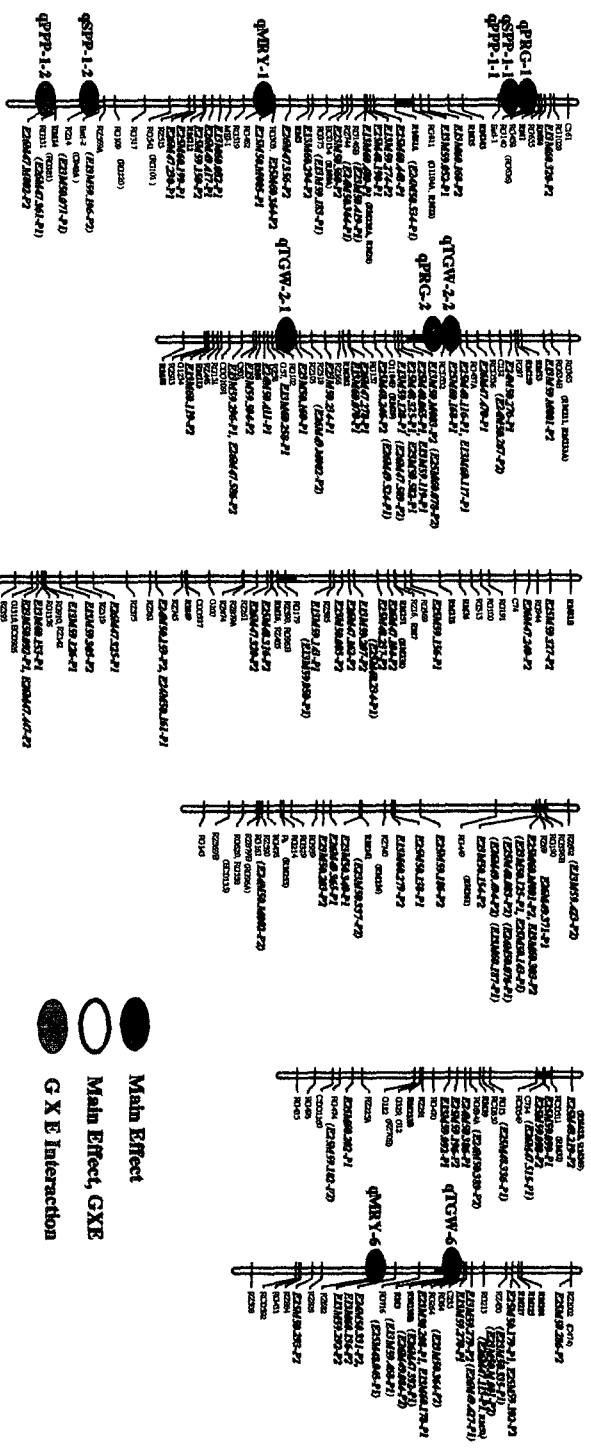
Materials and Methods :

o Population : Milyang23/Gihobyeo RILs - F11('95), F12 ('96), F13 ('97)
o Experimental fields : Iksan, Milyang
o Molecular map : 736 RFLP, SSLP, AFLP markers
  - RFLPs, SSLPs (Dr. SR McCouch), RFLPs (Dr. T Sasaki)
  - New cDNA markers (KRGRP), AFLP (co-work with KeyGene)
o QTLs analyzed : yield and yield components
o G x E analysis : AMMI model
o QTL analysis & permutation test : Qgene(V2.30b_AA), QTL Cartographer(V1.13)
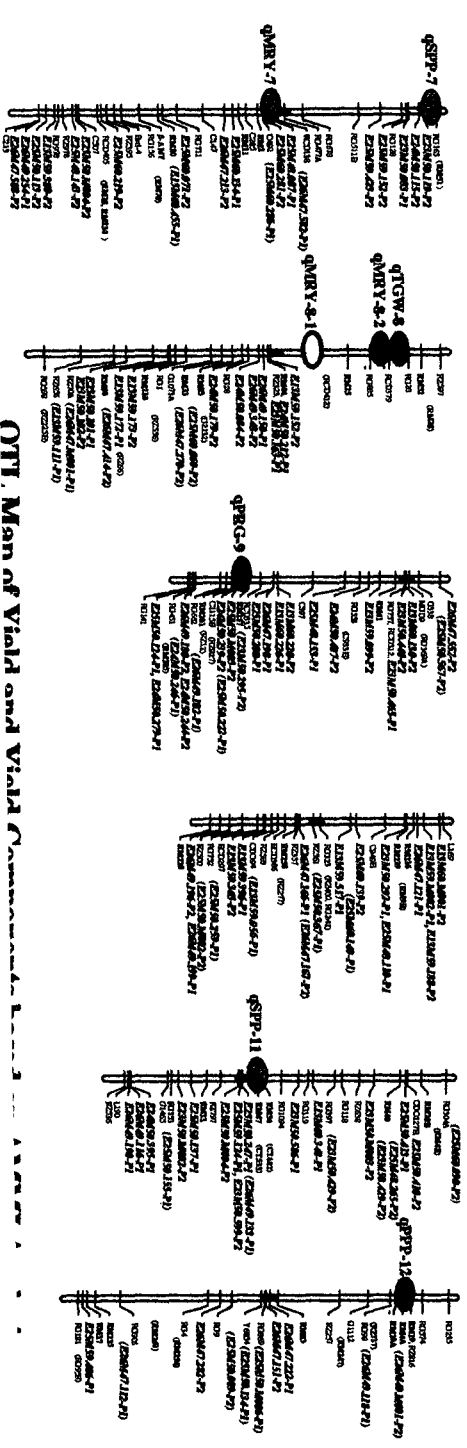
Results and Discussion :

Thousands of putative quantitative trait loci (QTLs) have been identified with many different rice populations, but one wonders how many will go the distance and give breeders the payoff of improved cultivars. The problem with QTL detection as it appears from statisticians perspective is that early-generation QTL experiments with few replications and few locations have considerable noise that increase Type I and II error rates, so many putative QTLs are not real and repeatable. To use markers linked to QTLs of interest for map-based cloning or marker-assisted selection (MAS), QTLs which show the genotypic main effects may be discriminated from QTLs with G x E interaction. The additive main effects and multiplicative interaction (AMMI) model has emerged as a powerful analytical tools for genotype x environment studies. A recombinant inbred population of rice, consisting of 164 RILs derived from a cross between Milyang 23 (Tongil type) and Gihobyeo (Japonica type), was used for mapping quantitative trait loci (QTLs) of yield and yield components. Yield and yield components were investigated for three years (1995-1997) in Honam region and for two years (1996-1997) in Yeongnam region of Korea. The dataset for five-environments was used to analyze for AMMI model. The molecular map used for QTL analysis covers 1,984cM with an average interval size of 2.8cM, involving 736 markers of RFLP, RAPD, AFLP and SSLP (Cho et. al. TAG 97:370-380). A total of eighteen QTLs were identified on yield and yield components: fourteen QTLs were detected with main effects; three QTLs were identified with GxE interaction; one QTLs showed main effects and GxE interaction.

QTL Map of Yield and Yield Components...

Main Effect

Main Effect, GXE

G X E Interaction

1 2 3 4 5 6 7 8 9 10 11 12

qPPP-1-1
qSPP-1-1
qPRG-1
qMRY-1
qPPP-1-2
qSPP-1-2
qPRG-1-2

qPRG-2
qPRG-2-2
qTGW-2-1

qMRY-7
qSPP-7
qTGW-8
qMRY-8-2
qMRY-8-1

qPRG-9

qSPP-11
qPPP-12

qMRY-6
qTGW-6