



Genetic Dissection of QTL Associated with Grain Yield in Diverse Environments



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Objectives

- Identify QTL associated with grain yield (GY) in diverse environments
- Identify QTL associated with traits related to genotype x environment interaction (GEI: IPC1, IPC2, and GYsd)
- Elucidate the effect of QTL x QTL (QQI) and QTL x environment interactions (QEI) on grain yield

Materials and Methods

❖ A total of 159 F_{8:10} recombinant inbred lines (RILs) were used in the present study, which were derived from the cross Rio Blanco x IDO444 (Chen et al., 2012)

❖ Grain yield (ton/hectare) of the parents and 159 RILs were evaluated in six diverse environments in southeastern Idaho: 0506 Aberdeen (06AB, full irrigation), 0607 Arbon Valley (07AR, rainfed), 0607 Rockland (07RK, rainfed), 0910 Aberdeen (10AB, terminal drought), 0910 Blackfoot (10BF, terminal drought), 1011 Rockland (11RK, rainfed)

❖ The GEI effect was represented using the first two interaction principal components of (IPC1 and IPC2) across six environments, which were calculated based on the additive main effects and multiplicative interaction (AMMI) model (Gauch et al., 2011)

❖ Standard deviation of GY across six environments (GYsd) was also calculated to represent the GEI effect (Ungerer et al. 2003)

❖ Genetic map used in the QTL analysis included 413 SNP, 342 DArT, 106 SSR, and 1 sequence-tagged-site (STS) markers, representing 21 wheat chromosomes except 1D and 5D

❖ Composite interval mapping (CIM) of GY, IPC1, IPC2, and GYsd were conducted using Windows QTL Cartographer 2.5 (Wang et al., 2012)

❖ QEI and QQI were tested by ANOVA method using the peak markers of the QTL associated with GY in R (R Core Team, 2012)

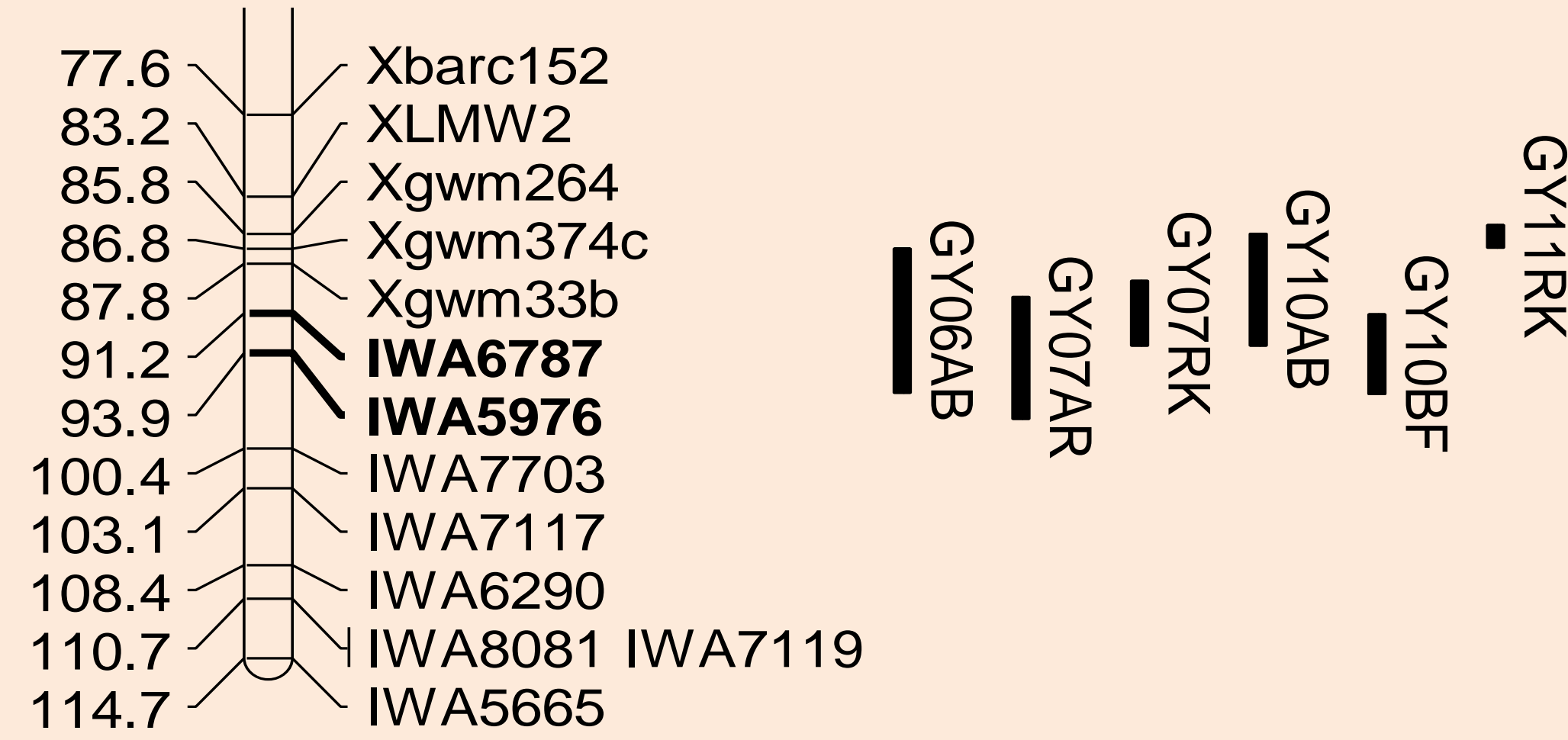


Fig. 1 Chromosome location of *Q.Gy.ui-1B.2* associated with grain yield (GY) in six environments: 06AB, full irrigation; 07AR, 07RK and 11RK, rainfed; 10AB and 10BF, terminal drought.

Trait	QTL	R ² (%)	Co-located with	Env.
IPC1	Q.Gypc1.ui-2B	8	Q.Gy.ui-2B.2	06AB
	Q.Gypc1.ui-3B	15	Q.Gy.ui-3B.1	06AB
IPC2	Q.Gypc2.ui-3B	5	Q.Gy.ui-3B.2	10BF
	Q.Gypc2.ui-4B	17	Q.Gy.ui-4B	10AB
GYsd	Q.Gypc2.ui-7A.1	5	Q.Gy.ui-7A.2	10AB
	Q.Gysd.ui-1A	6	Q.Gy.ui-1A	10AB
	Q.Gysd.ui-2B	7	Q.Gy.ui-2B.2	06AB
	Q.Gysd.ui-3B	12	Q.Gy.ui-3B.1	06AB
	Q.Gysd.ui-4B	8	Q.Gy.ui-4B	10AB

Table 2 Comparison of chromosome locations of QTL for GEI and QTL for grain yield. 9 of the 13 GEI QTL co-located with the GY QTL, indicating that some environment-specific GY-QTL control responses to environmental changes.

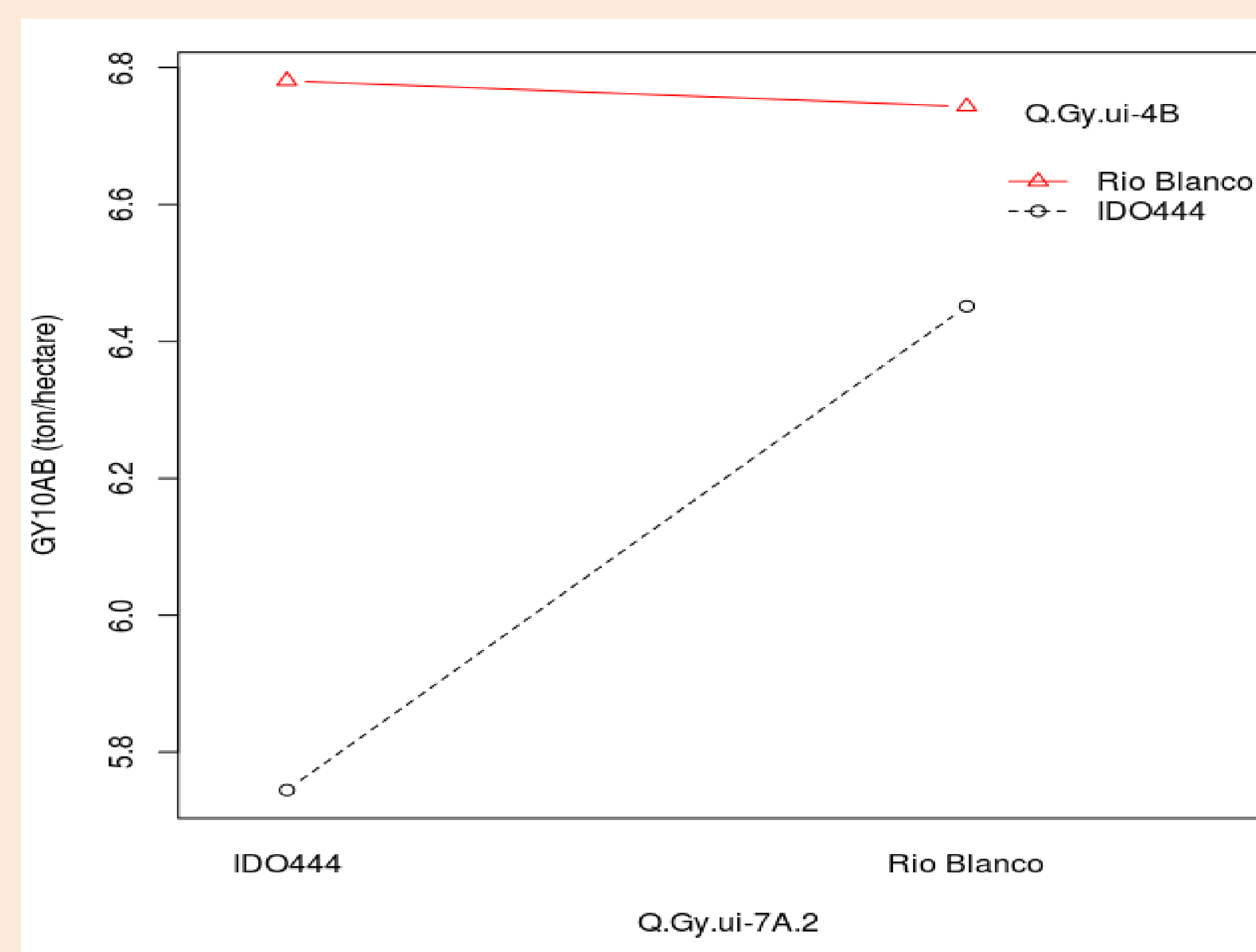


Fig. 2 *Q.Gy.ui-4B* x *Q.Gy.ui-7A.2* interaction identified in 10AB. *Q.Gy.ui-4B* had epistatic effect on *Q.Gy.ui-7A.2*, and selection of *Q.Gy.ui-4B* alone is enough to increase GY in 10AB.

Results and Discussion

- A total of 17 QTL were associated with grain yield and located on 11 chromosomes (1A, 1B, 2B, 2D, 3B, 4B, 5A, 5B, 6B, 7A, and 7B)
- A novel QTL *Q.Gy.ui-1B.2* was identified in all 6 environments, explaining 6 – 22% of the grain yield variation (Fig. 1)
- A total of 13 QTL were associated with traits (IPC1, IPC2, and GYsd) related to genotype by environment interaction (GEI)
- Nine of the 13 GEI QTL were located in the flanking regions of the QTL associated with grain yield (Table 2)
- QQI and QEI were common and complex identified in the present study (Table 1, Fig. 2 and Fig. 3)
- Examining QQI and QEI may help developing the desirable selection strategies for grain yield in diverse environments (Table 1, Fig. 2 and Fig. 3)

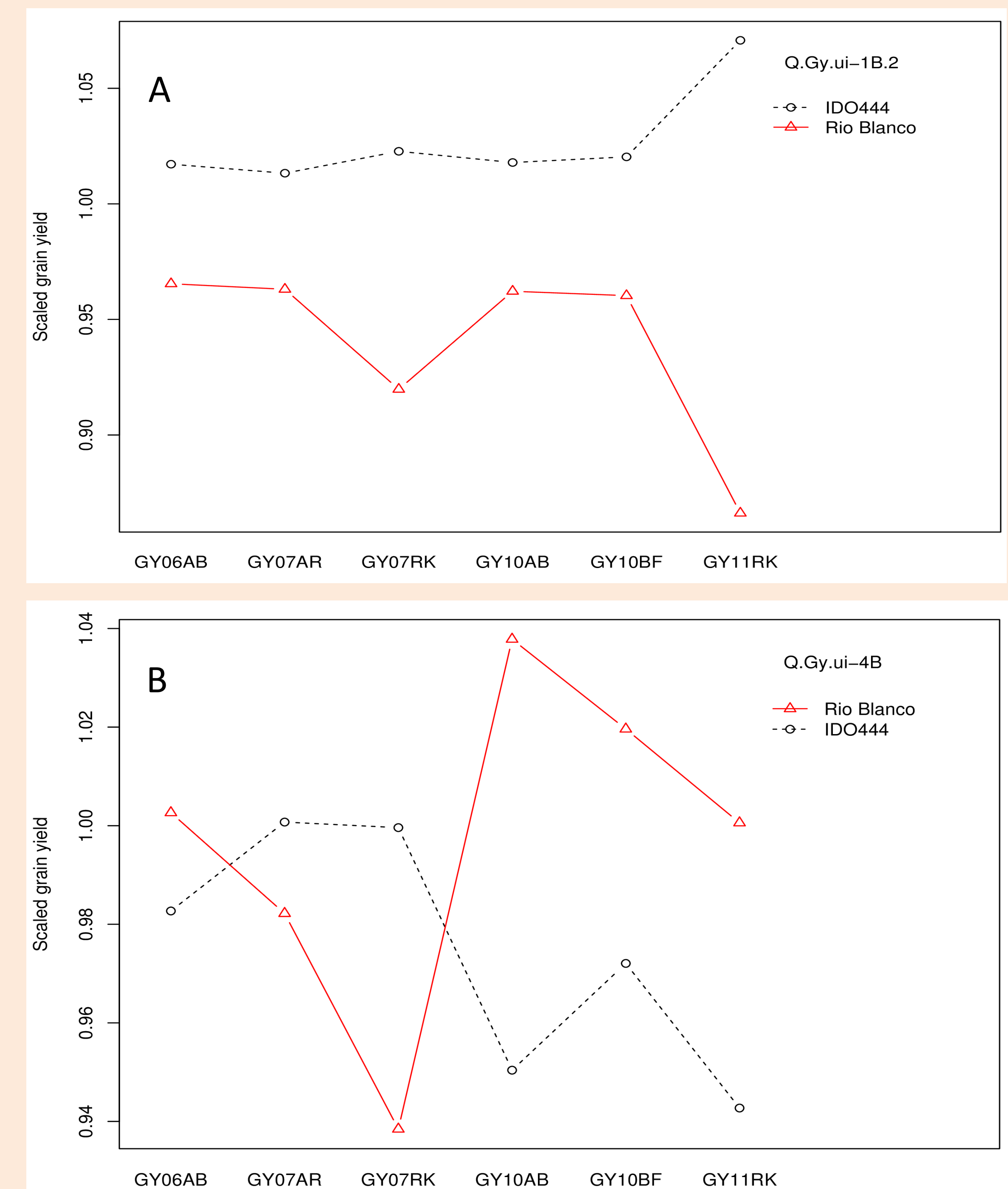


Fig. 3 Two types of QTL x environment interactions (QEI) A: changes in magnitude; B: changes in direction

QTL1	QTL2	Environment	R ² (%)
Q.Gy.ui-1A	Q.Gy.ui-1B.2	10AB	17
	Q.Gy.ui-3B.1	10AB, 10BF	12
Q.Gy.ui-1B.2	Q.Gy.ui-4B	07RK	9
	Q.Gy.ui-4B	07RK	11
Q.Gy.ui-3B.1	Q.Gy.ui-4B	10BF	9

Table 1 QQI among four major QTL. QTL *Q.Gy.ui-1A* and *Q.Gy.ui-4B* had significant interaction effect with the rest QTL, respectively. QQI is common between QTL, and it is necessary to check QTL network in a QTL mapping study

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