Supporting Information Legends

Supplementary Figure Legends

Supplementary Figure S1 Change of the effective correlation coefficient between individuals. Panel A: Change of the effective correlation when the number of markers increases in the situation where the LD between two consecutive markers is constant. As the number of markers increases, the total genome size also increases. Panel B: Change of the effective correlation as the marker density changes in the situation where the total genome size is fixed. Panel C: Change of the effective correlation between individuals when the genome size increases in the situation where the total number of markers is fixed. Panel D: Change of the effective correlation as the sample size increases in the situation where the number of markers, the genome size and the polygenic effect are constant.

Supplementary Figure S2 Comparison of minimum detectable QTL (h^2_{QTL}) between the new method (MixedPower) and an existing method (GWAPower) under seven different sample sizes.

Supplementary Figure S3 Comparison of the theoretical powers to the empirical powers from simulation studies using the kinship matrix of 210 recombinant inbred lines (RIL) of rice under the additive model, where the 0.05/10 = 0.005 threshold p-value was used to declare statistical significance. Smooth curves are theoretical power functions and open circles are empirical power functions obtained from simulations. The power functions are evaluated under three levels of polygenic contribution represented by the ratios of the polygenic variance to the residual variance ($\lambda = \sigma^2_\xi / \sigma^2$)

Supplementary Figure S4 Theoretical power functions using the kinship matrix of 210 recombinant inbred lines (RIL) of rice under the additive model under three levels of $\lambda = \sigma^2_\xi / \sigma^2$, where the 0.05/1619 = 0.00003088 threshold p-value was used to declare statistical significance.

Supplementary Figure S5 Theoretical power functions using the kinship matrix of 278 hybrid rice under the additive plus dominance model with three levels of $\lambda = \sigma^2_\xi / \sigma^2$, where the 0.05/1619 = 0.00003088 threshold p-value was used to declare statistical significance.

Supplementary Figure S6 Theoretical power functions using the kinship matrix of 524 rice cultivars under $\lambda = 1$ and three levels of correlation between the population structure and the genotype indicator of the marker under study (r_{QZ}) , where the 0.05/180,000 = 2.777E-7 threshold p-value was used to declare statistical significance.

Supplementary Figure S7 Comparison of the theoretical powers to the empirical powers from simulation studies using the kinship matrix of 500 individuals of 20 full-sib families (25 members per family) and the kinship matrix of 500 individuals of 20 half-sib families (25 members per family). Smooth curves are the theoretical power functions and open circles are the empirical powers obtained from simulations.

Supplementary Figure S8 Comparison of the theoretical powers of 500 individuals of full-sib families to 500 individuals of half-sib families (upper panels) and comparison of the theoretical powers of $\lambda = 1$ to $\lambda = 2$ (lower panels).

Supplementary Note Legends

Supplementary Note S1: Non-centrality Parameter of Association Test for Loci with Multiple Genotypes.

Supplementary Note S2: Non-centrality Parameter for Association Test with Population Structure.

Supplementary Note S3: Proof That the Correlation Between *Q* and Z_k Is r_{QZ}

Supplementary Note S4: R Functions and Examples Calling These R Functions

Supplementary Data Legends

Supplementary Data S1 Marker inferred kinship matrix of 210 recombinant inbred lines of rice. The matrix was calculated from 1619 bins (synthetic markers).

Supplementary Data S2 Marker inferred kinship matrix of 278 hybrids of rice. The matrix was calculated from 1619 bins (synthetic markers).

Supplementary Data S3 Marker inferred kinship matrix of 524 rice cultivars. The matrix was calculated from 180,000 SNPs.

Supplementary Data S4 Population structure (*Q*) of the 524 rice cultivars, where *indica* rice is coded in 1 and *japonica* rice is coded 0.

Supplementary Data S5 Minimum detectable QTL (h^2_{QTL}) for a population with variable sample sizes (*n*) and polygenic contribution (λ) when there are 100*k* markers evenly distributed on a 30 Morgan genome.

Supplementary Data S6 Effective correlation (ρ) between individuals with variable sample sizes (*n*) and polygenic contribution (λ) when there are 100*k* markers evenly distributed on a 30 Morgan genome.

Supplementary Data S7 Additive relationship matrix of 500 individuals of a population consisting of 20 full-sib families (25 members per family).

Supplementary Data S8 Additive relationship matrix of 500 individuals of a population consisting of 20 half-sib families (25 members per family).