Supplementary Material

**Genetic Dissection of *qPCG1*for a Quantitative Trait Locus for Percentage of Chalky Grain in Rice (*Oryza sativa* L.)**

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**Supplementary Table 1.** Molecular markers for mapping

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| --- | --- | --- | --- |
| Markers  | Forward primer (5' - 3') | Reverse primer (5' - 3') | Physical location |
| Z92 | GCACGGTTCTCTTTCTGTGATAGC | TTTCGAAGACCGTAGTAGCAGTGG | 26,486,863 |
| Z3 | AAAGAAAACATCCTTGACTTCCCACC | CCTTCTGAGAGCGCCTGGGTAT | 30,093,838 |
| RM212 | CCACTTTCAGCTACTACCAG | CACCCATTTGTCTCTCATTATG | 33,054,687 |
| Z345 | TTTTGAGATTTGGACTCACG | TCTTCTTACCTACACTTAGTCCT | 33,450,419 |
| Z361 | ATAATTGTTTTCTGGGTTCGG | CTACCTCTCTGTTCCCTCAC | 34,041,678 |
| MM5509 | ATCTACAAACGGAACCGTCG | CATAGATCGCACTCGGGTCT | 34,046,636 |
| RM11782 | GGAGTGTTTGTAGGACTGACACG | ACATTACCCGAATCAGGATAGG | 34,173,600 |
| MM5525 | GGCCTTAATAGGAAGTTGTTTCC | CCCGCACAGGTGTACAATC | 34,185,183 |
| MM5529 | AAAATTGGACACGGAAACCC | CCATCCCACCATAGGAGCTA | 34,200,601 |
| Z521 | TTGAACAGGAGGTCTAGTGA | CGCTCTTCCTCCATTAGACA | 34,285,570 |
| Z383 | GTTGCACGCAAAACGCCGCTA | GTCTTGCTTGCTCTCGGTGG | 34,702,058 |
| Z393 | ATGTTTCAATTATTGCGGCTG | TATTATCAAAATTTGGTAAGGC | 34,895,116 |
| Z395 | TTAACACCTATATCAAACGGAG | GCCGCCGCCAACTCAGGAA | 34,994,733 |
| C1-15 | CAACCCCTCCAAATACCTGA | ACCGTGTTCATGCCTTTCAC | 35,191,728 |
| Z405 | ACGCTCTATTTGTTTTCGCTT | GCCTGTTTGTTTCTCATCGTAT | 35,263,542 |
| Z255 | GAAACATTGTAAATACACTAGG | AATCCGAAAACACTTACCCTC | 35,430,824 |
| Z270 | AAAGATGAAGTTGGGAACTCAC | TAATGGACACTTTATTTTCCGT | 35,717,717 |
| RM11872 | CATCCCAATCTGGCCTTGACTAAGC | TTCTCGGGAGGTGGAGGACAGG | 36,389,840 |
| 1-41 | GAGGTACTTCCTCCGTTTCAC | AGTCAGCTCACTGTGCAGTG | 36,735,315 |
| RM11906 | GCTCGCTAAACACACTAGACATTTCC | CATAGGCAGATGAAGGCAACTCG | 37,123,128 |
| Z214 | CGCGCAAGTGACCTCGAT | GCACAATAGGCTAACTATACCTCT | 38,044,545 |
| Z219 | GGTGTTTCCTCGTCTGTT | TAAGTATAAGCATAACAAAACGAC | 38,240,460 |
| Z230 | CTGGAACAACTTTCGATGCTG | CATGAGAATGCCTGACTGGAT | 38,803,308 |
| RM3520 | CTGCAAATGCACAGGAATCAGG | TCCTCTCGCCTTTCTTTCTCTCC | 40,253,719 |
| RM12276 | GTCGACGGCTTCCTCAAGATTGG | TGAGACCTCTGTGAAGGCACTCG | 43,044,320 |

**Supplementary Table 2.** Phenotypic value of percentage of chalky grains (PCG) and descriptive statistic in type 1, 2 and 3 of P1, P2 and P3 in Fuyang (FY) and Lingshui (LS)

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Place | Population | Genotype | PCG(%) | SD | CV | Range | Skewness | Kurtosis |
| FY | P1 | Type 1 | 6.99  | 4.78  | 0.684  | 0.50-20.22 | 1.021  | 0.524  |
| Type 2 | 3.92  | 3.39  | 0.865  | 0.17-13.50 | 1.326  | 1.322  |
| Type 3 | 5.71  | 4.33  | 0.759  | 0.60-23.33 | 1.679  | 4.322  |
| P2 | Type 1 | 8.26  | 5.59  | 0.676  | 1.50-27.90 | 1.416  | 3.022  |
| Type 2 | 4.71  | 2.86  | 0.607  | 0.33-9.83 | 0.498  | -0.858  |
| Type 3 | 6.89  | 4.13  | 0.599  | 0.67-17.17 | 0.391  | -0.729  |
| P3 | Type 1 | 9.31  | 8.38  | 0.900  | 3.17-31.83 | 2.578  | 7.205  |
| Type 2 | 4.56  | 3.12  | 0.684  | 0.17-11.67 | 0.702  | -0.308  |
| Type 3 | 4.61  | 2.82  | 0.611  | 0.67-13.50 | 1.237  | 1.691  |
| LS | P1 | Type 1 | 43.71  | 9.94  | 0.227  | 14.40-62.54 | -0.752  | 1.654  |
| Type 2 | 30.83  | 9.49  | 0.308  | 17.24-56.23 | 1.193  | 2.265  |
| Type 3 | 34.70  | 9.76  | 0.281  | 10.21-51.71 | -0.538  | 0.300  |
| P2 | Type 1 | 40.49  | 10.30  | 0.254  | 27.00-63.38 | 0.518  | -0.339  |
| Type 2 | 31.44  | 10.72  | 0.341  | 5.96-52.07 | 0.219  | -0.011  |
| Type 3 | 37.45  | 11.69  | 0.312  | 12.50-65.41 | 0.631  | 0.139  |
| P3 | Type 1 | 41.44  | 13.38  | 0.323  | 16.56-63.48 | 0.099  | -0.801  |
| Type 2 | 37.51  | 10.91  | 0.291  | 12.52-54.16 | -0.326  | -0.752  |
| Type 3 | 38.75  | 13.92  | 0.359  | 17.45-66.35 | 0.285  | -1.096  |

**Supplementary Table 3.** Number and description of genes in the region between marker MM5509 and MM5525 on the long arm of chromosome 1

|  |  |
| --- | --- |
| Genes’ Number | Description |
| 7 | cytochrome P450 |
| 6 | expressed protein |
| 3 | hypothetical protein |
| 1 | retrotransposon protein |
| 1 | 50S ribosomal protein |
| 1 | thylakoid lumenal 20 kDa protein |
| 1 | cytokinin-N-glucosyltransferase 1 |
| 1 | indole-3-acetate beta-glucosyltransferase |
| 1 | cyclin |
| 1 | proline-rich family protein |
| 1 | tubulin/FtsZ domain containing protein |
| 1 | UBA/TS-N domain containing protein |
| 1 | OsFBX27 - F-box domain containing protein |

**Supplementary Figure 1.** **Schematic diagram of RH method**

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**Supplementary Figure 2.** Frequency distributions of type 1, type 2 and type 3 in three populations in Lingshui and Fuyang. (A), (B) and (C) are frequency distributions of populaiton1, 2 and 3 respectively in Lingshui and (D), (E) and (F) are frequency distributions of populaiton1, 2 and 3 respectively in Fuyang. Blue, red and green represent type 1, 2 and 3 respectively.****