# Dissection of quantitative trait loci for root characters and day length sensitivity in SynOpDH wheat (*Triticum aestivum* L.) bi-parental mapping population

**Supplementary Files**

**Figure Legends**

**Figure S1:**  Histograms of the phenotypic values in bread wheat for total root biomass (RM), shallow root weight (SRW), deep root weight (DRW), shoot biomass (SM), grain yield (GY), number of fertile tillers (FT), number of tillers (NT), harvest index 1 (HI1), plant height (PH), days to anthesis (DTA) and root length (RL) for 2013 and 2014 experiments. Green and red arrows highlight the group that parents Opata M85 (Op) and Synthetic W7984 (Syn) fall into respectively. Refer to Table 1 for population and parent mean values.

|  |  |
| --- | --- |
| **2013** | **2014** |
| Syn Op |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |
|  |  |

**Figure S1:** Histograms of the phenotypic values in bread wheat for total root biomass (RM), shallow root weight (SRW), deep root weight (DRW), shoot biomass (SM), grain yield (GY), number of fertile tillers (FT), number of tillers (NT), harvest index 1 (HI1), plant height (PH), days to anthesis (DTA) and root length (RL) for 2013 and 2014 experiments. Green and red arrows highlight the group that parents Opata M85 (Op) and Synthetic W7984 (Syn) fall into respectively. Refer to Table 1 for population and parent mean values.

**Supplementary Tables**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Table S1: Genotype, Year and Genotype\*Year interactions General AOV tables for deep root weight (DRW), total root biomass (RM), shoot biomass (SM), shallow root weight (SRW), days to anthesis (DTA), plant height(PH), harvest index 1 (HI1), root length (RL), number of fertile tillers (FT) and grain yield (GY). | | | | | | | | | | | |
| DRW | | | | | | PH | | | | | |
| Source | DF | SS | MS | F | P | Source | DF | SS | MS | F | P |
| Genotype | 151 | 126.896 | 0.8404 | 2.67 | 0.0000 | Genotype | 151 | 67702 | 448.35 | 3.33 | 0.0000 |
| Year | 1 | 13.485 | 13.4853 | 42.82 | 0.0000 | Year | 1 | 2039 | 2038.82 | 15.13 | 0.0001 |
| Genotype\*Year | 151 | 37.575 | 0.2488 | 0.79 | 0.9608 | Genotype\*Year | 151 | 24406 | 161.63 | 1.20 | 0.0717 |
| Error | 607 | 191.150 | 0.3149 |  |  | Error | 608 | 81940 | 134.77 |  |  |
| Total | 910 |  |  |  |  | Total | 911 | 176086 |  |  |  |
| Grand Mean | 0.6514 |  |  |  |  | Grand Mean | 77.529 |  |  |  |  |
| CV | 86.14 |  |  |  |  | CV | 14.97 |  |  |  |  |
| RM | | | | | | HI1 | | | | | |
| Source | DF | SS | MS | F | P | Source | DF | SS | MS | F | P |
| Genotype | 151 | 3268.77 | 21.648 | 8.45 | 0.0000 | Genotype | 151 | 5.4359 | 0.03600 | 4.76 | 0.0000 |
| Year | 1 | 877.16 | 877.159 | 342.21 | 0.0000 | Year | 1 | 2.2214 | 2.22138 | 293.65 | 0.0000 |
| Genotype\*Year | 151 | 896.93 | 5.940 | 2.32 | 0.0000 | Genotype\*Year | 151 | 2.2752 | 0.01507 | 1.99 | 0.0000 |
| Error | 608 | 1558.45 | 2.563 |  |  | Error | 608 | 4.5994 | 0.00756 |  |  |
| Total | 911 | 6601.32 |  |  |  | Total | 911 | 14.5319 |  |  |  |
| Grand Mean | 4.4546 |  |  |  |  | Grand Mean | 0.3740 |  |  |  |  |
| CV | 35.94 |  |  |  |  | CV | 23.26 |  |  |  |  |
| SM | | | | | | RL | | | | | |
| Source | DF | SS | MS | F | P | Source | DF | SS | MS | F | P |
| Genotype | 151 | 175441 | 1162 | 13.75 | 0.0000 | Genotype | 151 | 225915 | 1496.13 | 4.20 | 0.0000 |
| Year | 1 | 154398 | 154398 | 1827.64 | 0.0000 | Year | 1 | 1539 | 1539.01 | 4.32 | 0.0381 |
| Genotype\*Year | 151 | 21849 | 145 | 1.71 | 0.0000 | Genotype\*Year | 151 | 68712 | 455.05 | 1.28 | 0.0241 |
| Error | 608 | 51364 | 84 |  |  | Error | 607 | 216215 | 356.20 |  |  |
| Total | 911 | 403052 |  |  |  | Total | 910 |  |  |  |  |
| Grand Mean | 46.495 |  |  |  |  | Grand Mean | 80.094 |  |  |  |  |
| CV | 19.77 |  |  |  |  | CV | 23.56 |  |  |  |  |
| SRW | | | | | | FT | | | | | |
| Source | DF | SS | MS | F | P | Source | DF | SS | MS | F | P |
| Genotype | 151 | 2384.48 | 15.791 | 9.10 | 0.0000 | Genotype | 151 | 7336.5 | 48.5859 | 5.12 | 0.0000 |
| Year | 1 | 673.28 | 673.277 | 388.00 | 0.0000 | Year | 1 | 0.2 | 0.1579 | 0.02 | 0.8975 |
| Genotype\*Year | 151 | 700.16 | 4.637 | 2.67 | 0.0000 | Genotype\*Year | 151 | 2436.8 | 16.1380 | 1.70 | 0.0000 |
| Error | 608 | 1055.04 | 1.735 |  |  | Error | 608 | 5774.7 | 9.4978 |  |  |
| Total | 911 | 4812.96 |  |  |  | Total | 911 | 15548.1 |  |  |  |
| Grand Mean | 3.8034 |  |  |  |  | Grand Mean | 14.114 |  |  |  |  |
| CV | 34.63 |  |  |  |  | CV | 21.84 |  |  |  |  |
| DTA | | | | | | GY | | | | | |
| Source | DF | SS | MS | F | P | Source | DF | SS | MS | F | P |
| Genotype | 151 | 178634 | 1183.0 | 51.59 | 0.0000 | Genotype | 151 | 26504.5 | 175.5 | 6.03 | 0.0000 |
| Year | 1 | 37448 | 37447.7 | 1632.99 | 0.0000 | Year | 1 | 44294.2 | 44294.2 | 1520.92 | 0.0000 |
| Genotype\*Year | 151 | 13344 | 88.4 | 3.85 | 0.0000 | Genotype\*Year | 151 | 6567.1 | 43.5 | 1.49 | 0.0005 |
| Error | 608 | 13943 | 22.9 |  |  | Error | 608 | 17707.0 | 29.1 |  |  |
| Total | 911 | 243369 |  |  |  | Total | 911 | 95072.8 |  |  |  |
| Grand Mean | 65.401 |  |  |  |  | Grand Mean | 17.698 |  |  |  |  |
| CV | 7.32 |  |  |  |  | CV | 30.49 |  |  |  |  |

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table S2:** QTL associated with, grain yield (GY), shoot biomass (SM), total root biomass (RM), shallow root weight (SRW), deep root weight (DRW), fertile number of tillers (FT), root length (RL), days to anthesis (DTA) and flag leaf width (FLW) in the SynOpDH population with 122 lines (Lines with vernalization requirement are excluded). | | | | | | | | |
| **Trait** | **Year** | **Chromosome** | **Position** | **LeftMarker** | **RightMarker** | **LODa** | **PVE(%)b** | **Additivec** |
| GY | 2013 | 2D | 68.2300 | 579 | 1212 | 6.4743 | 22.0620 | 2.2977 |
| 2014 | 71.2300 | 745 | 250 | 7.8059 | 23.8856 | 3.2973 |
| SM | 2013 | 2A | 45.0000 | 374 | 262 | 7.9988 | 12.2215 | -4.2352 |
| 2014 | 46.0000 | 374 | 262 | 5.5280 | 8.9103 | -4.8328 |
| 2013 | 2D | 68.2300 | 579 | 1212 | 25.2312 | 54.4679 | 8.8281 |
| 2014 | 68.2300 | 579 | 1212 | 23.2015 | 53.4729 | 11.6824 |
| RM | 2013 | 2A | 47.0000 | 262 | 10 | 3.4541 | 8.7349 | -0.4018 |
| 2014 | 45.0000 | 374 | 262 | 6.4722 | 13.2787 | -0.9279 |
| 2013 | 2D | 68.2300 | 579 | 1212 | 10.0880 | 29.1641 | 0.7244 |
| 2014 | 68.2300 | 579 | 1212 | 16.4521 | 40.7664 | 1.6054 |
| SRW | 2013 | 2A | 45.0000 | 374 | 262 | 3.1992 | 8.6137 | -0.3230 |
| 2014 | 40.0000 | 1017 | 374 | 7.1893 | 15.0230 | -0.8500 |
| 2013 | 2D | 71.2300 | 745 | 250 | 8.7053 | 25.6886 | 0.5500 |
| 2014 | 68.2300 | 579 | 1212 | 16.8759 | 41.1759 | 1.3874 |
| DRW | 2013 | 2D | 68.2300 | 79 | 1212 | 7.2126 | 23.9542 | 0.1732 |
| 2014 | 71.2300 | 45 | 250 | 7.0987 | 23.5061 | 0.2337 |
| FT | 2013 | 4D | 0.0000 | 838 | 570 | 3.8062 | 9.4812 | -1.1818 |
| 2014 | 0.0000 | 838 | 570 | 3.7903 | 11.6982 | -1.0396 |
| RL | 2013 | 2D | 68.2300 | 579 | 1212 | 8.3675 | 22.4475 | 7.8546 |
| 2014 | 65.2300 | 579 | 1212 | 4.6290 | 14.8319 | 7.5856 |
| DTA | 2013 | 2A | 39.0000 | 1017 | 374 | 13.2580 | 23.7258 | -6.5016 |
| 2014 | 40.0000 | 1017 | 374 | 12.2099 | 24.2725 | -7.1430 |
| 2013 | 2D | 68.2300 | 579 | 1212 | 20.8195 | 42.6439 | 8.5657 |
| 2014 | 68.2300 | 579 | 212 | 18.2941 | 39.8006 | 9.0006 |
| FLW | 2013 | 2D | 71.2300 | 745 | 250 | 4.6911 | 14.8899 | 0.0779 |
| 2014 | 71.2300 | 745 | 250 | 7.2375 | 20.7909 | 0.1400 |

Plants were grown in 1 m PVC tubes under well-watered conditions until maturity for two seasons. Peak positions (cM) with the highest LOD score, left and right markers, the logarithm of the odds (LOD) scores, percent phenotypic effects, and additive effects.

a LOD score of 3.45 was used for the declaration of QTL.

b Phenotypic variation explained by QTL

c Additive effect of QTL

d LOD threshold value of 2.5 was used for the QTL declaration.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Table S3:** Phenotype associated chromatin regions (Marker \*Trait Associations) of the SynOpDH population that were detected only one year (2013 or 2014) for thousand-grain weight (1000gW), grain yield (GY), harvest index 1 (HI 1), shoot biomass (SM), total root biomass (RM), shallow root weight (SRW), deep root weight (DRW), fertile number of tillers (FT), number of tillers (NT), plant height (PH), root length (RL), days to anthesis (DTA) and flag leaf width (FLW). | | | | | | | | |
| **Trait Name** | **Year** | **Chromosome** | **Position (cM)** | **Left Marker** | **Right Marker** | **LODa** | **PVE (%)b** | **Additivec** |
| 1000GW | 2013 | 2D | 68.230 | synopGBS579 | synopGBS1212 | 4.1908 | 11.3699 | -2.8223 |
| 5D | 222.000 | synopGBS737 | synopGBS576 | 3.0333 | 8.0156 | -2.3689 |
| GY | 2013 | 2A | 43.000 | synopGBS374 | synopGBS262 | 3.0219 | 7.0736 | -1.3578 |
| 2014 | 4A | 42.850 | synopGBS1186 | synopGBS1416 | 3.4356 | 8.1081 | -1.9788 |
| HI | 2014 | 2A | 71.000 | synopGBS1475 | synopGBS916 | 3.1259 | 7.9469 | 0.0239 |
| 2D | 68.230 | synopGBS579 | synopGBS1212 | 5.3637 | 14.0689 | -0.0317 |
| SM | 2013 | 5D | 113.000 | synopGBS1282 | synopGBS656 | 3.4005 | 3.9694 | 2.4099 |
| 2014 | 4A | 56.850 | synopGBS525 | synopGBS325 | 3.9367 | 4.0702 | -3.4387 |
| 7D | 89.480 | synopGBS251 | synopGBS1449 | 2.7692 | 2.8441 | 2.8528 |
| RM | 2013 | 5D | 144.000 | synopGBS1273 | synopGBS613 | 3.3553 | 6.5519 | 0.3898 |
| SRW | 2013 | 5A | 125.000 | synopGBS902 | synopGBS147 | 3.3893 | 6.0144 | -0.3039 |
| 5D | 142.000 | synopGBS1273 | synopGBS613 | 3.8496 | 6.9980 | 0.3357 |
| DRW | 2013 | 3A | 19.000 | synopGBS706 | synopGBS1260 | 3.0382 | 6.7136 | -0.0961 |
| 6A | 91.000 | synopGBS1239 | synopGBS1401 | 3.5921 | 8.1762 | -0.1062 |
| 2014 | 7D | 89.480 | synopGBS251 | synopGBS1449 | 2.6581 | 5.7383 | 0.1144 |
| FT | 2013 | 1B | 82.960 | synopGBS1482 | synopGBS1086 | 3.4165 | 6.8507 | 0.9444 |
| 2D | 68.230 | synopGBS579 | synopGBS1212 | 10.3159 | 22.7059 | 1.7173 |
| 2014 | 5A | 127.000 | synopGBS147 | synopGBS429 | 2.9280 | 7.3109 | 0.7986 |
| 7B | 111.370 | synopGBS952 | synopGBS1301 | 3.3965 | 8.5685 | -0.8669 |
| NT | 2013 | 2A | 44.000 | synopGBS374 | synopGBS262 | 2.5128 | 5.8713 | -0.9645 |
| 2D | 68.230 | synopGBS579 | synopGBS1212 | 9.7382 | 23.4817 | 1.9231 |
| 4A | 0.000 | synopGBS838 | synopGBS570 | 2.9509 | 6.3075 | -1.0105 |
| 2014 | 7B | 111.370 | synopGBS952 | synopGBS1301 | 2.7123 | 8.3323 | -1.0951 |
| PH | 2013 | 2A | 42.000 | synopGBS1017 | synopGBS374 | 3.4211 | 7.5067 | -1.9319 |
| 2D | 66.230 | synopGBS579 | synopGBS1212 | 2.8781 | 6.7032 | 1.8191 |
| 4A | 27.850 | synopGBS1339 | synopGBS82 | 3.2091 | 7.0017 | -1.8652 |
| 5A | 47.000 | synopGBS851 | synopGBS826 | 4.5801 | 10.3250 | 2.2620 |
| 6D | 81.000 | synopGBS965 | synopGBS1413 | 2.5778 | 5.5599 | 1.6770 |
| 2014 | 6B | 86.000 | synopGBS1461 | synopGBS1235 | 2.7812 | 8.3059 | 1.2236 |
| RL | 2013 | 3B | 105.000 | synopGBS753 | synopGBS1241 | 2.9651 | 6.0136 | -3.9662 |
| 6A | 93.000 | synopGBS1239 | synopGBS1401 | 5.5205 | 12.0558 | -5.6851 |
| 7D | 32.480 | synopGBS254 | synopGBS773 | 2.5756 | 5.2144 | 3.7107 |
| 2014 | 6B | 108.000 | synopGBS900 | synopGBS286 | 2.6452 | 5.8114 | 4.7592 |
| DTA | 2013 | 5A | 69.000 | synopGBS293 | synopGBS1405 | 2.9316 | 3.3273 | -2.5959 |
| 5B | 66.000 | synopGBS1315 | synopGBS1269 | 3.8163 | 4.3380 | 2.9661 |
| 5D | 134.000 | synopGBS371 | synopGBS611 | 4.2059 | 4.9476 | 3.2116 |
| FLW | 2013 | 5A | 127.000 | synopGBS147 | synopGBS429 | 6.5515 | 14.8346 | -0.0776 |
| 2A | 26.000 | SynopGBS399 | SynopGBS855 | 3.1872 | 6.6993 | -0.0524 |
| 2014 | 5B | 130.000 | synopGBS1330 | synopGBS127 | 3.3704 | 6.2238 | -0.0784 |
| 2A | 42.000 | synopGBS1017 | synopGBS374 | 3.8694 | 7.2358 | -0.0848 |

Plants were grown in 1 m PVC tubes under well-watered conditions until maturity for two seasons. Peak positions with the highest LOD score left and right markers, the logarithm of the odds (LOD) scores, percent phenotypic effects, and additive effects.

a LOD threshold score of 2.5 was used.

b Phenotypic variation explained by associated loci

**c** Additive effect of specific loci.