Identification of quantitative trait loci for seedling root traits from Tibetan semi-wild wheat (Triticum aestivum ssp. tibetanum)

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<td>Ma, Jian; Sichuan Agricultural University, Triticeae Research Institute Luo, Wei; Sichuan Agricultural University, Triticeae Research Institute Zhang, Han; Sichuan Agricultural University, Triticeae Research Institute Zhou, Xiao-Hong; Sichuan Agricultural University, Triticeae Research Institute Qin, Na-Na; Sichuan Agricultural University, Triticeae Research Institute Wei, Yu-Ming; Sichuan Agricultural University, Triticeae Research Institute Liu, Yaxi; Sichuan Agricultural University, Triticeae Research Institute Jiang, Qian-Tao; Sichuan Agricultural University, Triticeae Research Institute Chen, Guo-Yue; Sichuan Agricultural University, Triticeae Research Institute Zheng, You-Liang; Sichuan Agricultural University, Triticeae Research Institute Lan, Xiu-Jin; Sichuan Agricultural University, Triticeae Research Institute</td>
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<td>Keyword:</td>
<td>Tibetan semi-wild wheat, recombinant inbred line, root trait, quantitative trait locus, correlation</td>
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Identification of quantitative trait loci for seedling root traits from
Tibetan semi-wild wheat (*Triticum aestivum* ssp. *tibetanum*)

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Abstract

As a primitive hexaploid wheat resource distributed only in Tibet, Tibetan semi-wild wheat (*Triticum aestivum* ssp. *tibetanum* Shao) possesses unique characteristics that could be exploited in wheat breeding program. A good root system could offer a stable platform for the above-ground components. Aiming at detecting possible excellent locus for root traits from Tibetan semi-wild wheat, we here identified QTLs for root traits using a recombinant inbred line population derived from a cross between Tibetan semi-wild wheat Q1028 and Zhengmai 9023. A total of 15 QTLs on 8 chromosomes were detected, including four major QTLs, *QMrl.sau-7B*, *QTrl.sau-4B*, *QAd.sau-7A* and *QSa.sau-4B*. The phenotypic variation explained by each of these QTLs ranges from 5.67 to 16.68%. Positive alleles of 6 QTLs were derived from Q1028. Several novel QTLs for root traits were identified. In addition, significant correlations were detected amongst root traits and agronomic traits. Taken together, the results suggested that Tibetan semi-wild wheat and the newly identified novel QTLs could be useful in future breeding programs.

Keywords Tibetan semi-wild wheat, recombinant inbred line, root trait, quantitative trait locus, correlation
Introduction

Common wheat (*Triticum aestivum* L., 2n=6x=42, AABBDD) is one of the most important food crops in the world. With the increase of population, improving yield of wheat has become an important target of breeding work. However, the current annual rate of increase in wheat productivity is considerably lower than the demanded by global wheat consumption (Reynolds et al. 2012).

As an important organ to absorb water and minerals, a root system plays a major role in the growth and development and even yield in crops (Moudal and Kour 2004; Partha et al. 2004; Rogers and Benfey 2015). Compared with root traits, the above-ground components including plant height and harvest index have always been focused on in wheat improvement programs, mainly due to the difficulties related to root recovery and evaluating root traits in situ. Another two limitations, i.e. broad phenotypic plasticity of root traits in response to changes in soil conditions and lack of high-throughput and cost-effective screening techniques, make root studies highly challenging as well (Fitter 2002; Manschadi et al. 2008; Poorter and Nagel 2000). Despite of these restricted conditions, some appreciable progress has been made to date on identification of QTLs for important root traits (Bai et al. 2013; Ehdaie et al. 2016; Kabir et al. 2015; Liu et al. 2013; Ren et al. 2012). For instance, Maccaferri et al. (2016) detected several QTLs for root length, root number and root growth angle in the whole genome of tetraploid wheat except 4A and 5B, Ayalew et al. (2017) located some QTLs for root length on 1A, 1B, 2D, 3A, 5A, 6A and 7B in hexaploid wheat. Furthermore, quite a few of QTLs for root diameter, surface area and root volume have been reported by Petrarulo et al. (2015) and Shang et al. (2016).

Tibetan semi-wild wheat (*T. aestivum* ssp. *tibetanum*) is a hexaploid wheat found only in Tibet (Shao et al. 1980), with unique and primitive characteristics such as hulled glumes and brittle rachis (Jiang et al. 2014). It is characterized by numerous desirable characteristics, such as tolerance to nutrition deficiency and strong seed dormancy which can be introduced by crossing with common wheat breeding (Jiang et al. 2015; Sun et al. 1998). Thus, identification and the utilization of desirable genes from Tibetan semi-wild wheat could be important to develop modern wheat cultivars.

Most recently, we identified QTLs controlling seed dormancy (Jiang et al. 2015), brittle rachis and threshing ability (Jiang et al. 2014), and important agronomic traits (Luo et al. 2016) of *T. aestivum* ssp. *tibetanum* accession Q1028 collected in our institute. In addition, a recent study reported a few QTLs controlling root traits using RILs derived from common wheat and Tibetan semi-wild wheat (Kabir et al. 2015), broadening our knowledge on Tibetan semi-wild wheat for breeding as well. It is documented that more than 140 accessions of Tibetan semi-wild wheat with high genetic diversity were collected (Liu 2010). As part of our systematic work to exploit breeding potentialities of Tibetan semi-wild wheat in cultivar development, we, here, report on QTLs controlling root traits of Tibetan semi-wild wheat accession Q1028.
different from that used in Kabir et al. (2015).

Materials and methods

Plant material

In this study, a total of 186 RILs derived from a cross between Tibetan semi-wild wheat accession Q1028 (female parent) and a wheat cultivar Zhengmai 9023 (male parent, ZM9023) were used to investigate root traits. Q1028 shows a longer root system than ZM9023 (Fig. 1). Furthermore, Q1028 has longer flowering date, taller plant height, higher spikelet number per spike and larger tiller number than ZM9023. While ZM9023 has higher thousand-grain weight than Q1028 (Luo et al. 2016).

Hydroponic culture

The commonly used hydroponic culture system (Kabir et al. 2015; Ren et al. 2012) was employed to study the root morphological parameters of wheat seedlings in the present study. The experiments were conducted in greenhouse of the Triticeae Research Institute of Sichuan Agricultural University. The settings for the greenhouse were: 20 (±4) °C day/night temperature and 65/85 % day/night relative humidity, and a 16-h photoperiod.

The experiment was repeated for three times to increase the credibility of root trait measurements. Each replicated experiment was performed in a completely randomized design. For each replicated experiment, twenty uniformly sized seeds from each line were surface-sterilized by soaking in 10 % sodium hypochlorite for 5 min and then, rinsed three times with deionized water. Seeds were then germinated on three layers of filter paper saturated with water in petri dishes at room temperature for a week. After removing residual endosperm materials, four equal sized germinated seeds of each line having shoots of about 1 cm were transferred to plastic tray. The plastic trays (50 cm × 40 cm × 30 cm) contain Hoagland nutrient solution to supply mineral nutrition and air pump to supply oxygen (An et al. 2006). The nutrient solution was replaced twice in a week.

Phenotypic data

Root and shoot tissues were collected separately four weeks after transplanting for measuring root traits. Maximum root length (MRL, the length between the roots base and the tip of the longest root, cm/plant) was measured using a ruler. The collected roots were scanned by Epson Expression 10000 XL. The output root imagines were analyzed by Win-RHIZO developed by Regent Instruments Canada Inc. (Ottawa, ON, Canada) for the following traits: total root length (TRL, the sum of the length for all the roots including primary and lateral roots from a single measured plant, cm/plant), root surface area (SA, the area of all the roots from a single measured plant,
cm²/plant), root average diameter (AD, the average diameter of all the roots from a single measured plant, cm/plant), root volume (RV, the total size for all the roots from a single measured plant, cm³/plant) and number of root tips (RTN, the total tips of all the roots from a single measured plant, n/plant). Root dry weight (RDW, g/plant) and shoot dry weight (SDW, g/plant) were measured by electronic scale after the fresh roots and shoot had been dried to a constant weight at 100 °C. The root/shoot ratio (RSR, RDW/SDW) was calculated. Five agronomic traits investigated in our previous study (Luo et al. 2016) were employed for correlation analysis, including flowering date (FD), plant height (PH), tiller number (TN), spikelet number per spike (SNS) and 1000 grains weight (TGW). The best linear predictors (BLUPs) were calculated for the measured root traits (from three repeated experiments) and agronomic traits (from different growth seasons) and were further used for the following analysis. Frequency distribution and the correlation between traits were calculated using SPSS version 20.0 for Windows (SPSS Inc., Chicago, IL). The estimated broad-sense heritability of the investigated traits was calculated as follows: \( h^2 = \sigma^2_G/(\sigma^2_G + \sigma^2_e/r) \), where \( \sigma^2_G \) is the genetic variance, \( \sigma^2_e \) is the residual variance, and \( r \) is the number of replicates per genotype. Student’s t-test \( (P < 0.05) \) calculated by SPSS was used to evaluate the differences of the investigated traits between the parents.

**QTL mapping**

The BLUPs of 12 seedlings of each RIL from three replicates was used to detect root QTLs. A whole-genome genetic map constructed previously (Jiang et al. 2014) was adopted for QTL mapping. The genetic map was constructed using a population of 186 RILs with 564 DArT makers and 117 SSR markers. These markers were distributed in 22 linkage groups and covered a total genetic distance of 2,727 cM (Jiang et al. 2014). The relative positions of contiguous markers were tested through Kosambi mapping function. QTL analysis was initially conducted using QTL IciMapping version 3.2 which was followed by inclusive composite interval mapping (ICIM) (Wang et al. 2012). Thereafter, single marker analysis (SMA) was applied to ascertain the QTLs’ authenticity. LOD ≥ 2.5 was used to determine the presence of a QTL (Lin et al. 1996). QTLs were named according to the rules of International Rules of Genetic Nomenclature (http://wheat.pw.usda.gov/ggpages/wge/98/Intro.htm).

**Results**

**Phenotypic analysis**

The phenotypes values for each trait varied among different lines (Table 1; Fig. 1). Significant differences between parents were detected for MRL, TRL, SA, AD, RV, MRL and RTN (Table 1). For example ZM9023 exhibits higher values of TRL, RSA, RV and RTN than Q1028. However, Q1028 shows longer MRL and larger AD than ZM9023 (Table 1).
The transgressive segregation in the RIL population were observed for all traits (Fig. 2). The frequency distributions of the investigated traits showed continuous variation with approximately normal distributions indicating that the traits are quantitative in nature and are suitable for QTL analysis. The heritability value of RSR was the lowest in this study (only 5%) (Table 1). Furthermore, a concentrated heritability values ranged from 62 % to 85 % indicating that the other 8 traits are stable and mainly controlled by genetic factors (Table 1).

**Correlation between root and agronomic traits**

The phenotypic correlations among the investigated root and agronomic traits are shown in Table 2. Significant correlations were detected amongst most of the traits. The correlation coefficients ranged from 0.008 to 0.988 (Table 2). FD was significantly correlated with SDW and MRL as well as all other agronomic traits with correlation coefficients ranging from 0.144 to 0.689 ($P < 0.05$). Significant positive correlations were also detected between PH and 6 seeding traits including RDW, SDW, TRL, SA, RV and RTN with the coefficients ranging from 0.255 to 0.329 ($P < 0.01$). TN was significantly negatively correlated with TGW and AD ($P < 0.01$) but positively correlated with SNS, MRL and RTN ($P < 0.05$ or 0.01). SNS showed significantly negative correlation with TGW and significantly positive correlation with RDW, SDW and MTL. TGW was significantly correlated with MRL, TRL, SA and RV ($P < 0.01$).

Significant correlations were also detected among seeding traits (Table 2). Significantly positive correlations were detected between RDW and all of the other seeding traits except AD, and the coefficients ranged from 0.297 to 0.852 ($P < 0.01$). Unsurprisingly, SDW was significantly negatively related to RSR ($r = -0.186$), but it was significantly positively correlated with several seeding traits including RDW, MRL, TRL, SA, RV and RTN ($0.295 \leq r \leq 0.847$). MRL was significantly correlated with TRL, SA, RV and RTN ($P < 0.01$). TRL showed highly significant correlations with PH, TGW and all the seeding traits except RSR ($P < 0.01$). AD was significantly negatively correlated with TN, TRL and RTN ($P < 0.01$). SA was significantly correlated with PH, TGW and all of the seeding traits ($0.230 \leq r \leq 0.988$, $P < 0.01$) except AD and RSR. RV was significantly correlated with all of the seeding traits ($0.204 \leq r \leq 0.948$) except RSR. RTN was significantly correlated with PH, TN and all the seeding traits except RSR (Table 2).

**QTL detection**

In the present study, a total of 15 QTLs for seven root traits were identified with a single QTL explaining 5.67–16.68 % of phenotypic variation observed (Table 3, Fig. 3). The LOD values ranged from 2.54 to 7.75 (Table 3). The 15 QTLs were distributed on 8 chromosomes and they were 1B, 3B, 3D, 4B (4 QTLs), 5B, 6B, 7A (5 QTLs) and 7B. The additive effects of 6 QTLs were positive with Q1028 increasing.
Four QTLs for MRL were detected and they were mapped on chromosomes 3B, 6B, 7A, and 7B (Fig. 3). The phenotypic variation explained by these QTLs ranged from 6.18 to 16.68% (Table 3). The positive allele of QMrl.sau-7B was contributed by ZM9023 and those of the remaining QTLs were contributed by Q1028. The QTL, QMrl.sau-7B, was a major QTL which explained 16.68% of variation.

Two QTLs for TRL, QTrl.sau-4B and QTrl.sau-7A, were detected explaining 12.56% and 5.67% of the phenotypic variation, respectively. The positive alleles of these two QTLs were contributed by ZM9023.

For AD, a major (QAd.sau-7A) and two minor QTLs (QAd.sau-3D and QAd.sau-5B) with 12.18%, 8.74%, and 5.83% phenotypic variation explained were identified on 7A, 3D, and 5B, respectively (Fig. 3, Table 3). The positive alleles of QAd.sau-3D and QAd.sau-7A were contributed by Q1028 and that of QAd.sau-5B was contributed by ZM9023.

One QTL only for RV was detected and it was mapped on chromosome 4B (Fig. 3). It explained 8.79% of the phenotypic variation and the positive allele was from ZM9023 (Table 3).

A major QTL for SA was also detected on 4B (Fig. 3). It explained 10.61% of the phenotypic variation and the positive allele was from ZM9023 (Table 3).

Two QTLs for RTN were detected on 4B and 7A (Fig. 3). QRtn.sau-4B and QRtn.sau-7A explained 8.00% and 8.61% of the phenotypic variation, respectively. The positive alleles of these QTLs were all from ZM9023 (Table 3).

Two QTLs for RSR were located on 1B and 7A. QRsr.sau-1B explained 6.80% of the phenotypic variation and QRsr.sau-7A explained 5.73% of that (Table 3). Furthermore, the positive alleles of the two QTLs were from ZM9023 and Q1028, respectively.

**Discussion**

A good root system could offer a stable platform for the above-ground components. To explore desirable genes for root traits of wheat, we investigated several root traits of a RIL population derived from the Tibetan semi-wild wheat Q1028 and a wheat cultivar ZM9023. ZM9023 showed clear advantages in six out of the eleven assessed seeding traits, indicating its breeding potential as a national wheat cultivar. A total of 15 QTLs on 8 chromosomes were detected. The phenotypic variation explained (PVE) by each of these QTLs ranged from 5.67 to 16.68% and 4 were considered as major
QTLs with a higher than 10% of PVE. Positive alleles of 6 QTLs were derived from Q1028. Significant correlations were detected amongst most of root traits and several agronomic traits. As the expression of QTL is easily affected by environment factors, the BLUP model was adopted to correct the environmental effects aiming at increasing the reliability and facticity of the detected QTLs (Doligez et al. 2013).

### Possible potential of Tibetan semi-wild wheat in breeding program

The values of MRL and AD for Tibet semi-wild wheat Q1028 were significantly higher than those for ZM9023. Reportedly, a deep root system could facilitate the plant to extract water stored in deep soil layers to avoid drought stress (Boyer 1996; Ludlow and Muchow 1990). It is also reported that increased root diameter was related to drought tolerance in rice (*Oryza sativa* L.) because thicker roots are characterized by large xylem vessels with improved axial conductance and are more efficient in penetrating deep soil layers to extract water (Clark et al. 2008; Fukai and Cooper 1995). Given that Tibetan semi-wild wheat was found only in Tibet, a relatively dry growth environment (Shao et al. 1980), it is thus understandable that Tibetan semi-wild wheat has adapted by increasing rooting depth and root diameter to capture water and nutrition from the deeper layers of soil to avoid drought stress. Therefore, Tibetan semi-wild wheat could be utilized as an excellent genetic resource in breeding program aiming at improving tolerance to drought.

It was documented that more than 140 accessions of Tibetan semi-wild wheat with high genetic diversity were collected (Liu 2010). Exploring various genotypes of Tibetan semi-wild wheat with desirable genes could facilitate ongoing of wheat improvement. For example, an accession of Tibetan semi-wild wheat (i.e. Zang 1817) had been used to construct a RIL population and detected QTLs controlling root traits (Kabir et al. 2015). Aiming at identifying more desirable genes from different genotypes of Tibetan semi-wild wheat, we created a RIL population derived from Tibetan semi-wild wheat Q1028 and a cultivar ZM9023 for detecting QTLs responsible for root traits. Genotypes of Tibetan semi-wild wheat (Q1028 and Zang 1817) are different in phenotypes including plant height (Q1028: 139.0 cm; Zang 1817: 96.7 cm), spike length (Q1028: 12.7 cm; Zang 1817: 11.2 cm), thousand grain weight (Q1028: 21.3 g; Zang 1817: 26.7 g) (Liu et al. 2014; Luo et al. 2016). For the traits determined in both study, i.e. MRL, TRL, (R)SA, AD (RVOL), RTN (TIP), some novel QTLs were detected in the present study, such as QTLs for MRL, TRL and AD on 7A. Of these newly identified QTLs, positive alleles of QMrl.sau-7A and QAd.sau-7A are derived from Q1028. In addition, it was notable that transgressive segregation was detected in all of the nine traits, and some lines showed better phenotype than their parents (Fig. 2). The lines which expressed transgressive segregation in multiple traits were also propitious to be applied in breeding programs. Taken together, the results reported here combined with those from Kabir et al. (2015) suggested that Tibetan semi-wild wheat can be used as a valuable gene resource in breeding wheat.
Comparison of QTLs detected in this study with those reported previously

Numerous QTLs for root traits have been detected by using various populations (Ayalew et al. 2017; Bai et al. 2013; Ibrahim et al. 2012; Kabir et al. 2015; Liu et al. 2013; Maccaferri et al. 2016; Ren et al. 2012). Both the present study and that reported by Kabir et al. (2015) detected QTLs for MRL on 3B and 7B. Ibrahim et al. (2012) detected QTLs for TRL on 7A as this study. As the markers used for QTL mapping were different, the detailed comparison of the markers flanking a given QTL is not realistic. In this study, we also detected several QTLs that have not been detected previously to our knowledge. For example, QMr1.sau-7A and the QTLs for AD on 3D and 5B were newly identified in the present study. The fact that the QTLs for MRL, TRL, AD, RTN and RSR were identified in 7A suggests that chromosome 7A could play a major role in growth and development of root and its function.

Co-mapped and closely linked QTLs controlling different root traits

QTL clusters have been reported in previous studies (Kabir et al. 2015; Luo et al. 2016). The co-located QTLs for different traits were detected in specific chromosomal intervals in the present study. Two QTL clusters distributed on chromosomes 4B and 7A were identified (Fig. 3). Co-localization of QTLs indicates the close association of the traits. The loci for TRL, SA, RV and RTN on 4B are most likely controlled by a same gene, given that the positive alleles of these loci came from the same parent ZM9023. The cluster on 7A consisting of three QTLs for AD, RTN, and TRL mapped between wPt-4515 and Xgpw3220 was identified. The positive alleles for QTRL.sau-7A and QRTn.sau-7A were contributed by male parent ZM9023 and the positive allele of QAd.sau-7A was contributed by female parent Q1028. The resolution of the genetic map constructed in this study should be further improved to determine whether these traits are controlled by the two different alleles of the same locus.

The relationships among root and agronomic traits

In this study, SA showed significantly positive correlation with PH, TGW, SDW and other root traits except AD and RSR (Table 2). Water and nutrient absorption from the soil is directly proportional to contact areas between soil and roots (Caassen and Barber 1976; Yoshida and Hasegawa 1982). It was reported that the absorptive capacity of wheat roots increases with SA (Narayanan et al. 2014). The increased intakes through increased SA might help plant to improve the above-ground biomass production including SDW and TGW. As TRL, RV and RTN were significantly positively correlated with SA ($r \geq 0.805$, $P < 0.01$), it is thus understandable that these three root traits were also significantly positively correlated with SDW.

A positive correlation between SDW and RDW ($r = 0.833$, $P < 0.01$; Table 2) was
detected in the present study, being consistent with previous studies in wheat
(Narayanan et al. 2014), pea (McPhee 2005) and chickpea (Serraj et al. 2004). As
discussed above, the raised nutrients absorbed through increased root surface might
help to improve the biomass of SDW. In turn, the surplus photosynthate of the
increased shoot growth might be transported to roots and thus increase RDW
(Narayanan et al. 2014). And the mutual-promotion pattern might explain the
significant correlations between root traits and agronomic traits including PH, TN,
SNS and TGW.

Our previous study detected a QTL for TN on 6B where the MRL QTL $Q_{Mrl.sau-6B}$
was located (Luo et al. 2016). In the present study, TN showed significant correlation
with MRL and RTN. Furthermore, significant correlations between PH and RDW,
TRL, SA, RV and RTN ($P < 0.01$) were also detected. We thus suggest that some root
and yield-related traits could be controlled by a single gene. For example, it was
reported that there were genes or QTLs likely controlling both plant height and root
traits (Bai et al. 2013; Ehdai et al. 2016; Kabir et al. 2015). This might be another
reason that root traits were significantly related to agronomic traits (such as SNS and
TGW).

FD showed significant correlation with MRL. It is known that a plant with longer
growth period need to absorb more water and nutrients from deeper soil layers to
complete the period from vegetative to reproductive stage (Salvador R and Pearce R
1995). Therefore, longer roots could undoubtedly benefit the absorption and
utilization of the water and nutrients and thus help the growth and development of a
plant. The fact that Q1028 showed a longer growth stage (Luo et al. 2016) and root
length than ZM9023 may further explain the significant correlation between root traits
and FD in this study.

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Province.

**References**

nitrogen uptake in relation to the early growth of wheat (*Triticum aestivum* L.). Plant

Ayalew, H., Liu, H., and Yan, G. 2017. Identification and validation of root length


Table 1 Phenotypic variation and heritability ($H^2$) of investigated traits for RIL population. The data of the parents were the average of the three repetitions, and that for lines were BLUP values.

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<td>ZM9023 ± SD</td>
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<tr>
<td>RDW (g)</td>
<td>0.051 ± 0.012</td>
<td>0.053 ± 0.010</td>
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<tr>
<td>SDW (g)</td>
<td>0.19 ± 0.01</td>
<td>0.21 ± 0.03</td>
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<tr>
<td>MRL (cm)</td>
<td>44.99 ± 6.00**</td>
<td>36.17 ± 6.43</td>
</tr>
<tr>
<td>TRL (cm)</td>
<td>645.33 ± 118.88**</td>
<td>989.97 ± 86.55</td>
</tr>
<tr>
<td>AD (cm)</td>
<td>0.33 ± 0.022**</td>
<td>0.31 ± 0.018</td>
</tr>
<tr>
<td>SA (cm$^2$)</td>
<td>67.60 ± 14.90**</td>
<td>97.21 ± 12.37</td>
</tr>
<tr>
<td>RV (cm$^3$)</td>
<td>0.56 ± 0.14**</td>
<td>0.76 ± 0.13</td>
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<tr>
<td>RTN (n/plant)</td>
<td>1235.83 ± 234.04**</td>
<td>2614.24 ± 397.89</td>
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<tr>
<td>RSR</td>
<td>0.27 ± 0.05</td>
<td>0.25 ± 0.01</td>
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* Significant at the 0.05 probability level.

** Significant at the 0.01 probability level.

RDW, Root dry weight; SDW, Shoot dry weight; MRL, Maximum root length; TRL, Total root length; AD, Root average diameter; SA, Root surface area; RV, Root volume; RTN, Number of root tips; RSR, root/shoot ratio.
Table 2 Correlation coefficients between investigated traits in the RIL population.

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<th>TGW</th>
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<td>FD</td>
<td>0.298**</td>
<td>0.257**</td>
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<td>0.329**</td>
<td>0.103</td>
<td>0.329**</td>
<td>-0.122</td>
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<td>0.308**</td>
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<td>TN</td>
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<td>SNS</td>
<td>-0.391**</td>
<td>0.157*</td>
<td>0.194**</td>
<td>0.193**</td>
<td>0.075</td>
<td>0.087</td>
<td>0.091</td>
<td>0.104</td>
<td>0.124</td>
<td>-0.032</td>
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<td>TGW</td>
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<td>-0.053</td>
<td>0.243**</td>
<td>0.232**</td>
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<td>RDW</td>
<td>0.833**</td>
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<td>0.784**</td>
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<td>0.828**</td>
<td>0.852**</td>
<td>0.578**</td>
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<td>SDW</td>
<td>0.295**</td>
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<td>0.029</td>
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<td>0.847**</td>
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<td>0.186†</td>
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<td>MRL</td>
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<td>-0.003</td>
<td>0.313**</td>
<td>0.316**</td>
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<td>TRL</td>
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<td>0.948**</td>
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<tr>
<td>AD</td>
<td>-0.127</td>
<td>0.035</td>
<td>-0.460**</td>
<td>0.085</td>
<td>0.073</td>
<td>0.094</td>
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<tr>
<td>SA</td>
<td>0.986**</td>
<td>0.805**</td>
<td>0.731**</td>
<td>0.094</td>
<td>0.081</td>
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<td>RV</td>
<td>0.731**</td>
<td>0.094</td>
<td>0.081</td>
<td>0.081</td>
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<tr>
<td>RTN</td>
<td>-0.081</td>
<td>0.081</td>
<td>0.081</td>
<td>0.081</td>
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</table>

* Correlation is significant at the 0.05 level
** Correlation is significant at the 0.01 level

The BLUP values for a given trait were used for correlation analysis. FD, Flowering date; PH, Plant height; TN, Tiller number; SNS, Spikelet number per spike; TGW, Thousand grains weight; RDW, Root dry weight; SDW, Shoot dry weight; MRL, Maximum root length; TRL, Total root length; AD, Root average diameter; SA, Root surface area; RV, Root volume; RTN, Number of root tips; RSR, root/shoot ratio.
Table 3 QTLs controlling maximum root length (MRL), total root length (TRL), root average diameter (AD), root surface area (SA), root volume (RV), number of root tips (RTN) and root/shoot ratio (RSR) detected in the RIL population of wheat derived from the Q1028 × ZM9023 cross.

<table>
<thead>
<tr>
<th>Trait</th>
<th>QTL</th>
<th>Chromosome</th>
<th>Interval</th>
<th>LOD</th>
<th>PVE (%)</th>
<th>Add.</th>
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<tr>
<td>MRL</td>
<td>QMrl.sau-3B</td>
<td>3BS</td>
<td>Xgpw7452-wPt-6047</td>
<td>4.43</td>
<td>9.85</td>
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<td>QMrl.sau-6B</td>
<td>6BS</td>
<td>wPt-2564-wPt-8183</td>
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<td>6.94</td>
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<td>QMrl.sau-7A</td>
<td>7AS</td>
<td>wPt-744715-Xgpw3208</td>
<td>3.20</td>
<td>6.18</td>
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<td>QMrl.sau-7B</td>
<td>7B</td>
<td>Xgpw4444-Xgpw3111</td>
<td>7.75</td>
<td>16.68</td>
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<td>TRL</td>
<td>QTrl.sau-4B</td>
<td>4BL</td>
<td>Xbarc1096-Xwmc47</td>
<td>4.51</td>
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<td>7AS</td>
<td>wPt-4515-Xgpw3220</td>
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<td>AD</td>
<td>QAd.sau-3D</td>
<td>3DS</td>
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<td>QAd.sau-5B</td>
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<td>wPt-4515-Xgpw3220</td>
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<td>12.18</td>
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<td>SA</td>
<td>QSa.sau-4B</td>
<td>4BL</td>
<td>Xbarc1096-Xwmc47</td>
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<td>10.61</td>
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<td>RV</td>
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<td>RTN</td>
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<td>RSR</td>
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<td>QRsr.sau-7A</td>
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<td>5.73</td>
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</table>

* The left and right flanking markers of the interval of the logarithm of odds (LOD) peak value for a given QTL.
† Percentage of the phenotypic variation explained.
‡ Additive effect of a QTL. Positive values of additive effect indicate that alleles from Q1028 in the direction of increasing the traits scores, and the negative values indicate that alleles from ZM9023 in the direction of increasing the score.
§ The arm location of QMrl.sau-7B is difficult to analysis. Xgpw4444 and Xgpw3111 were belonged to 7BS and 7BL, respectively.
Figure legends

Fig. 1 Comparison of root systems for ZM9023 and Q1028. Scale represents 10 cm.

Fig. 2 Frequency distributions of the root traits from the RIL population. Data was based on BLUP values of the investigated experiments. The black arrow indicates the value of Q1028 and the white arrow indicates ZM9023.

Fig. 3 QTLs for the root traits of the RIL population. Abbreviations for traits are: MRL, Maximum root length; TRL, Total root length; AD, root average diameter; SA, Root surface area; RV, root volume; RSR, root/shoot ratio; RTN, number.
Fig. 1 Comparison of root systems for ZM9023 and Q1028. Scale represents 10 cm.

122x279mm (300 x 300 DPI)
Fig. 2 Frequency distributions of the root traits from the RIL population. Data was based on BLUP values of the investigated experiments. The black arrow indicates the value of Q1028 and the white arrow indicates ZM9023.

73x63mm (300 x 300 DPI)
Fig. 3 QTLs for the root traits of the RIL population. Abbreviations for traits are: MRL, Maximum root length; TRL, Total root length; AD, root average diameter; SA, Root surface area; RV, root volume; RSR, root/shoot ratio; RTN, number.

76x85mm (600 x 600 DPI)