Genetic variation in specific root length in Scandinavian wheat and barley accessions

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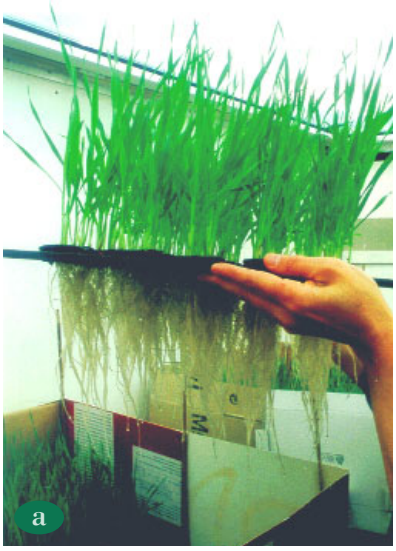

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Legend to pictures, opposite page

a Cereal accessions during growth in circulating low-P nutrient solution, here lifted up to show the roots.
b Cereal accessions grown in circulating low-P nutrient solution at harvest. Three replicates, each comprised of five single plants, of the accessions that produced most or least total dry matter (DM), respectively. These accessions were barley cv. Dønnes (to the left, most DM) and barley cv. Tunga (to the right, least DM).
c Preparation of pots for growth of single plants in low-P soil without nutrient supply.
d Single plant of barley cv. Dønnes at harvest after 2 weeks growth in low-P soil without nutrient supply. Nutrient deficiency symptoms are obvious, as shown by red leaf sheath (P-deficiency) and yellow leaf tips (N-deficiency).

Picture a were taken by Birgitte Løes; b, c and d by Anne-Kristin Løes.

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ABSTRACT

Specific root length (SRL, m root g^{-1} root dry matter) was studied in a broad selection of old and presently grown accessions of spring wheat and barley from Norway and Sweden, at sub-optimal phosphorus conditions in nutrient solution and soil. The results indicated that genotype did not have a significant effect on SRL. A close relationship between root length (RL) and root weight (RW) was found, and more than 70% of the variation in root lengths was explained by root weights of representative and homogenous root samples. In nutrient solution, the relationship between RL and RW was described by the regression equations RL = 0.32RW – 0.19 (R^2 = 0.74) for wheat and RL = 0.20RW + 0.73 (R^2 = 0.56) for barley. In the soil experiment, the relationships between RL and RW were described by the equations RL = 0.15RW + 0.95 (R^2 = 0.67) for wheat and RL = 0.16RW + 0.50 (R^2 = 0.77) for barley. Hence, in screenings of a large number of cereal genotypes, the root length (y-axis) may be estimated with good accuracy by records of root weight (x-axis) and an appropriate regression equation.

Abbreviations: CV = coefficient of variance (%), CH = clustered herringbone (root type), DM = dry matter, H =herringbone (root type), RL = root length, RW = root weight, SRL = specific root length (m root g^{-1} root dry matter)

INTRODUCTION

The total root surface of a plant is important for capturing water and nutrients from soil. At sub-optimal nutrient concentrations in soil a large root surface is of advantage, especially for absorbing less mobile nutrients such as phosphorus (P). A large root surface is achieved by a combination of reduced mean root diameter and elongation of the relatively thinnest roots (Fitter, 2002). The specific root length (SRL) expressed as m root g^{-1} root dry matter (DM) integrates root length and fineness. From a given amount of root DM, a plant with fine roots (large SRL value) produces a relatively larger root system. SRL has been suggested as a useful trait in breeding of P-efficient varieties (Clark, 1983; Sattelmacher et al., 1994). Root characteristics such as total root length (Römer et al., 1988), root length density (Egle et al., 1999) and root length per plant dry matter (Nielsen & Schjørring, 1983) have been shown to vary considerably between cereal genotypes. For further references on genotypic variation in these root characteristics, see O'Toole & Bland (1987) or Manske &Vlek (2002). However, with respect to the specific root length, information on the genetic variation in cereal species is rudimentary, often based on studies with few lines or varieties and often non-consistent. Significant variation was found between eight barley varieties in nutrient solution (Schjørring & Nielsen, 1982), but for six winter wheat varieties grown in the field, the differences were smaller, and not consistent from one sampling to another (Welbank et al., 1974). Therefore, the value of SRL in breeding programmes is yet difficult to assess. Errors in sampling and measuring root length, even with modern image analysis systems, add to the reasons for the discrepancies. Hence, simple ways of comparing the size of root systems of large number of genotypes are desired. Root length is measured by line intersection (Newman, 1966) or scanning methods (Richner et al., 2000), which are both time-consuming.

We studied the root development of old and recent Scandinavian spring wheat and barley accessions at sub-optimal P conditions in circulating nutrient solution and soil. Based on the results of these studies, this paper aims to discuss the influence of cereal genotype and root morphology on SRL, and to test the possibility whether less laborious root weight determination can be a good indicator of the root length of cereal genotypes.

MATERIAL AND METHODS

Plant material and overview of experiments

A selection of 17 spring wheat and 35 spring barley accessions, ranging from old land races collected around 1900 to modern lines not yet released, was investigated for root development and SRL. One Scottish land race, Scots Bere, was also included in the material, as it is adapted to a low soil pH. The pedigree of the accessions is shown in Table 1. Before starting the experiments all accessions were grown in the same field to multiply seed under comparable conditions. Two experiments in climate chamber were conducted, one with all accessions in low-P nutrient solution and the other with 15 accessions in low-P soil. SRL was measured at harvest in each experiment. Due to differences in nitrogen (N) availability, the growth and development of the plants was very different in nutrient solution and soil, but this should not hamper a comparison of genotypes within each experiment.

Table 1. Pedigree or geographical origin, year of approval or collection, and specific root length (SRL) values for spring barley and wheat accessions arranged by increasing SRL value in nutrient solution, and for a subset of 15 accessions additionally in low-P soil. Abbreviations: S = Swedish (all other accessions are of Norwegian origin), 2r = 2-row barley (others are 6-row), n.r. = not released at the time of the study, Dw = Dwarf line for breeding purpose only. LSD = Least significant difference, 5%

Genotype	Pedigree or origin, year of approval or collection	Nutrient sol.	Low-P soil
		SRL m g-1 root DM	
BARLEY			
Fager	HN355-93/Thule, 2000	186	
Tore	Lise/Clermont, 1986	199	
Fløya	Pur. line of land race Ørnes, N Norway, 1918	200	
Lise	(Asplund x Ds295) x Varde, 1960	200	
Jadar	Land race, SW Norway, 1900-1910	208	
HDw021, Dw	Lise x Ashdon /x Tore / xTore	209	
Asplund, S	Purified line from 2-row barley, 1900-1910	210	
Thule	Ensenada/Bamse//H313-248, 1993	215	
Finnebygg	Land race, central Norway, 1900-1910	216	
Skjåk	Land race, central Norway, 1900-1910	218	224
Varde	Asplund x Maskin (1924), 1939	219	
Maskin	Purified line of land race Bjørneby, 1910	222	
Olsok	Bode/Agneta, 1994	224	
Jarle	Jadar x(Asplund x Maskin)(1932), 1952	228	
Mari, 2r	Mutation in Sv. Bonus (1963), 1977	228	
Herse	Asplund x Maskin, 1939	234	182
Tyra, 2r	Sold/Sv71164, 1988	236	
NK95036	Tyra/P-13, n.r.	236	
NK94682	Arve//HS72-8/MØ75-278/3/PH107, n.r.	239	
SWE018, S, 2r	Meltan x Svani, Sweden, n.r.	240	
Domen, 2r	Maskin x Opal B, 1949	240	
Gunilla, 2r	Birgitta x Sv Å 56888, 1973	257	223
Gaute	SvN82114/V13647-77, 2000	258	216
SWE9306, S, 2r	Derkado x Sv84580, n.r.	259	
Refsum, 2r	Land race, S Norway 1900-1910	263	229
SWE9319, S, 2r	Meltan x Svani, Sweden, n.r.	265	
Tunga	Fræg x (Juli x Rigel), 1975	268	233
Arve	Agneta//Otra/Vigdis, 1990	273	
Dønnes	Land race from N Norway, < 1900	275	205
SWE013, S, 2r	Goldie x Svani, Sweden, n.r.	280	243
Olve, 2r	Gunilla/Lilly, 1994	283	243
Møyar, 2r	Domen x Herta, 1964	295	
SWE019, S, 2r	Meltan x Svani, Sweden, n.r.	295	
Scotch Bere	Adapted to soil pH (H2O) 4.5, land race from Scotland	303	
Herta, 2r	Kenia x Isaria, 1941	329	235
LSD barley		*75*	*49*
WHEAT			
Diamant, S (or Diamant II)	Kolben x Steninge, 1928 (Diamant x Ekstra Kolben, 1938)	255	193
NK97520	SvB87293/Bastian, n.r.	279	
Brakar	T8058/T8073//T8080/Bastion, 1995	288	173
Bastian	Baijo/Runar/3/Yactana//Norin10/Brevor/5,1989	289	
Møystad	Mö043-40 x KärnII, 1966	292	
Østby	Land race, S Norway, 1900-1910	304	
Reno	Els x (Tammi x KärnII), 1975	304	197
Børsum	Land race, S Norway, 1900-1910	312	197
Norrøna	FramII x Sopu, 1952	313	
NK97535	Reno/Genesis//Drabant /Hanno, u.a.	316	
Rollo	KärnII x Norrøna, 1963	318	
Sibirian	Land race, 1900-1910	320	
Ås	Purified line from land race, 1900-1910	323	
NK98602	Brakar/ Rida x T2038, n.r.	331	
SnøggII	(Jo3 x Sibirisk) x Ås1927, 1940	334	
NK0058, Dw	Brakar/T1022	339	187
NK97537	T4023/WW27328, n.r.	340	
LSD wheat		*98*	*39*

Nutrient solution experiment

Seeds were germinated on filter paper and the seedlings were grown for 3 weeks in a circulating well-aerated nutrient solution in a climate chamber (light intensity 130 mE s^{-1} m^{-2}, light/dark period 16/8 h, temperature 18 °C day, 15 °C night and 75% relative humidity). There were three replicates; each composed of five single plants fixed in a strip of foamed plastic. The initial complete basic nutrient solution was according to Gahoonia et al. (1999), except that a lower P concentration (25 mM as compared to 50 mM) was used. The nitrate concentration was 5 mM; no ammonium was added. To adjust pH close to 5.5 and to keep the electrical conductivity at 0.67 mS m^{-1}, a complete maintenance solution as described by Gahoonia et al. (1999), or only ammonium nitrate solution was added (if pH increased without change in electric conductivity). Although no visual signs of P deficiency were observed, the value of the N/P ratios in plant DM at harvest according to Gorshkova (1978) indicated a moderate P stress during growth. At harvest and root measurements, the plants were extending, DC 32 (Zadoks et al., 1974).

Soil experiment

Five genotypes of wheat and ten of barley (five 2-row, five 6-row) producing contrasting plant DM in nutrient solution were chosen and grown in low-P soil in the same climate chamber at the same conditions as mentioned. The soil was topsoil (0-30 cm, 15% clay, 18% silt, 65% sand, 1.5% total C) taken from a field where no P was added since 1966, and 60 kg N, 60 kg potassium (K) $ha^{-1}y^{-1}$ had been added as mineral fertilisers to cereals. The concentration of Olsen-P (Olsen & Sommers, 1982) was 4.5 mg P kg^{-1} and exchangeable K (Knudsen et al., 1982) was 60 mg kg^{-1} dry soil. Other soil chemical characteristics were pH (H2O) 6.0, pH ($CaCl_2$) 4.9, and soil mineral N 26 mg nitrate and 11 mg ammonia kg^{-1} dry soil (Bremner & Keeney, 1966). After sieving through 5 mm-mesh, 800 g soil (water content 12%) was filled into plastic pots and one vigorous seedling planted in each pot. There were 5-7 replicates (pots) per genotype and four of these were sampled for root length measurement. The plants were grown until growth diminished and the plants had developed significant nutrient deficiency symptoms, after approximately three weeks. By then, the plants had developed 3-5 leaves, DC 13-15 (Zadoks et al., 1974). The soil surface was covered with aluminium foil to prevent evaporation. The pots were placed on water absorbing cloth where distilled water was added when necessary. The correlation between SRL value and final water content of soil was very weak (R^2 = 0.13), and as all plants developed very similarly it is unlikely that differences in water availability influenced the nutrient supply of the plants.

Without external supply of N and P the plants grew slowly, and the genotypes were harvested in the sequence as deficiency symptoms (yellow leaf tips and purple leaf sheaths) appeared. Hence, 2-row-barley was harvested on days 15-19 from planting, 6 row-barley on days 18-20 and wheat genotypes on days 19-22. The correlation between SRL and harvest day was negligible (R^2 = 0.09).

Sampling and length measurement of roots

The roots from nutrient solution grown plants were stored moist in dark at 4 °C until length measurements, when two or three roots, 10-30 cm long, were randomly taken from the root mass of each genotype replicate. The roots from the soil experiment were gently washed, and immersed in water. A representative sample was cut off and carefully pulled out and stored dark at 4 °C in 15% alcohol solution.

For length measurement, the root samples were spread in distilled water in a glass tray placed on a flat bed scanner (ScanJet IIcx) and the scanned images were stored. The root samples were collected from the trays, dried at 70 °C and weighed. The digital image files were analysed by Dt-Scan Software (Delta-T Devices, Cambridge, England) to measure root length (RL). In Dt-Scan, the standard calculation procedure measures the RL by dividing the total area of the image by mean diameter. RL values obtained by this procedure were considerably over-estimated as compared to those measured by hand (Table 2). This is because shade and root debris particles were interpreted as image area and system limitation did not allow setting a limit to particle size for excluding this noise. The procedure "Object scan" measures the perimeter of objects, and here a lower limit of particle size could be set. The values for object perimeter/2 were close to the values measured manually (Table 2) when the limit was set to 0.03 mm^2. The roots from nutrient solution were scanned at a resolution of 300 DPI (dots per inch), but as we realised that 150 DPI gave a sufficient quality, this resolution level was used for the roots from soil.

SRL was calculated as the RL divided by the weight of the scanned root sample.

Table 2. Values of root length obtained by hand measurement compared to values obtained by different analyses with Delta T Scan software. The analysis "Object Scan" gives the perimeter of stick-like objects; the root length is the perimeter/2. Here, a lower limit of the size of scanned objects could be set. The analysis "Root length, Newman-Head" calculates the root length from the root image area. No limit of objects could be set and hence, shade and root debris exaggerated the root length values. Perimeter/2 values were used in the present study.

Sample	Hand measured	Perimeter/2	Newman-Head
1	1401 mm	1404 mm	1828 mm
2	1559 mm	1663 mm	2500 mm
3	1616 mm	1623 mm	2568 mm
4	1902 mm	1950 mm	2372 mm
5	2235 mm	2726 mm	3585 mm
6	2576 mm	2381 mm	4022 mm

Statistical analysis

The effect of variety and root type on SRL was analysed by variance analysis (Anova or GLM, SAS Institute, 1989). Tukey's t-test was used to analyse if accessions were significantly different. Levels of significance are shown in the text as *P* values. For information on the variability of the data, the coefficient of variance, CV (standard deviation / average value *100%) is referred for each statistical analysis.

RESULTS

Root morphology

The roots from the solution experiment had quite distinct morphology and could be divided in two categories (Figure 1). One category was composed of 1st and 2nd order roots, and ended by a long zone where roots of 2nd order had not yet developed (Figure 1). Such roots were called "herringbone" (H) roots, according to Fitter (2002). The other group had a more dichotomous architecture, and was called "clustered herringbone" (CH, Figure 1). A much shorter part of CH roots was 1st order root, and the roots of 2nd order had developed 3rd order roots. Thereby, the 2nd order CH roots looked similar to the H roots, only with smaller root diameters. As the H roots had usually not developed roots of 3rd order, whereas the CH roots had many roots of 3rd order, the H roots were probably younger than the CH roots. It may be assumed that CH roots were seminal and H roots were nodal, as the CH roots were localised at the inner parts of the root mass. Due to the growing conditions and because in wheat and barley the distance between the base of the 1st and 2nd internode (where the seminal and nodal roots, respectively, develop) is very short, which roots were seminal and nodal could not be distinguished.

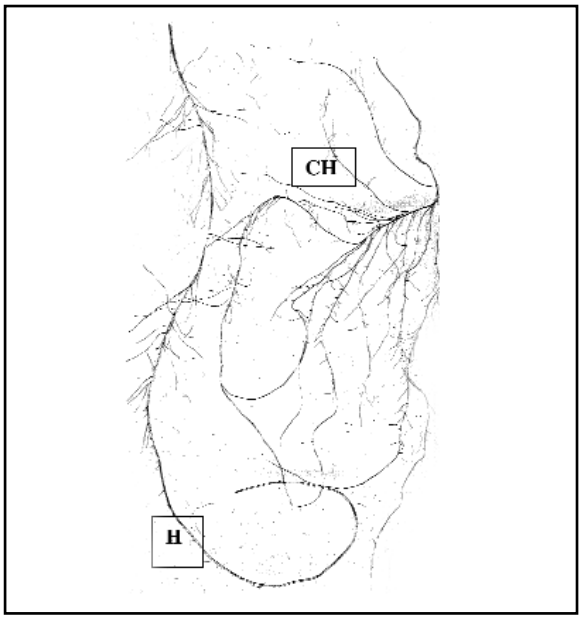

Figure 1. Roots from barley SWE9319 grown for 21 days in low-P nutrient solution. To the left typical "herringbone" roots (H); to the right, typical "clustered herringbone" roots (CH).

By the random sampling procedure, initially, only H roots were sampled. After the CH roots were revealed, efforts were made to sample both kinds of roots from each variety. Each root sample was classified as H root, CH root or a mixture of both. For barley, 6% of the samples consisted of CH roots, 47% of H roots and 47% were a mixture. For wheat, 22% of the samples were CH roots, 25% were H roots and 53% were a mixture.

Roots from the soil experiment were generally slightly curled H roots of 1st and 2nd order. As compared to the H roots from nutrient solution, the roots of 2nd order from soil were often very elongated. In some cases, roots of 3rd order had developed. No typical CH-roots were found in soil.

Specific root length of H and CH root types

In nutrient solution, H and CH root type clearly affected SRL values, both for wheat and barley (P = 0.007 and 0.0001, and CV 15 and 20%, respectively). No significant interaction was found between root type and variety. From the visual observations, the H roots were generally coarser than the CH roots. For H roots the mean SRL values were 223 m g^{-1}root DM for barley and 264 for wheat. For CH roots, the mean values were 327 for barley and 344 for wheat. The variation in SRL values within the H and CH roots of both species was large, with extreme values for H roots being 115 and 312 m g^{-1} root DM for barley and 190 and 370 for wheat. For CH roots, the corresponding values were 226 and 369 in barley, and 259 and 400 in wheat. The main factor contributing to larger SRL values for H roots was the length of the 2nd order roots (Figure 2, upper panel), which had a lower root diameter than 1st order roots. The length of 2nd order roots was much larger for a sample from NK98602 (wheat) with SRL = 370 than for cv. "Fager" (barley), SRL = 115. For the CH roots, the number of 2nd order roots and hence the root branching seemed to be the main reason for increased SRL values (Figure 2, bottom panel). Cv. "Fager" had a SRL value of 226 and a less branched CH root than the accession "Ås" (wheat) with a SRL value of 392. This shows that relatively lower root diameters within each root order, increased lengths of higher order roots (with lower diameters) as well as increased root branching are mechanisms by which the fraction of the root system that is composed of fine roots, and hence the SRL value, may be increased.

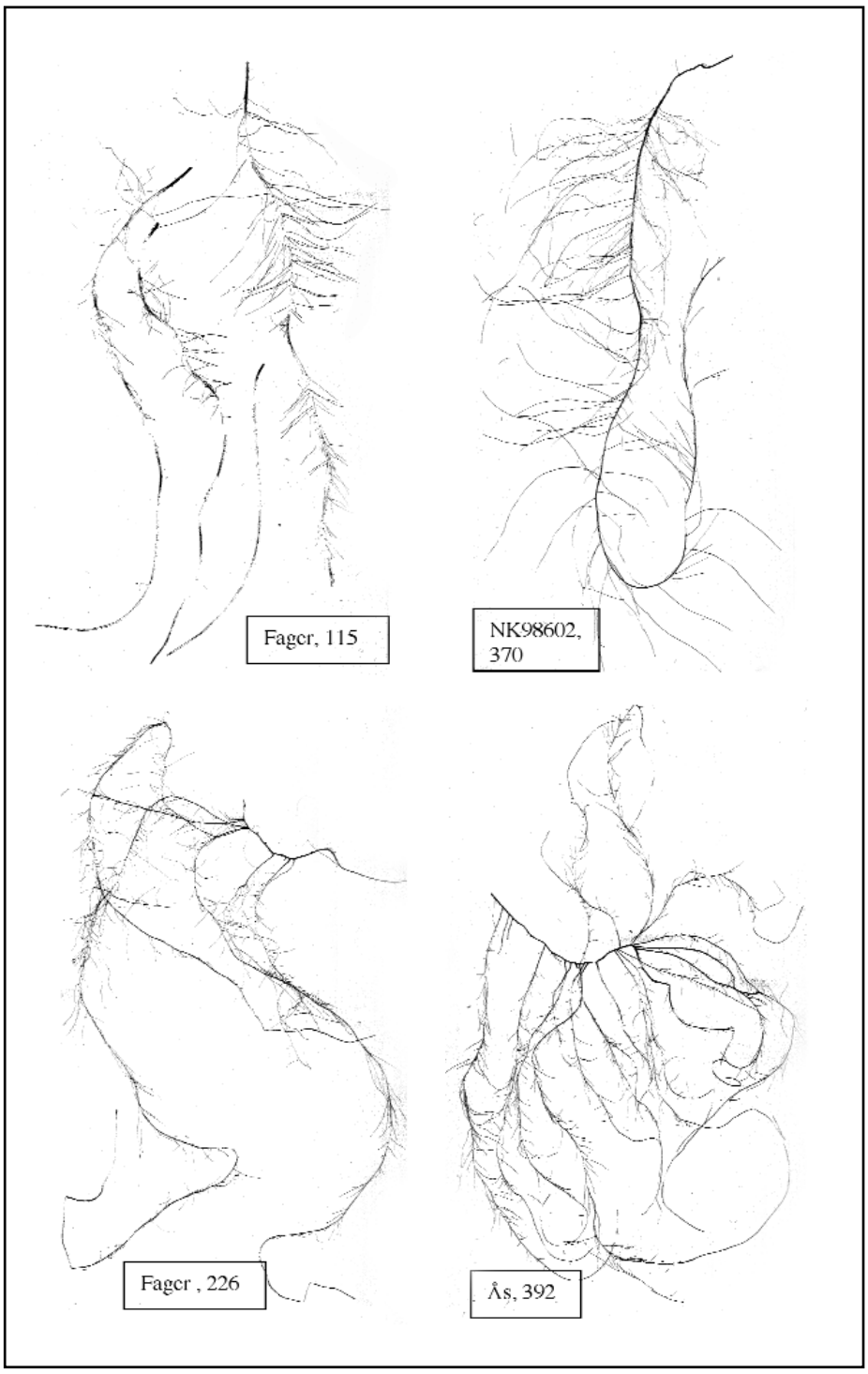

Figure 2. H (herringbone) and CH (clustered herringbone) root samples of wheat and barley accessions with contrasting values of specific root length (SRL). Upper panel H roots, lower panel CH roots. To the left, low SRL values, to the right, high values. SRL values, m g-1 root DM, are shown for each picture.

Genetic variation in specific root length (SRL)

The average SRL values for the barley and wheat accessions are shown in Table 1. The SRL of barley accessions ranged from 186 for cv. "Fager" to 329 for cv. "Herta" in the nutrient solution experiment. These were the only two among the 35 accessions, which differed statistically (P = 0.02, CV = 19%) in SRL values. For the 17 wheat accessions in nutrient solution, there was no effect of genotype on SRL (P = 0.95, CV = 19%). The lowest value was for cv. "Diamant" (255) and the highest for NK97537 (340). In the soil experiment there were no statistically significant differences in SRL neither for wheat nor for barley accessions (P = 0.64 and 0.31, CV = 14 and 15%, respectively). The difference between the lowest and highest SRL value was smaller in soil as compared to nutrient solution. In barley, the SRL varied between 182 and 243, and in wheat between 173 and 197.

Specific root length of wheat vs. barley

In nutrient solution, the mean SRL for wheat was significantly higher (309) than for barley (242, P = 0.0001, CV 20%). When the subset of accessions that were used in the soil experiment was analysed separately, the average SRL for wheat (5 accessions) was 300 and for barley (10 accessions) it was 263. The difference was statistically significant (P = 0.03, CV 18%). In the soil experiment, however, wheat had a somewhat lower (189) SRL value than barley (223, P = 0.0003, CV 31%). Hence, there appeared to be no general difference in SRL values between the two cereal species. The reason for a larger SRL value of wheat than barley in nutrient solution may be a larger fraction of H roots in the barley as compared to the wheat root samples.

Relation between root weight and length

There was a significant correlation between root weight and root length ($P < 0.001$) in each of the two experiments. In nutrient solution (Figure 3), the relationship between root weight (RW, x-axis) and root length (RL, y-axis) could be described by the regression equations RL = 0.32*RW – 0.19 for wheat (R^2 = 0.74) and RL = 0.20*RW + 0.73 (R^2 = 0.56) for barley. The wheat root samples were more homogenous with respect to the amount of H and CH roots than the barley samples, which explain the larger coefficient of variation for wheat than for barley. In the soil experiment (Figure 4), the relationships between RW and RL were described by the equations RL = 0.15*RW + 0.95 (R^2 = 0.67) for barley and RL = 0.16*RW + 0.50 (R^2 = 0.77) for wheat. A closer correlation between RW and RL in the soil experiment was probably due to that the soil root samples comprised a larger part of the total root system, on average 9.1% of the root mass, as compared to 4.5% in nutrient solution. Further, there were more replicates per genotype.

The data presented suggested that there was a close relationship between root weight and root length both for wheat and barley. More than 70% of the variation in root length was then explained by the variation in root weight. Hence, root weight of homogenous roots of wheat and barley can be a good indicator of root length.

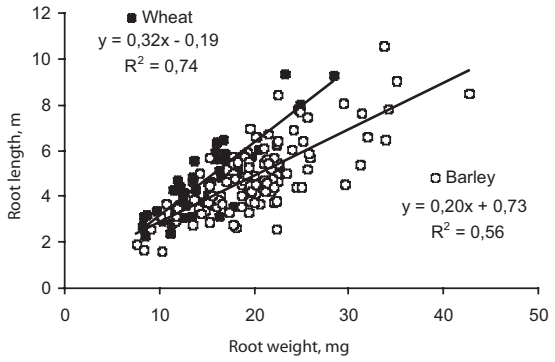

Figure 3. Relation between dry weight and length of scanned root samples of 17 wheat and 35 barley accessions grown in nutrient solution with sub-optimal P availability.

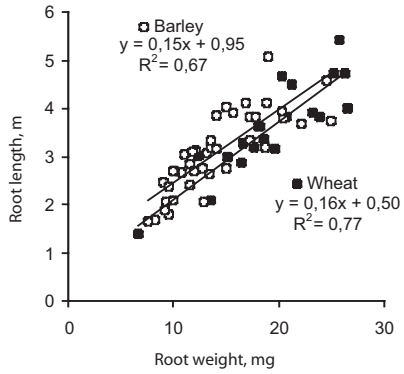

Figure 4. Relation between dry weight and length of scanned root samples of 5 wheat and 10 barley accessions grown in soil with sub-optimal P availability.

DISCUSSION

Data variability

The present root data must be seen in the light of a large variability, especially in nutrient solution where the least significant differences (LSD values) were 31-32% of the total average for barley and wheat, respectively (Table 1). Römer & Schenk (1998) reported a comparable variability, where the LSD values for total root length were 39-48% of the average for 24 barley genotypes grown with varying P-availability. One of the reasons for the large data variability in the present study may be the small sample size and number of replicates (3) in nutrient solution, where the CV was 19%. With four replicates and a larger average sample size, the CV decreased, to 14-15%. This shows that a considerable part of the variability in SRL within genotype is due to a natural background variation, so that most probably there is a limit as to how much the CV would decrease with larger samples and more replicates. All of this highlights the difficulties related to root sampling and length measurements for detection of variation in root characteristics of cereal varieties and emphasises the need to explore simpler ways of comparing root systems.

Root type in relation to root origin

In nutrient solution, the roots were classified into the categories "herringbone" (H) and "clustered herringbone" (CH). The CH-roots were located to the inner part of the root mass, and hence assumed to be of seminal origin. In soil, seminal roots are generally finer and more densely branched (Kutschera, 1960) as compared to nodal roots, which strengthens this assumption. The number of H as compared to CH roots per genotype replicate would have been valuable information, but it was not recorded in the present study. The theoretical maximum number of seminal roots in wheat and barley is 10 (Manske & Vlek, 2002), but normally, far less seminal root primordia develop. In a study of Norwegian wheat and barley genotypes, Heen (1980a) found 5-6 seminal roots per plant grown in field. Contrary to the number of seminal roots, the number of nodal roots is strongly influenced by the degree of tillering, and was found to be approximately 10 roots per plant by a tillering density of 4-5 shoots (Heen, 1980a).

The number of seminal roots is influence by genotype, but the number of seminal roots was only found to vary between 4 and 6 in a study of nine wheat accessions (Robertson et al., 1979). The impact of genotype on the number of nodal roots is small (Heen, 1980a). In the present study, it cannot be excluded that the number of seminal roots was affected by genotype. However, as the tiller density was not recorded, it can not be excluded that the number of nodal roots was affected by genotype, because the significant variation among genotypes in DM production may have been linked to a variation in numbers of tillers and thereby, of nodal roots. Hence, it is probable that the amount of H (nodal) and CH (seminal) roots sampled from each genotype in nutrient solution was not representative, and this may have obscured potential genetic differences in SRL. However, the effect of such biased sampling was not substantial. If biased sampling should have obscured potential differences, it should be expected that the lowest SRL values should have been found for genotypes where only H roots were sampled, and opposite that the highest SRL values should be found for genotypes where only CH roots were sampled. The only significant difference in SRL between genotypes was observed between barley cv. "Herta" and "Fager". Cv. "Herta" with the largest SRL value had a mixture of H and CH roots in all root samples, whereas cv. "Fager" (lowest SRL value) had two root samples with H and one with a CH root. Hence, the samples included both H and CH roots for both genotypes. Two other accessions of barley, cv. "Fløya" and "Dønnes", had only H root samples, but had SRL values well above "Fager" (Table 1).

No effect of genotype on SRL within root type

What the present study clearly demonstrated was that within root type, there was no significant effect of genotype on root fineness. In a subset of 17 barley accessions in nutrient solution where two replicates were comprised of H roots (n = 34), no significant difference in SRL was found (P = 0.46, CV = 21%). The mean SRL values in the subset ranged from 150 m g^{-1} root DM for cv. "Fager" to 288 for cv. "Møyar", and were roughly comparable to the difference found when all replicates of all barley genotypes were considered. In another subset, comprised of five barley and five wheat accessions where one replicate was H and one was CH root (n = 20), no relation was found between the SRL value for H and CH root from the same genotype (P = 0.56). In the soil experiment, mostly seminal roots were present because nodal roots develop when the fourth mainstem leaf appears (Manske & Vlek, 2002) and the soil-grown plants in our study had developed only 3-5 leaves at harvest. In the soil experiment, no effect of genotype on SRL was found at all. This emphasises that when a variation among genotypes in SRL is found, it is most probably related to differences in the number of seminal and nodal roots, and not that some genotypes have a lower average root diameter and/or increased root branching as compared to others.

Conflicting results from previous studies

Some previous studies have reported differences among genotypes in SRL; for eight barley cultivars (Schjørring & Nielsen, 1982), two wheat cultivars (Horst & Wiesler, 1986) and six maize cultivars (Nielsen & Barber, 1978). However, in a field study with six wheat varieties during two seasons (Welbank et al., 1974), no genetic variation in SRL was found. It is not clear from the above-mentioned previous studies whether attention was given to seminal and nodal roots. In the present study, where a considerably larger amount of genotypes were compared, no clear effect of genotype on SRL was found. Our data suggested that the impact of genotype on root fineness of wheat and barley might not be significant. Hence, when a large number of wheat and barley accessions are considered, the root fineness may be considered uniform and homogeneous.

Root length – weight: a close correlation

In the present study, there was a close relationship between root weight and root length (Figures 3 and 4), especially when the root samples were representative and homogenous such as in soil. For such root samples, a large proportion (> 70 % of the variation in root length) could be explained by root weight. This is in accordance with Atkinson (2000), and with Heen (1980b) who found a coefficient of determination as high as R^2 = 0.98 for the relation between length and dry weight of hand-measured root pieces of barley. Hence, the root length may be estimated from the weight of homogeneous and representative root samples by using appropriate regression equations as mentioned above in the results. This significantly simplifies the laboratory work in screening of genotypes for root characteristics.

CONCLUSIONS

The present study indicated that the SRL of seminal roots was larger than for nodal roots grown in nutrient solution. Within each root type there was no significant effect of genotype on SRL. The influence of genotype on SRL within spring wheat and barley was not significant as compared to other conditions influencing this complex plant characteristic. Hence, in cereal genotype screenings where a large number of accessions are to be compared, the initial assessments of root size can be done with reasonable good accuracy by recording root weight. Although such assessments may not substitute measurement of actual root length for detailed studies in connection with uptake of nutrients and water, they may significantly simplify the initial screening of cereals and perhaps also other grasses for their root systems. In this study the relationships between root weight and root length of wheat and barley, whose root fineness is fairy uniform as compared to woody roots, are presented. Therefore, as described by Atkinson (2000), the close correlation between root length and weight found in the present study may not be valid for woody roots.

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