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Review

Breeding for increased nitrogen-use efficiency: a review for wheat (*T. aestivum* L.)FABIEN CORMIER¹, JOHN FOULKES², BERTRAND HIREL³, DAVID GOUACHE⁴, YVAN MOËNNE-LOCCOZ^{5,6,7,8} and JACQUES LE GOUIS^{7,8}

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With 2 figures and 4 tables

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Abstract

Nitrogen fertilizer is the most used nutrient source in modern agriculture and represents significant environmental and production costs. In the meantime, the demand for grain increases and production per area has to increase as new cultivated areas are scarce. In this context, breeding for an efficient use of nitrogen became a major objective. In wheat, nitrogen is required to maintain a photosynthetically active canopy ensuring grain yield and to produce grain storage proteins that are generally needed to maintain a high end-use quality. This review presents current knowledge of physiological, metabolic and genetic factors influencing nitrogen uptake and utilization in the context of different nitrogen management systems. This includes the role of root system and its interactions with microorganisms, nitrate assimilation and its relationship with photosynthesis as postanthesis remobilization and nitrogen partitioning. Regarding nitrogen-use efficiency complexity, several physiological avenues for increasing it were discussed and their phenotyping methods were reviewed. Phenotypic and molecular breeding strategies were also reviewed and discussed regarding nitrogen regimes and genetic diversity.

Key words: bread wheat — breeding — nitrogen uptake efficiency — nitrogen-utilization efficiency

Nitrogen-use efficiency (NUE) has been the subject of a wealth of literature and underpinning projects for its improvement. There seems to be consensus on the need to increase NUE in breeding, but, to the best of our knowledge, NUE has not been the target of dedicated breeding programmes. Rather, it has been improved through the indirect selection for yield, in environments targeted by breeding programmes. Sadras and Richards (2014) have suggested that indirect selection for yield serves as a benchmark for any alternative approach. Several studies have evaluated *a posteriori* breeding improvement of NUE (Ortiz-Monasterio et al. 1997, Guarda et al. 2004, Muirinen et al. 2006, Cormier et al. 2013). For example, Cormier et al. (2013) quantified NUE improvement at 0.13 kg DM/kg N/year between 1985 and 2010 in France. Supposing an average French grain yield of 7 t/ha and assuming a reference NUE value between 37.8 kg DM/kg N (Cormier et al. 2013) and 33.3 kg DM/kg N (average value for wheat used in French balance sheet N recom-

mendation methods; Meynard 1987), this equates to a saving of approximately 6–8 kg N/ha after 10 years of genetic improvement. From an economic standpoint, the variations in fertilizer N/grain price ratio essentially determine the quantity of N applied. The impacts of this volatility on on-farm NUE and required N savings can be shown in two examples. Firstly, 10 years of breeding (*i.e.* a saving of 6–7 kg N/ha) can compensate for a variation in N/grain price ratio from 5 to 6, that is 16% of the total observed volatility over the past 10 years (Cohan 2009). Secondly, over the same 10-year period, Sylvester-Bradley and Kindred (2009) showed that this price ratio has varied from 3 to 9 (Sylvester-Bradley and Kindred 2009), leading to a necessity to increase NUE from 23.8 to 28.6 kg DM/kg N requiring almost 40 years of breeding progress.

Overall, this leads us to conclude that breeding programmes need to tackle NUE more efficiently than it has been doing at the current rate.

Definitions of NUE

The concept of nitrogen-use efficiency (NUE) has been widely used to characterize plant responses to different levels of nitrogen (N) availability. It is important to distinguish the concept of NUE and the NUE as a phenotypic trait.

Several definitions and evaluation methods have been suggested (reviewed in Good et al. 2004, Fageria et al. 2008). Moll et al. (1982) defined the most use of NUE, at least among breeders, which computes the grain dry mass divided by the total N available to a plant. It is divided into two components:

$$\text{NUE} = \text{NUpE} \times \text{NUEtE},$$

where NUpE is the N-uptake efficiency calculated as the total amount of N in above-ground plant at harvest divided by the available N in soil, and NUEtE is the utilization efficiency calculated as the grain dry mass divided by the total amount of N in above-ground plant at harvest. When different genotypes are compared, the computation of these components faces two main

issues: (i) the complex estimation of N available to the crop and (ii) the estimation of the total amount of N in the above-ground plant.

N available to the crop results from residual soil N at sowing and then aerial N deposition, mineralization of organic N and the actual availability of applied N. Thus, the estimation of N available to the crop is complex, and an often-used proxy has been the total amount of applied mineral N fertilizer added to an estimation of residual soil N at sowing or after winter. For 15 barley genotypes, Bingham *et al.* (2012) compared different methods to estimate available N. The first one was independent of genotype and used only residual soil N after winter and applied N fertilizer. The two others were dependent on the genotype and required a control without N fertilization (N^0). Available N for the fertilized treatment (N^T) was then estimated either (i) by adding the above-ground plant N at harvest for N^0 to the applied N fertilizer or (ii) by adding soil N at harvest to (i). Bingham *et al.* (2012) showed that genotype rankings were very similar between the three methods, and thus, the simplest method can be used.

However, as discussed in Cormier *et al.* (2013), this can lead to an overestimation of NUE in low N situations and to an underestimation of NUE in high N situations, making comparison and/or joint analyses of different studies difficult. Experimenting a large collection of genotypes, Cormier *et al.* (2013) suggested estimating available N from the distribution of the total plant N at harvest. They proposed to use the total amount of N in above-ground plant at harvest of the top 5% genotypes as an estimation of N that was available to the whole series.

To estimate the total amount of N in the plant, usually only the aerial parts are sampled. Not taking into account N in the roots would increase NUtE and decrease NUpE. However, measuring the quantity of root N (in the first 30-cm soil layer) of a set of cultivars grown at two N levels, Allard *et al.* (2013) showed that only a small fraction of total N is partitioned to the roots (about 4% or 10 kg/ha at harvest). Here again, the genotype rankings were very similar with or without taking into account root N.

Looking at the successes and debates that agitated other scientific communities may help to improve the approaches on wheat NUE. Ecologists developed another decomposition of NUE. Originally called 'nitrogen utility', Hirose (1971) defined it as the flux ratio of dry mass productivity for a unit of N taken up from the soil. Berendse and Aerts (1987) suggested dividing it into two components to make it biologically meaningful in a context of perennial species in a steady-state system (*i.e.* annual biomass production = annual biomass loss; annual N uptake = annual N loss). Thus, NUE was defined as the product of the nitrogen productivity rate (NP; dry mass growth per unit of plant N) and the mean time residence of N (MRT). Later, Hirose (2011) revisited this definition and specified how it should be calculated to make it also suitable for non-steady-state systems such as annual crops.

Compared to Moll *et al.* (1982), this definition has the potential to deliver a dynamic vision of NUE, which is directly related to photosynthetic activity along the plant cycle. Nevertheless, it only focuses on N utilization, as plant efficiency in extracting N from the soil is not taken into account. However, in annual crops, this is an important parameter to consider as substantial amounts of N fertilizer are applied, implying environmental and economic issues.

In a similar way, in the water-use efficiency (WUE) community, it has been explicitly decided not to account for water

available to the plant. The focus has been on viewing yield as the final objective through Passioura's (1977) seminal equation:

$$GY = WU \times WUE \times HI,$$

where WU is the water use (mm transpired), WUE is the water-use efficiency (kg above-ground dry matter/mm water transpired) and HI is the harvest index (kg grain/kg above-ground dry matter).

In relation to NUE formalization, NUtE would then be equivalent to $WUE \times HI$. NUpE would be an equivalent to WU divided by the quantity of water available to a plant. The approach could be taken further by simply targeting nitrogen use (NU) as kg N absorbed by the plant instead of NUpE; in much the same way that WU is seen as (arguably) the most important target in improving water response (Blum 2009). This would also avoid dividing an already rather imprecise variable (NU) by an even more imprecise one (available N). Yet, environmental and economic issues are different in NUE where minimizing the loss of fertilizer applied (*e.g.* by leaching) and maximizing N uptake for increasing grain protein concentration lead to a focus also on NUpE. Moreover, not to account for N available to the crop would imply using genotype-dependent methods (*e.g.* repeated controls) to compare varietal behaviour between different stress intensities or to characterize genotype \times stress interactions, if confounding effects need to be eliminated.

Criticisms of the initial WUE equation have heavily contributed to the identification and to the prioritization of approaches and traits. The first has been to recognize that the three terms of the equation are clearly not independent (Blum 2009, Tardieu 2013). Typically, as WU increases, WUE decreases because WU scales to biomass (Blum 2009), as does N absorption (Lemaire *et al.* 2007, Sadras and Lemaire 2014). Consequently, an excessively narrow focus on WUE may be counterproductive (Blum 2009). Although the underlying physiological reasons for this are very different between nitrogen and water, framing the nitrogen community in much the same way as the water community could help in placing the focus on NU and on systematically accounting for the total biomass when evaluating NU, as advocated by Sadras and Lemaire (2014).

As in water and ecologist communities, research on NUE could also be disconnected from the NUE definition of Moll *et al.* (1982) and focus on a dynamic approach. Indeed, NUpE and NUtE are calculated at the end of the crop cycle. However, total N in the plant varies during the cropping season and has a critical interaction with HI: once grains are growing, they become an N sink, and growers, breeders and the wheat industry have to manage the contradictory objectives of high yields and high protein contents (Feil 1997, Jeuffroy *et al.* 2002, Oury and Godin 2007). First of all, pre-anthesis and postanthesis phases should be clearly separated. Regarding the postanthesis phase, the grain protein deviation (GPD; deviation from the yield-protein linear regression) criterion suggested by Monaghan *et al.* (2001) and Oury and Godin (2007) allows breeders specifically to select for high protein content without the associated yield penalty. Bogard *et al.*'s (2010) analysis of GPD showed that this metric was tightly related to the deviation between pre-anthesis N uptake and postanthesis N uptake, meaning the obvious: crops that are both high yielding and high in protein content absorb large quantities of nitrogen. In other words, the analysis of Bogard *et al.* (2010) places NU as a key factor without focusing on NUpE. Looking at the pre-anthesis phase has the advantage of not having to deal with the yield-protein trade-off. Studying N

impacts on yield, grain number per area can become the criterion to target instead of yield. Indeed, it removes the grain weight elaboration, which occurs postanthesis. And as suggested by Meynard (1987), at least in western European situations, N will essentially have an impact on grain number per area, and kernel weight will often add noise due to other stresses. This would also mean that HI would essentially be replaced by a fertility index, implying complex phenotyping although it may allow for a better characterization of N response regarding the phenologic stage.

Traits Influencing N-Uptake Efficiency

Root size and morphology

Nitrate is readily leached through the soil profile. Consequently, the primary root traits to improve for enhanced N capture include rooting depth and rooting density, especially for postanthesis N uptake (Foulkes et al. 2009). A deeper relative distribution of roots could comprise part of an ideotype to maximize N capture, and further improvements in root architecture could focus on root proliferation at depth in wheat (Carvalho and Foulkes 2011). Indeed, root length density (root length per unit volume of soil) is often below a critical threshold of 1 cm/cm³ (Barraclough et al. 1989, Gregory and Brown 1989) for potential nitrate capture at lower depths in the rooting profile (Ford et al. 2006, Reynolds et al. 2007).

Genetic variation in root system size has been widely reported in wheat (e.g. O'Toole and Bland 1987, Hoad et al. 2001, Ehdaie and Waines 2003, Ford et al. 2006), but root distribution varies strongly with soil characteristics, nutrient availability and mechanical impedance. In wheat, the use of synthetic wheat derivatives, incorporating genes from the diploid wild species *Triticum tauschii* (D genome) with deeper rooting systems (Reynolds et al. 2007), may help in the development of cultivars with relatively deeper rooting systems. In addition, the wheat-rye translocation in 'Kavkaz' for the short arm of chromosome 1 (1RS) has been observed to have increased root biomass at depth (Ehdaie et al. 2003). And tall landraces from China and Iran have larger root biomass than semi-dwarf cultivars descended from CIMMYT breeding material (Ehdaie et al. 1991, Ehdaie and Waines 1993, 1997, Ehdaie 1995). It may also be possible to increase root length density at depth without extra carbon input by modifying specific root length (root length per root biomass; Carvalho et al. 2014). Although it is well established that plants respond to N deficiency by increasing the ratio of root biomass to total plant biomass (root dry weight ratio; RDWR) due to the functional equilibrium between the growth of the root and shoot (Barraclough et al. 1989, Dreccer et al. 2000, Robinson 2001), there are to date no reports of genetic variation in the dynamic responses of RDWR to N supply.

Direct selection for root system architecture traits (length, biomass, density, lateral root dispersion) has been associated with improved water and/or nutrient uptake in wheat (Hurd 1964), upland rice (Price et al. 2002) and maize (Lynch 2007). Indirect selection for lower canopy temperatures might also be taken as an indication of a greater root uptake capacity, but higher stomatal conductance would produce a similar signal (Reynolds et al. 2009). Root hairs provide another potential mechanism to maximize N capture, and two genes for root hair elongation, *RTH1* and *RTH3*, have been identified in maize (Hochholdinger and Tuberosa 2009). Root architecture and root function are likely to be multigenic and hence much more difficult to select for (Hall and Richards 2013). Therefore, breeding for root charac-

teristics has seldom been implemented to date, principally because of the difficulties of scoring root phenotypes directly and the absence of suitable proxy measurements. Nevertheless, marker-assisted selection may be especially useful to pyramid multiple traits, such as root angle, root length, root weight and root-to-shoot ratio, which are associated with main effect of quantitative trait loci (QTL) in wheat (Sharma et al. 2011, Hamada et al. 2012, Bai et al. 2013, Atkinson et al. 2015), even if a better understanding of the biology of these traits and the potential synergies and trade-offs between traits is required (Lynch 2007). For example, the expression of length and density of root hairs may be synergistic (Ma et al. 2001), and there may be antagonistic interactions between biomass allocation to different root classes due to competition for assimilates (Walk et al. 2006).

Root N transporter systems

In most countries, the commercial mineral forms of N commonly applied to crops are anhydrous ammonia, urea, ammonium sulphate and ammonium nitrate (Robertson and Vitousek 2009, Andrews et al. 2013). In addition, farmyard manure is also able to supply a considerable amount of N fertilization (Hooda et al. 2000, Körschens et al. 2013). Mineral N fertilizers are particularly soluble for easy assimilation by crops. Both urea and ammonia are converted to nitrate (NO₃⁻) at different rates depending on the nature of the soil and of the climatic conditions (Jarvis et al. 2011). Thus, NO₃⁻ is the main source of N for most crop species, whether inorganic or organic N is provided to the plant (Nasholm et al. 2009, Gioseffi et al. 2012).

Ammonium (NH₄⁺) is the ultimate form of inorganic N available to the plant. Most of the NH₄⁺ incorporated by the plant into organic molecules originates from NO₃⁻ reduction, although metabolic pathways such as photorespiration, phenylpropanoid metabolism, utilization of N transport compounds and amino acid catabolism can generate NH₄⁺ (Lea and Mifflin 2011). In cultivated soil, NH₄⁺ concentration is generally ten times lower than NO₃⁻ concentration (Nieder et al. 2011), but substantial amounts of ammonium (NH₄⁺) can remain despite active nitrification by soil microorganisms. Both NO₃⁻ and NH₄⁺ enter the root apoplast mostly by diffusion or mass flow, respectively (Crawford and Glass 1998). Then, there are taken up via an active transport system by means of proteins termed high- and low-affinity transporters and located in the root cell plasma membrane (Loqué and von Wirén 2004, Glass 2009, Dechorgnat et al. 2011).

In higher plants, there are basically three different NO₃⁻ transport systems that operate depending on the NO₃⁻ concentration in the surrounding root environment. The first one is an inducible high-affinity transport system (iHATS) that is induced in the presence of low concentration of NO₃⁻ in the range of 1 to 200 μM depending on the plant species (Pace and McClure 1986, Siddiqi et al. 1990). In wheat, it was reported that the iHATS has a Michaelis constant (*K_m*) value of approximately 27 μM and requires 10 h for full induction by NO₃⁻ (Goyal and Huffaker 1986). The second one is a constitutively expressed high-affinity transport system (cHATS) that is present even in the absence of NO₃⁻. Both systems exhibit a typical Michaelis-Menten saturation profile when the external NO₃⁻ concentration reaches a certain threshold. The third one is represented by a non-saturable low-affinity transport system (LATS) that dominates when NO₃⁻ in the external medium exceeds 250 μM, operating in the 0.5–1 mM concentration range (Siddiqi et al. 1990, Von Wirén et al. 1997).

Recent studies showed that NO_3^- transport systems can also play versatile roles in sensing NO_3^- in plant development, pathogen defence and stress response (Wang *et al.* 2012a). Although NH_4^+ ions can be passively taken up by plant roots, different root NH_4^+ transporter systems (Ludewig *et al.* 2007) allow the direct uptake of NH_4^+ ions and operate across a wide range of NH_4^+ concentrations (Loqué and von Wirén 2004). However, it is likely that in agricultural soils, NH_4^+ uptake operates mainly through the low-affinity transport system (LATS), which is part of the NH_4^+ permeases in the ammonium transporter/methylammonium permeases/Rhesus (AMT/MEP/Rh) family (Von Wirén and Merrick 2004). The K_m values for NH_4^+ influx in different species range between 1 and 200 μM (Bradley and Morris 1991, Wang *et al.* 1993), fitting with the average NH_4^+ soil concentration, which rarely rises beyond 50 μM (Marshner 1995). In wheat, it was reported that the iHATS has a K_m value of approximately 50 μM and requires 6 h for full induction by NH_4^+ (Goyal and Huffaker 1986).

NO_3^- transporters in higher plants are represented by two main gene families, namely the NRT1 PTR (nitrate transporter, peptide transporter) family (NPF), which now regroups the previous NRT1/PTR genes, and the NRT2 family also called the major facilitator superfamily (MFS; Lérán *et al.* 2014). An excellent review describing the different members of the NO_3^- and NH_4^+ transporters and the regulatory mechanisms affecting root N-uptake systems, especially on the model species *Arabidopsis*, has recently been published by Nacry *et al.* (2013). This review emphasizes that expression and activity of most N-uptake systems are regulated both by the concentration of their substrate and by a systemic feedback control of metabolites representative of the whole-plant N status. In cereals in general and wheat in particular, there is far less information on root NO_3^- and NH_4^+ transport systems and their regulations. This is mainly because most of the pioneer work was conducted using the model plant *Arabidopsis*, due to the ease of obtaining mutants and transgenic plants altered in the expression of the different NO_3^- and NH_4^+ transporters (Miller and Smith 1996, Von Wirén and Merrick 2004, Miller *et al.* 2007, Garnett *et al.* 2009, Xu *et al.* 2012). Nevertheless, gene structure and phylogeny of high- or low-affinity transport systems have been studied in a number of grasses including rice, maize, sorghum, *Brachypodium* and wheat (Yin *et al.* 2007, Plett *et al.* 2010, Girin *et al.* 2014). Moreover, a comprehensive overview of the complex phylogeny and gene expression patterns of 16 members of the NPF family in wheat has been recently published (Buchner and Hawkesford 2014). This study highlighted the complex pattern of expression of the nitrate transporters, mainly due to the presence of multiple co-orthologous genes that are differentially expressed according to the plant tissue, NO_3^- availability and leaf senescence during the N assimilation and N remobilization processes. In the wheat NO_3^- HATS system, earlier studies have also demonstrated that five genes (*TaNRT2.1*, *TaNRT2.2*, *TaNRT2.3*, *TaNAR2.1* and *TaNAR2.2*) are induced by abscisic acid when NO_3^- is not present (Cai *et al.* 2007). In contrast to the inhibitory effect of glutamine generally observed in other species, glutamine was able to induce the expression of *NRT2* genes in the absence of NO_3^- (Cai *et al.* 2007).

In addition, it has also to be considered that under agronomic conditions, both efficiency and the regulation of NO_3^- -uptake systems may be enhanced by the presence of mycorrhizal associations (Hawkins and George 2001), humic substances (Cacco *et al.* 2000), allelopathic compounds such as coumarin (Abe-navoli *et al.* 2001) and plant root growth-promoting bacteria (Mantelin and Touraine 2004) or inhibited when the CO_2 con-

centration is rising in the atmosphere (Bloom *et al.* 2014). Therefore, when studying the genetic basis of inorganic N uptake, environmental interactions must be taken into account together with the capacity of the plant to capture and transport NO_3^- or NH_4^+ . This implies that in combination with modelling approaches (Bertheloot *et al.* 2011), further research is required to obtain an understanding of the regulation of the NO_3^- and NH_4^+ HATS and LATS throughout the entire plant developmental process (Kong *et al.* 2013). It will also be necessary to evaluate the contribution of direct NH_4^+ uptake to the wheat N economy, as the available information on the NH_4^+ transport systems at both the molecular and physiological levels remains fragmentary in wheat (Causin and Barneix 1993, Sjøgaard *et al.* 2009) and in other cereals such as maize (Gu *et al.* 2013) and rice (Gaur *et al.* 2012). However, for wheat that preferentially uses NO_3^- instead of NH_4^+ as the main N source, an increase in NH_4^+ uptake may not be beneficial to the plant when the ion is applied to the soil (Angus *et al.* 2014).

Another field of investigation is the use of urea as a synthetic fertilizer in conventional agriculture (Andrews *et al.* 2013, Karamos *et al.* 2014). Indeed, to date, urea is mainly used as a source of N fertilizer (as converted forms through soil mineralization after application) and the contribution of plant urea uptake and metabolism as an intact molecule in a physiological and agricultural context has not been thoroughly investigated. Nevertheless, it is well known that plants possess leaf and root transporters to absorb urea and can hydrolyse and use it very efficiently (Witte 2011). Two distinct transport processes for urea have been identified in rice exhibiting a linear or a Michaelis–Menten kinetics (Wang *et al.* 2012b). Moreover, it is encouraging to note that when a rice urea transporter was overexpressed in *Arabidopsis*, a positive effect was observed both on urea uptake at low concentration and on plant growth (Wang *et al.* 2012b). In wheat, compared to other inorganic N sources, urea uptake was very low. Moreover, its kinetics of uptake was difficult to measure (Criddle *et al.* 1988). However, in some cases when applied at an optimum timing after anthesis, an increase in grain protein content or yield has been observed (Gooding and Davies 1992, Rawluk *et al.* 2000). More recently, in spring wheat, it has been shown that seed yield and N uptake were generally greater with polymer-coated urea than with urea alone (Malhi and Lemke 2013). Even if the efficiency of foliar application of urea in wheat and other cereals remains questionable, it is attractive in terms of environmental benefit. Thus, more research is required both at physiological and at the molecular levels.

Interaction with micro-organisms

Plant roots, including those of wheat, release a variety of organic substrates (*e.g.* organic acids and sugars), exudates and other rhizodeposits (Nguyen 2003). This creates a particular fraction of soil in contact with roots named rhizosphere and favourable to the development of microorganisms. Plant rhizosphere is largely colonized by soil microorganisms, at levels of typically 10^8 to 10^9 bacteria per gram of rhizosphere soil and 1 to 1.5 m of fungal filaments per cm^2 of root surface (Moënne-Loccoz *et al.* 2014). This microbial community contains a broad range of taxa differing from bulk soil community due to the selective effects of roots (Buée *et al.* 2009). Some of them, including pathogens as well as non-pathogenic microorganisms, may enter roots and reside within intercellular space or even within plant cells (Behl *et al.* 2012, Moënne-Loccoz *et al.* 2014). This also occurs in wheat (Germida and Siciliano 2001).

The composition and physiological activities of root-associated microbial communities are influenced by many factors, such as soil characteristics, farming practices, climatic conditions and wheat genotypes (Mazzola et al. 2004). Indeed, rhizodeposition can differ between wheat cultivars (Wu et al. 2001) leading to differences in various aspects of the rhizosphere microbial ecology (Germida and Siciliano 2001). Therefore, it would be of prime interest to develop breeding strategies tailored both to suppress root pathogens and to promote root colonization by plant-beneficial microbial partners (Hetrick et al. 1995, Lammerts van Bueren et al. 2011), especially those with the potential to enhance (i) N availability in the rhizosphere, (ii) root system and architecture, (iii) systemic plant metabolism and (iv) microbial phytoprotection (Fig. 1). This is all the more relevant because breeding is typically carried out under optimal conditions. Thus, phenotypic traits involved in interaction between plant and growth-promoting rhizobacteria may have been neglected (Den Herder et al. 2010).

Soil microorganisms in the rhizosphere are major players in the availability of N for plant roots (Richardson et al. 2009). On the one hand, N availability for roots may be reduced by microbial competition as various soil bacteria and fungi use ammonium and nitrate as N sources (Nelson and Mele 2006) and/or transform nitrate to gaseous N by denitrification (Herold et al. 2012). Nevertheless, plants can limit denitrification by releasing inhibitory secondary metabolites (Bardon et al. 2014), but so far this property is not documented in cultivated cereals. Attempts are currently made to introduce into wheat a chromosome of *Leymus racemosus*, a wild relative of wheat, containing the ability for biological nitrification inhibition (Subbarao et al. 2007, Ortiz et al. 2008). On the other hand, N availability is enhanced by microbial mineralization of organic N yielding ammonium in the rhizosphere. This entails the proliferation of bacterial and fungal decomposers, as well as protozoan predators (Bonkowski 2004) and mycorrhizal fungi (Atul-Nayyar et al. 2009). In wheat, this priming effect reaches higher levels at the flowering

stage (Cheng et al. 2003), and root colonization by mycorrhizal fungi as well as positive mycorrhizal effects on plant nutrition and yield is genotype dependent (reviewed in Behl et al. 2012). N availability for roots is also improved by N fixation. Thus, the community of N fixers (functional group) plays a key role for plant N nutrition (Hsu and Buckley 2009). Unlike in legumes, in wheat and in other cereals, conversion of N_2 into NH_3 does not entail root-nodulating rhizobia, but it can be performed by other non-nodulating N-fixing bacteria and part of the N fixed may be acquired by the plant (Behl et al. 2012). N-fixing bacteria occur naturally in soils including in the wheat rhizosphere (Nelson and Mele 2006, Venieraki et al. 2011), and inoculation with N fixers may enhance wheat yield (Kapulnik et al. 1987, Hungria et al. 2010, Behl et al. 2012, Neiverth et al. 2014). Their diversity and activity fluctuate with both plant species (Perin et al. 2006, Rardon et al. 2014) and cultivar (Coelho et al. 2009) including in wheat (Christiansen-Weniger et al. 1992, Manske et al. 2000, Venieraki et al. 2011). For example, the N-fixing bacterium *Klebsiella pneumonia* strain 342 can relieve N deficiency and enhance plant N levels (Iniguez et al. 2004) depending on cultivar (Manske et al. 2000).

Enhanced acquisition of water and mineral nutrients can be expected if the root system colonizes soil more extensively. Under *in vitro* conditions, wheat inoculation with rhizosphere bacteria may enhance root number and/or length, as well as root hair elongation (Dobbelaere et al. 1999, Combes-Meynet et al. 2011). These inoculation effects on root system architecture and biomass have been also evidenced in soil-grown wheat (Baldani and Baldani 2005, Veresoglou and Meneses 2010). Indeed, many bacteria and fungi modify root system architecture by manipulating plant hormonal balance, in particular by producing phytohormones such as auxins (Ortiz-Castro et al. 2009), cytokinins (Cassán et al. 2009, Moubayidin et al. 2009) or gibberellins. Gibberellins are produced by several rhizosphere bacteria and fungi (Bottini et al. 2004), including wheat strains (Upadhyay et al. 2009), thereby promoting primary root elonga-

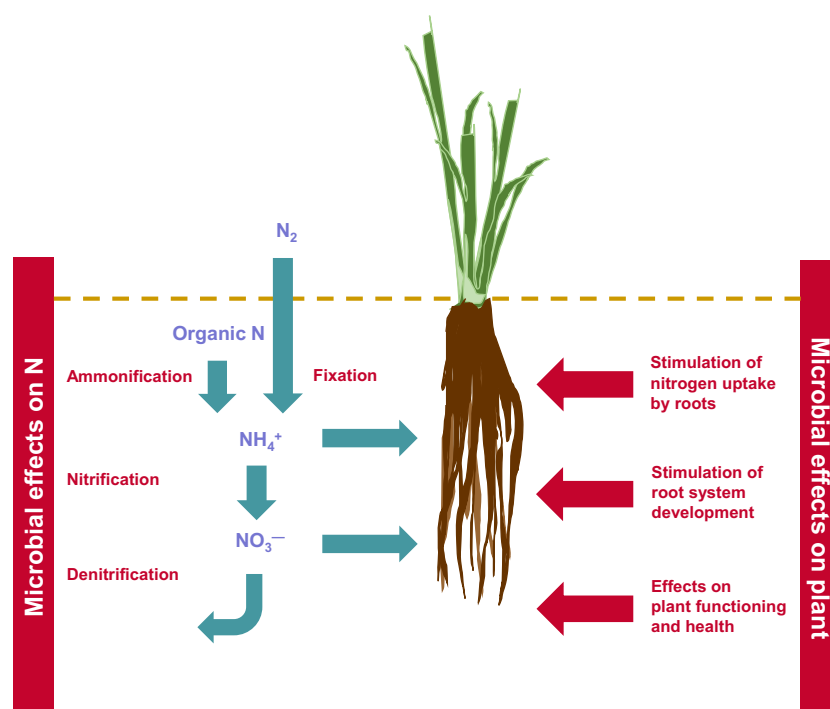


Fig. 1: Summary of microbial effects

tion and lateral root extension. For example, the wheat bacterium *Azospirillum brasilense* Sp245 synthesizes abscisic acid, which modifies lateral root development, and inoculation resulted in higher abscisic acid concentration in *Arabidopsis* (Cohen *et al.* 2008). Other root-branching signals especially 2,4-diacetylphloroglucinol (Brazelton *et al.* 2008) and nitric oxide (Creus *et al.* 2005) may also be implicated, including in wheat (Pothier *et al.* 2008, Couillerot *et al.* 2011). Their effects appear to take place via an auxin signal transduction pathway (Brazelton *et al.* 2008, Molina-Favero *et al.* 2008). Microbial interference with ethylene metabolism in roots may also be responsible for modifying wheat root system architecture (Upadhyay *et al.* 2009) by a direct microbial production of ethylene (Graham and Linderman 1980), or a reduction in ethylene concentration in plant roots by the deamination of ethylene precursor 1-aminocyclopropane carboxylic acid (Prigent-Combaret *et al.* 2008), thereby diminishing ethylene-mediated root growth repression (Glick 2005).

Microorganisms can induce systemic changes in plant physiology. For instance, a wide range of *Arabidopsis* genes displayed different expression levels upon inoculation with the plant-beneficial bacterium *Pseudomonas putida* (Srivastava *et al.* 2012). Microbial inoculation may also modify plant proteomic profiles (Mathesius 2009) and metabolomics profiles, both for primary metabolites (including rice shoot contents in amino acids; Curzi *et al.* 2008) and for secondary metabolites in maize (Walker *et al.* 2012) and wheat (Fester *et al.* 1999). There are also indications that some rhizosphere bacteria may directly affect N metabolism in plants. Oil seed rape (*Brassica napus* L.) roots inoculated with *Achromobacter* strain U80417 displayed enhanced net influx rates of NO_3^- (Bertrand *et al.* 2000). Added to that, genes coding for two nitrate transporters (NRT2.5 and NRT2.6) were expressed at higher levels in *Arabidopsis* upon inoculation with *Phyllobacterium brassicacearum* STM196 (Mantelin *et al.* 2006). Tomato exposure to the bacterial metabolite 2,4-diacetylphloroglucinol increased the net root efflux of amino acids (Phillips *et al.* 2004). In wheat, nitrate reductase activity of *Azospirillum brasilense* Sp245 inside roots is thought to contribute to N assimilation (Baldani and Baldani 2005). However, information is scarce, and relevance for wheat remains to be further investigated.

A range of root-associated microorganisms promote plant health, by inhibiting root pathogens and/or triggering systemic induction of plant defence mechanisms (Couillerot *et al.* 2011, Almario *et al.* 2013). For instance, wheat inoculation with the bacterium *Pseudomonas fluorescens* Q8r1-96 resulted in cultivar-dependent, defence-related transcript accumulation in roots (Maketon *et al.* 2012). Thus, microbial phytoprotection effects are also important to consider and investigate.

Traits Influencing N Utilization Efficiency

Nitrate assimilation

After being taken up by the roots, nitrate [NO_3^-] is then reduced to nitrite [NO_2^-] in the cytosol through the reaction catalysed by the enzyme nitrate reductase (NR; EC 1.7.1.1) using NAD(P)H as electron donors. The NR enzyme represents the first step in the pathway of NO_3^- assimilation. The NR enzyme is positively regulated by NO_3^- and light at the transcriptional level and is down-regulated at the post-transcriptional level by reversible phosphorylation during the dark period (Kaiser *et al.* 2011). In hexaploid wheat, two genes encoding NADH-NR have been identified (Boisson *et al.* 2005). NO_3^- reduction is followed by the reduction of NO_2^- to NH_4^+ catalysed by the enzyme nitrite

reductase located in the plastids (NiR; EC 1.7.7.1; Sétif *et al.* 2009). NiR forms a complex with ferredoxin that provides electrons for the reduction of NO_3^- to NH_4^+ (Sakakibara *et al.* 2012). NH_4^+ is then incorporated into the amino acid glutamate through the action of two enzymes. The first reaction catalysed by the glutamine synthetase (GS; EC 6.3.1.2; Lea and Mifflin 2011) is considered as the major route facilitating the incorporation of inorganic N into organic molecules in conjunction with the second enzyme glutamate synthase (GOGAT; EC 1.4.7.1; Suzuki and Knaff 2005), which recycles glutamate and incorporates C skeletons in the form of 2-oxoglutarate into the cycle. Then, the amino acids glutamine and glutamate are used as amino group donors to all the other N-containing molecules, notably other amino acids used for storage, transport and protein synthesis and to nucleotides used as basic molecules for RNA and DNA synthesis (Lea and Mifflin 2011, Fig. 2).

In higher plants, including wheat, several isoenzymic forms of GS and GOGAT exist which are located in different cellular compartments and differentially expressed in organs or cell types according to the developmental stage. Indeed, the GS exists as a cytosolic form (GS1) present in a variety of organs and tissues such as roots, leaves, phloem cells, and a plastidic form (GS2) is located in chloroplasts and in plastids of roots and etiolated tissues. The relative proportions of GS1 and GS2 at protein level vary within the organs of the same plant and between plant species, each GS isoform playing a specific role in a given metabolic process, such as photorespiratory ammonia assimilation, nitrate reduction, N translocation and recycling (Lea and Mifflin 2011). In wheat and other C3 cereals, both at the transcriptional and at enzyme activity levels, GS2 predominates throughout the entire plant developmental cycle, although its activity can decrease by half after the flowering period. One GS1 isoenzyme is constitutively expressed in the phloem, while others are generally induced in the cytosol of senescing leaves (Kichey *et al.* 2005, Christiansen and Gregersen 2014, Yamaya and Kusano 2014). Detailed analyses of gene expression and cellular localization of the different wheat GS isoenzymes were performed in developing and senescing leaves as well as in a number of reproductive tissues (Kichey *et al.* 2005, Bernard *et al.* 2008). These studies highlighted that the complex GS isoenzyme pattern of expression was not only due to the hexaploid nature of the wheat genome, but also to the morphological complexity of leaves. In order to clarify the function of the different GS isoenzymes, a phylogenetic approach was taken, due to the lack of mutants or transgenic plants. This allowed for the clustering of the different genes encoding GS into different classes of biological functions, which were not necessarily conserved between C3 and C4 cereals (Thomsen *et al.* 2014). In the same way, GOGAT also exists in two forms that have specific roles during primary N assimilation or N recycling. A ferredoxin-dependent isoenzyme (Fd-GOGAT) is mainly involved, in conjunction with GS2, in the reassimilation of photorespiratory ammonia. A pyridine nucleotide-dependent isoenzyme (NADH-GOGAT; EC 1.4.1.14) is involved in the synthesis of glutamate in photosynthetic and non-photosynthetic organs or tissues, to sustain plant growth and development (Lea and Mifflin 2011).

Glutamate can also be generated by the incorporation of ammonia into 2-oxoglutarate by the glutamate dehydrogenase (GDH; EC 1.4.1.2; Lea and Mifflin 2011). However, a number of experiments using ^{15}N -labelling techniques and mutants deficient in GS and GOGAT have demonstrated that over 95% of the ammonia available to the plant is assimilated via the GS/GOGAT pathway (Lea and Mifflin 2011). Subsequently, it was

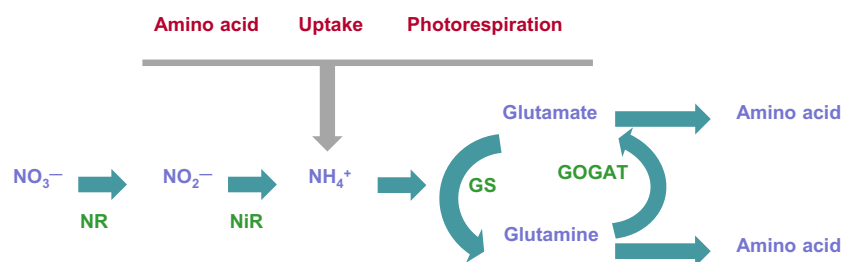


Fig. 2: Main N assimilation pathways in wheat

clearly shown that GDH operates in the direction of glutamate deamination to provide organic acids, notably when the root and leaf cells are carbon limited (Labboun et al. 2009, Fontaine et al. 2012). Recently, the hypothesis that GDH could play an important role in controlling not only glutamate homeostasis (Forde and Lea 2007, Labboun et al. 2009), but also the level of downstream and upstream carbon and N metabolites through the changes in its hetero-hexameric structure, has been put forward (Tercé-Laforgue et al. 2013). This function, which may also have a signalling role at the interface between C and N metabolism, may be of importance when there is a shortage of C under stress conditions or during several phases of plant growth and development. Moreover, transgenic studies performed on a number of model and crop species (Tercé-Laforgue et al. 2013) as well as quantitative genetic approaches performed on maize (Dubois et al. 2003) and wheat (Fontaine et al. 2009) strongly suggest that the reaction catalysed by NAD(H)-GDH is involved in the control of plant growth and productivity. Thus, further research is required to validate the function of GDH in crops such as wheat.

Over the last two decades, our knowledge of the various pathways involved in the synthesis of amino acids, particularly those derived from glutamate and glutamine, has been increased through the use of mutant and transgenic plants in which amino acid biosynthesis was altered. Amino acid biosynthesis is also of major importance for cereal growth and productivity (Howarth et al. 2008), and there are excellent reviews that extensively describe the current knowledge of this complex pathway and its regulation (e.g. Lea and Azevedo 2007, McAllister et al. 2012).

Leaf and canopy photosynthesis per unit N

Up to 75% of N in wheat leaves is located in mesophyll cells and is involved in photosynthetic processes, mainly as the chloroplastic enzyme Rubisco (Evans 1983). Thus, responses in N-limited crops often include reductions in total leaf area, leaf expansion and duration, leaf N and chlorophyll content, leaf stomatal conductance and photosynthesis per unit of leaf area (Sylvester-Bradley et al. 1990, Monneveux et al. 2005). These responses reduce radiation interception and radiation-use efficiency (above-ground biomass per unit radiation interception; RUE) and hence biomass (Foulkes et al. 2009) and yield. Canopy and leaf processes affecting photosynthesis per unit of N uptake include (i) radiation interception per unit of N uptake, (ii) optimizing vertical N distribution in relation to light in the canopy and (iii) leaf photosynthesis per unit of leaf N.

For a radiation interception of 95%, assuming a light extinction coefficient (K) value of 0.5, a green area index (green canopy area per unit of ground area; GAI) of 6 is required. Indeed,

$$K = -\ln(I/I_0)/L,$$

where I_0 is the incident radiation and I is the amount of radiation not intercepted by a canopy having a $\text{GAI} = L$.

At anthesis, modern wheat cultivars produce canopies with GAI values around 6 and hence achieve full interception at this stage (e.g. Moreau et al. 2012, Gaju et al. 2014). The only realistic way to increase fractional interception in the pre-anthesis phase is to increase fractional interception at the start of the stem elongation phase. However, in wheat, it is already around 60–70% (Shearman et al. 2005, Moreau et al. 2012). Thus, only marginal improvement seems possible. Physiological avenues for increasing fractional interception specifically under low N supply may be possible through an increased specific leaf N area (leaf area per unit leaf N; SLN) and/or a higher light extinction coefficient. Genetic variation in SLN has been associated with embryo size (López-Castañeda et al. 1996) and earlier canopy closure (Rebetzke and Richards 1999). The light extinction coefficient is mainly influenced by leaf angle. For modern wheat cultivars, light extinction is approximately 0.55 for photosynthetically active radiation (Thorne et al. 1988, Abbate et al. 1998, Moreau et al. 2012). These values are associated with semi-erect to erect leaf angles, which help to reduce light saturation in the upper canopy leaves boosting RUE. A higher value of K seems unlikely to be desirable due to the trade-off with RUE. Although desirable, more prostrate leaves during early vegetative growth and more upright leaves during later vegetative growth may be difficult to achieve in practice. In summary, although genetic gains in radiation interception per unit of N uptake may be possible during stem elongation, these gains seem likely to be small.

N distribution in canopies in relation to light attenuation also affects photosynthesis per unit of N uptake. Considering that the leaf N gradient is 'optimal' in accordance with the 'optimization theory' (Field 1983, Hirose and Werger 1987, Anten et al. 1995, Moreau et al. 2012), theoretical studies indicated that leaf N maximizes canopy photosynthesis when it parallels the light gradient, that is when the light (K_L) and N (K_N) extinction coefficients are equal. In wheat, observed N gradients are generally less steep than predicted with the 'optimization theory'; however, they do demonstrate that SLN follows an exponential gradient with vertical depth in the canopy (Critchley 2001, Pask 2009, Moreau et al. 2012). Possible reasons for this discrepancy have been discussed in detail by Kull (2002). There is relatively little information on genetic diversity in the vertical distribution of N in relation to light in the canopy. Nevertheless, Bertheloot et al. (2008) demonstrated with two French winter wheat cultivars (Apache and Isengrain) that the vertical distribution of N at anthesis was close to the optimum, as defined in the 'optimization theory', and only differed significantly at the end of grain filling. Similarly, genetic differences were not found for

five spring wheat genotypes grown in the Netherlands (Bindaban 1999). Moreau *et al.* (2012) analysed the vertical distribution of leaf N and light at anthesis for 16 wheat cultivars experimented in field trials in France and the United Kingdom (UK) in two seasons under two N levels. The N extinction coefficient with respect to light (K_N ; K_L) varied with N supply and cultivar. A scaling relationship was observed between (K_N ; K_L) and the size of the canopy for all the cultivars in the different environmental conditions. Interestingly, the scaling coefficient of the (K_N ; K_L – green area) index relationship differed among cultivars, suggesting that cultivars could be more or less adapted to low N environments.

Photosynthesis rate per unit of N affects NUtE. In C3 cereals such as wheat, the net light-saturated rate of leaf photosynthesis (A_{max}) typically increases to 20–30 $\mu\text{mol CO}_2/\text{m}^2/\text{s}$ at leaf N concentrations of 2 g N/m². Assuming an asymptotic relationship between A_{max} and leaf N concentration (Evans 1983, Sinclair and Horie 1989), there may be scope to decrease SLN while maintaining A_{max} . Indeed, because leaves of modern wheat genotypes typically accumulate more than 2.0 g N/m² under favourable conditions (Critchley 2001, Pask *et al.* 2012), NUtE could be increased by selecting for lower specific leaf N (leaf N content per unit leaf area; SLN) to decrease the transient ‘storage’ N components of leaves. A sensitivity analysis using the wheat Sirius crop model predicted that decreasing SLN in the range of 1–2 g/m² increased NUE by 10–15% when N was limiting (Semenov *et al.* 2007). However, under well-fertilized conditions, decreasing SLN below 2 g/m² may not be beneficial because the SLN required for maximal RUE in field-grown winter wheat in the UK and New Zealand was estimated to be 2.1 g/m² (Pask *et al.* 2012). Alternatively, increasing SLN above current values of 2–3 g/m² seems unlikely to be advantageous overall for NUtE as leaves may operate well below light saturation in the canopy (Reynolds *et al.* 2000), mesophyll cell size, leaf size and light interception may be reduced (Austin *et al.* 1982) and many chloroplasts may end up in a light-limited state due to intraleaf shading in thick leaves. Genetic variability in SLN amounts to 1.4–2.6 g/m² for 144 durum wheat genotypes (Araus *et al.* 1997), 2.1–2.4 g/m² for 17 durum wheat cultivars (Giunta *et al.* 2002) and 1.4–2.2 g/m² for 16 bread wheat cultivars (mean over a high and low N treatment, Moreau *et al.* 2012). SLN heritability in wheat is largely unknown. However, it is encouraging that the heritability for straw (leaf lamina, leaf sheath and stem) N at anthesis for winter wheat was >0.60 under low N (Laperche *et al.* 2006b), indicating that selection should be possible.

Rubisco catalyses a wasteful reaction with oxygen that leads to the release of previously fixed CO₂ and NH₃ and the consumption of energy during photorespiration. Consequently, at the metabolic level, there are several avenues to increase photosynthetic efficiency. These include (i) relaxing the photo-protected state more rapidly, (ii) reducing photorespiration through ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) with decreased oxygenase activity, (iii) improving Rubisco activity, (iv) faster regeneration of ribulose-1,5-bisphosphate (RuBP) and (v) introducing carbon-concentrating mechanisms associated with C4 photochemistry into C3 plants (see recent reviews by Reynolds *et al.* 2000, Parry *et al.* 2003, 2011, Long *et al.* 2006, Murchie *et al.* 2009, Zhu *et al.* 2010). These strategies all require modification of the photosynthetic components, which can only be achieved through genetic manipulation. Potential improvements in C3 cereals available from reduced photorespiration were estimated around 30% and those from other mechanisms in the 15–22% range (Long *et al.* 2006).

Alternatively, it may be possible to increase A_{max} by decreasing respiration in crops, although this has received less attention than photosynthesis partly due to difficulties in measurement. Respiration may consume 30% to 80% of the carbon fixed (Atkin *et al.* 2005) and is commonly divided into growth and maintenance components, each exerting differing effects. Respiration, increasing with temperature and depending on phenological stage (McCullough and Hunt 1993, Foulkes and Murchie 2011), may be positively but nonlinearly related to photosynthesis. High respiration rates (especially at night) can increase reactive oxygen species, leading to cell damage and affecting pollen viability (Prasad *et al.* 1999). Recent work highlighting the importance of increased night-time temperature with climate change on productivity in wheat (Tester and Langridge 2010, Lizana and Calderini 2013) and the high sensitivity of respiration to temperature in general suggests that the environmental responses of crop respiration to temperature changes is an important area on which to focus.

Post-anthesis N remobilization and senescence dynamics

In wheat, 35–42% of the N in the above-ground crop at anthesis is in the leaf lamina, 14–20% in the leaf sheath, 20–31% in the true stem and 16–23% in the ear under optimal N supply (Pask *et al.* 2012, Barraclough *et al.* 2014, Gaju *et al.* 2014). Under low N conditions, the proportion of the N in the ear increases relative to that in the other plant components (Barraclough *et al.* 2014, Gaju *et al.* 2014). In field experiments in the UK and New Zealand, on winter wheat, the accumulation and remobilization of structural, photosynthetic and reserve N was estimated in crop components under high N and low N conditions (Pask *et al.* 2012). At anthesis, reserve N accounted for 44% of above-ground N in optimally fertilized crops and was principally located in the true stem, but was observed in all crop components in non-limiting fertilizer N treatments. The efficiency of postanthesis N remobilization of true stem reserve N in the true stem was low (48%) compared to the leaf sheath (61%) and leaf lamina (76%), and in well-fertilized crops, significant quantities of non-remobilized reserve N remained in true stem at harvest.

A high capacity to absorb N in the true stem before flowering could theoretically favour a high maximum rate of N uptake and hence higher NU_pE (Foulkes *et al.* 2009). In addition, favouring a greater capacity to store N in non-photosynthetic organs (*i.e.* stem internodes) may enable the translocation of a larger amount of N to grains without reducing plant photosynthetic capacity (Bertheloot *et al.* 2008), although the respiratory cost of maintaining a large non-photosynthetic pool of storage N is unclear. In wheat, genetic variation in stem N content at anthesis is reported (Triboï and Ollier 1991, Critchley 2001, Pask 2009, Barraclough *et al.* 2014, Gaju *et al.* 2014), as well as in postanthesis N remobilization efficiency from the stem (Kichey *et al.* 2007, Pask 2009, Gaju *et al.* 2014). In maize, studies reported an early remobilization of N from the stem before the leaf lamina (Beauchamp *et al.* 1976, Friedrich and Schrader 1979). Thus, high stem N remobilization efficiency would potentially favour high NUtE through delayed senescence of the leaf lamina.

‘Stay-green’ phenotype refers to the capacity of a genotype to retain green leaf area for longer than a standard genotype during grain filling (Thomas and Smart 1993). Although under optimal conditions, wheat crops are, in general, little limited by the assimilate supply during grain filling (Dreccer *et al.* 2000, Borrás *et al.* 2004, Calderini *et al.* 2006); under low to moderate N fertilizer levels, there is evidence that yields can be

limited by postanthesis assimilate supply (Bogard et al. 2011, Gaju et al. 2011). ‘Stay-green’ phenotypes and broader genetic variation in senescence have been reported in hexaploid wheat (Silva et al. 2000, Verma et al. 2004, Joshi et al. 2007, Christopher et al. 2008, Chen et al. 2010, 2011, Bogard et al. 2011, Gaju et al. 2011, Derkx et al. 2012, Naruoka et al. 2012). N dynamics are an important factor in the maintenance of green leaf area in sorghum, with ‘stay-green’ in sorghum hybrids linked to changes in the balance between N demand and supply during grain filling resulting in a slower rate of N translocation from the leaves to the grain (Borrell and Hammer 2000, Van Oosterom et al. 2010a,b). The latter study showed that the onset and rate of leaf senescence were explained by a supply–demand framework for N dynamics, in which individual grain N demand was sink-determined and was initially met through N translocation from the stem and rachis, and then if these N pools were insufficient, from leaf N translocation. A correlation between postanthesis N remobilization efficiency and the onset of the rapid phase of canopy senescence was reported under low N conditions among 16 wheat varieties grown at sites in the UK and France (Gaju et al. 2014). A transcription factor (*NAM-B1*) accelerates senescence and increases N remobilization from leaves to grains in wheat (Uauy et al. 2006). Candidate regulatory genes that were members of the WRKY and NAC transcription factor families were related to senescence in controlled environment conditions (Derkx et al. 2012). In a winter wheat doubled-haploid mapping population, QTLs affecting leaf senescence and grain yield and/or grain protein concentration were identified associated with QTLs for anthesis date, showing that the phenotypic correlations with leaf senescence were mainly explained by flowering time influencing postanthesis N availability (Bogard et al. 2011).

These results suggested that a better understanding of the mechanisms determining postanthesis N remobilization and senescence associated with environmental characterization, particularly on their N availability during the postanthesis period, would offer scope to raise grain yield and/or grain protein content in wheat cultivars.

Optimizing grain protein concentration and composition

Structural and metabolic proteins are present in the starchy endosperm cells of the grain, and the predominant protein fraction in this tissue is the gluten storage proteins, comprising a mixture of monomeric gliadins and polymeric glutenins. These groups of proteins are present in approximately equal amounts and together account for about 60–70% of the total N in the endosperm tissue. The gluten proteins confer viscoelastic properties to dough crucial for processing wheat into baked food such as bread, pasta and noodles. A precise balance between gliadin and glutenin proteins is also required, as glutenins are predominantly responsible for dough elasticity (strength) required for bread making and gliadins for dough viscosity and extensibility required for making biscuits and cakes. The qualitative composition of the grain protein is a genetic characteristic, caused in part by differences in protein synthetic capacity (Shewry and Halford 2002, Ravel et al. 2009), while the rate, duration and grain protein quantitative composition (*i.e.* the ratio between the different protein fractions; Martre et al. 2003) can be modified by environmental conditions.

An inverse relationship exists between the grain protein concentration and grain yield (*e.g.* Kibite and Evans 1984, Simmonds 1995, Oury et al. 2003, Oury and Godin 2007, Bogard

et al. 2010), making the simultaneous genetic improvement of yield quantity and bread-making quality a difficult task. The physiological basis of this inverse relationship relates to competition between carbon and N for energy (Munier-Jolain and Salon 2005) and an N dilution effect by carbon-based compounds (Acreche and Slafer 2009). The grain protein deviation (GPD) is the deviation from the regression between grain yield and grain protein concentration (GPC). GPD can be used to identify genotypes having higher GPC than expected from their GY (Monaghan et al. 2001) and wheat lines that have a positive GPD among groups of wheat lines (Oury et al. 2003, Bogard et al. 2010, 2011). Genetic variability in GPD has been related to postanthesis N uptake (Monaghan et al. 2001, Bogard et al. 2010, 2011), which is in part associated with anthesis date (Bogard et al. 2011). Because the majority of grain N originates from remobilization (Pask et al. 2012, Gaju et al. 2014), rather than from postanthesis uptake, mechanisms to enhance reserve N accumulation in the canopy and efficiency of N remobilization should also be addressed in the genetic improvement of GPD (Hakwesford 2014). This may be the case using the already mentioned *NAM-B1* allele (Uauy et al. 2006) that increases N remobilization efficiency. An alternative to develop high-quality and N-efficient wheat lines is to modify grain protein composition to maintain dough strength and elasticity parameters with a lower GPC. In this sense, Guarda et al. (2004) observed that grain quality of cultivars introduced in Italy from 1900 to 1994 was increased although GPC was decrease.

For wheat grown for feed, distilling and biofuel markets (high ratio of starch to protein required), a higher NUTE will be associated with a lower GPC. The minimum GPC reported is in the range 6.8–7.2% (Martre et al. 2006, Kindred et al. 2008, Bogard et al. 2011), equivalent (assuming a conversion ratio of 5.7 between GPC and grain N %) to 1.2–1.3% grain N %. It is not certain whether it is possible to decrease the % of N below as there may be a minimum obligatory (approximately 1.5%; Sinclair and Amir 1992) for the synthesis of essential amino acids and structural and metabolic proteins.

Phenotyping for NUE

Root phenotyping methods

The lack of high-throughput and large-scale phenotyping methods for root traits remains a bottleneck to gene discovery and selection for such traits in breeding programmes (Fiorani and Schurr 2013). Progress in root measurement methodology has enhanced our ability to visualize, quantify and conceptualize root system architecture traits and their relationship to plant productivity (Lynch 1995). However, laboratory screens have focused mainly on seedlings, with seedlings growing on germination paper or in growth pouches (*e.g.* Hund et al. 2009, Bai et al. 2013, Atkinson et al. 2015). Thus, although several screening tests have been designed to generate accurate and robust data from seedlings grown under artificial conditions, these phenotypes have only rarely been extrapolated to field conditions, partly because of the pronounced plasticity of root growth and development processes. Laboratory-based methods can be limited in their ability to reproduce field-like conditions (Passioura 2006, 2010, Poorter et al. 2012). For example, soil environment × genotype interactions significantly affect the root length of wheat cultivars grown in sandy soil compared to agar plates (Wojciechowski et al. 2009). Encouragingly, seedling root traits based on paper-based germination screens were shown to be

linked to mature plant traits such as height and yield in recent studies on a Savannah \times Rialto DH winter wheat population (Atkinson *et al.* 2015); seedling root traits were associated with plant height in a winter wheat Avalon \times Cadenza DH population (Bai *et al.* 2013). At an intermediate scale, the use of soil-filled root observation chambers (rhizotrons or clear-pot) (*e.g.* Lobet *et al.* 2011, Nagel *et al.* 2012, Richard *et al.* 2015) and non-destructive digital imaging techniques offers some promises (Manschadi *et al.* 2006, 2010), as X-ray computed tomography (Gregory *et al.* 2003, Lontoc-Roy *et al.* 2006, Hargreaves *et al.* 2009, Mooney *et al.* 2012, Mairhofer *et al.* 2013), magnetic resonance imaging (Metzner *et al.* 2015) and mini-rhizotrons (Lontoc-Roy *et al.* 2006, MacFall and Johnson 2012, Poorter *et al.* 2012, Vamerali *et al.* 2012).

Field phenotyping methods for roots in cereals were reviewed by Manske and Vlek (2002) and Polomski and Kuhn (2002), including the use of rhizotrons, mini-rhizotrons and assessments of root parameters from soil cores (root washing and root counts/image analysis). There are two relatively high-throughput field phenotyping techniques: the core break method (Köpke 1979) and shovelomics (Trachsel *et al.* 2011). In the core break method, a root auger is used to take soil root cores from the field, the cores are then broken transversely and the roots on the exposed cross-sections counted (Manske *et al.* 2001). The number of roots visible is then used to estimate root length density and mass from established calibrations. A field study in Australia on a range of genotypes (cultivars, near-isogenic lines and recombinant inbred lines) by Wasson *et al.* (2014) indicated that the core break method can directly identify the variation in deep root traits to speed up selection. Shovelomics involves the excavation and visual scoring of crown roots extracted from the field. Results in maize have been shown to be well correlated with total plant depth and root system total length (Trachsel *et al.* 2011). Finally, soil coring, root washing and scanning have been successful in describing root system architecture traits of adult plants in the field and in controlled environment conditions and have been widely used as a standard technique to compare new methods against (Metzner *et al.* 2015). The measurement of the root system architecture traits from images is carried out using appropriate software. The most commonly used are the commercial WinRHIZO (Regent Instruments, Quebec, Canada) and the public domain IMAGEJ (Schneider *et al.* 2012).

The development of methods that measure changes in the root DNA concentration in soil could eliminate the need for separation of roots from soil and permit large-scale phenotyping of root genotypes and responses to environmental stresses in the field (Huang *et al.* 2013).

Canopy phenotyping methods

A major limitation to improving yield and N stress tolerance in wheat is obtaining high-throughput accurate phenotypes on thousands of breeding lines. Promising technologies for high-throughput field phenotyping include spectral reflectance to estimate biomass, canopy size and N content. Spectral reflectance indices (SRI) are based on the capacity of canopies to absorb and reflect specific wavelengths of solar radiation according to their structural and physiological characteristics. Currently, the most widely applied SRI are based on the relative reflectance in the visible (400–700 nm) and in the near infrared (700–1100 nm) due to the absorption of light by

chlorophyll and associated pigments [*e.g.* the normalized difference vegetation index (NDVI) (Araus *et al.* 2001)]. Using ground-based spectroradiometers, SRI have been developed to estimate crop biomass (Babar *et al.* 2006), green canopy area (Aparicio *et al.* 2002), leaf chlorophyll (Babar *et al.* 2006), 'stay-green' (Lopes and Reynolds 2012), grain yield (Gutierrez-Rodriguez *et al.* 2004, Gutierrez *et al.* 2010a,b) and grain protein content (Apan *et al.* 2006, Freeman *et al.* 2007). The recent development of field-portable spectroradiometers measuring wavelengths up to 2500 nm increases the capacity to phenotype wheat performance under N stress environments. In this sense, associations have been established between SRI measured during grain filling and grain yield and C isotope discrimination of the grain (Lobos *et al.* 2014). The challenge in the development of such techniques is to reach high-throughput both for data acquisition and for processing as well as to derive metrics that are meaningful with regard to canopy structure and function.

Alongside spectral reflectance, promising remote-sensing technologies for field-based phenotyping include chlorophyll fluorescence imaging to measure photosynthesis (Romer *et al.* 2011, Murchie and Lawson 2013) and infrared thermometry as a proxy for canopy photosynthesis (Olivares-Villegas *et al.* 2007, Saint Pierre *et al.* 2010). To date, the latter has been mainly applied under heat-stressed or water-stressed environments. Another remote-sensing technique that is now being adopted for field-based phenotyping in cereals to survey directly the 3D distribution of canopies is laser imaging detection and ranging (Lidar). This technology provides accurate estimates of crop height, cover, canopy structural properties (Lefsky *et al.* 2002, Omasa *et al.* 2007, Hosoi and Omasa 2009), crop biomass and N content (Eitel *et al.* 2014). Furthermore, laser scanning coupled with fluorescence has potential to evaluate photosynthetic performance (Romer *et al.* 2011). Additional techniques relevant to NUE field-based phenotyping are stereo- and colour imaging to determine canopy structure and ear density (Berger *et al.* 2010) and near infrared spectroscopy to measure protein and N content using calibrations derived from N combustion analyses (White *et al.* 2012). A full review of the above phenomics technologies is beyond the scope of this article. Fortunately, recent reviews of such phenomics methodologies are available (Furbank and Tester 2011, White *et al.* 2012, Araus and Cairns 2014).

Challenges that can limit the potential of ground-based sensor platforms (*e.g.* tractor-mounted sensors, phenomobiles) include the non-simultaneous measurement of different plots and vibrations resulting from uneven field surfaces. Some of these limitations can be addressed using high-resolution and low-altitude aerial platforms such as small unmanned aerial vehicles. The availability of unmanned aerial vehicles has rapidly increased in recent years, and several types, ranging from multicopters and helicopters to fixed wing, are now available (Lelong *et al.* 2008, Zhang and Kovacs 2012, Araus and Cairns 2014). These aerial platforms have an advantage over ground-based sensing platforms in generating surface maps in real time and measuring plant parameters from several plots at a time. However, high-quality camera systems often still exceed the payload of available drones. Automation of data processing and difficulties in the extraction of meaningful parameters are other reasons that presently restrict fast methodological advances. Satellites platforms, on the other hand, are currently limited by the frequency of measurements and spatial resolution.

Breeding for NUE

Estimation of genetic progress

Grain yield and the N demand to maximize yield evolved simultaneously (Guarda et al. 2004, Sylvester-Bradley and Kindred 2009), leading to an equal NUE of old and recent cultivars at their respective N optimum (Sylvester-Bradley and Kindred 2009). But when old and recent varieties are compared in the same N conditions, a significant genetic improvement of NUE was measured in various studies at different N levels (Table 1).

Ortiz-Monasterio et al. (1997) reported an NUE genetic progress of +0.4–1.1% per year depending on the N levels in spring CIMMYT varieties cultivated between 1962 and 1985. Sylvester-Bradley and Kindred (2009) also reported a significant trend between +0.35–0.58% per year comparing an old group of varieties (1977–1987) to a recent one (2001–2007) at two N levels (without N applied and with 200 kg/ha N applied). In the same way, Cormier et al. (2013) estimated genetic progress at +0.30–0.37% per year between 1985 and 2010 using 195 European elite winter varieties at optimal and suboptimal N levels. Only Muurinen et al. (2006), studying 17 spring wheat cultivars released between 1901 and 2000, observed a poorly significant genetic improvement of NUE ($P = 0.055$).

NUE is an integrative trait, and thus, its improvement could be the result of modification on several components. An increase in N harvest index (NHI) was assessed at +0.15% per year by Brancourt-Hulmel et al. (2003) and at +0.12% per year by Cormier et al. (2013). This improvement is independent of the semi-dwarf allele introgressions (Gooding et al. 2012) and is associated with a decrease in N content in straw at maturity (Cormier et al. 2013). It may result from a better translocation (portion of N absorbed after anthesis and allocated to the grain) and/or a better N remobilization. In summary, these results highlighted a breeding impact on N utilization. An increase in N uptake was also observed (Ortiz-Monasterio et al. 1997, Guarda et al. 2004, Sylvester-Bradley and Kindred 2009). Nevertheless, this conclusion has to be balanced as Foulkes et al. (1998) who studied in UK 27 cultivars released from 1969 to 1988 concluded that at zero N input, N offtake in grain decreased. Moreover, Cormier et al. (2013) could not conclude on this point due to a genetic variance for N uptake that was too low in a variety panel of 214 recent European elites.

To conclude, both N uptake and N utilization may have been increased by breeding with a relative efficiency affected by the N levels (Ortiz-Monasterio et al. 1997, Le Gouis et al. 2000). We should point out that this improvement is an indirect effect of breeding for grain yield at a constant N level as no specific targeted selection for NUE has been conducted.

Table 1: Assessment of yearly percentage genetic gain in nitrogen-use efficiency (NUE) from direct comparison of old and modern cultivars

Period	Genotypes	N level (kg N/ha)	NUE (% per year)	References
1962–1985	8	0	1.2	Ortiz-Monasterio et al. (1997)
		75	0.4	
		150	0.6	
1977–2007	24	300	0.9	Sylvester-Bradley and Kindred (2009)
		0	0.35	
		200	0.58	
1985–2010	195	150	0.37	Cormier et al. (2013)
		250	0.30	

Impact of G × N interactions on direct/indirect selection efficiency

In wheat, varieties are commonly selected and registered under high N conditions. Thus, genetic progresses in low N condition result from an indirect selection. Numerous studies detected significant G × N interactions for agronomic traits (*e.g.* Ortiz-Monasterio et al. 1997, Le Gouis et al. 2000, Laperche et al. 2006a, Barraclough et al. 2010, Cormier et al. 2013), meaning that the genetic values of varieties differ between N levels. Significance of G × N interactions directly affects the correlations of genetic values between N levels, and hence, the best varieties at high N may not be the best at low N. In other words, when G × N interactions are significant, indirect selection efficiency (ISE) is reduced. Nevertheless, selecting at high N for low N can be efficient when heritabilities in high N are higher than in low N. Indeed, a balance between the ability to select (heritabilities) and the genetic correlation between the environment used to select and the one where varieties will be tested is required. This balance is easy to understand when looking at the ISE formula (Falconer and Mackay 1996):

$$ISE = r_{G12} \times h_2/h_1,$$

where varieties are tested in condition 1, but selected in condition 2; h_1 and h_2 are the respective square roots of the heritability in the two conditions; and r_{G12} is the genetic correlation between conditions, considering an equal selection intensity in both conditions.

In wheat, studies reported both genetic variance decrease and environmental variance increase at low N compared to HN. Thus, heritabilities are usually lower under low N conditions (Brancourt-Hulmel et al. 2005, Laperche et al. 2006a), and indirect selection at high N can be an effective strategy to breed for low N conditions. However, few studies directly quantified this indirect selection efficiency (Brancourt-Hulmel et al. 2005, Przystalski et al. 2008, Annicchiarico et al. 2010, Cormier et al. 2013, Sarcevic et al. 2014). These studies have to be compared regarding N stresses and the number of genotypes used (Table 2). Using 270 breeding lines tested during 2 years in the same environment (northern France), Brancourt-Hulmel et al. (2005) assessed an ISE of 0.65–0.99 for grain yield with an N stress, which implied a mean yield reduction of 35% and genetic correlations between 0.83 and 0.89. Cormier et al. (2013) tested 225 commercial varieties. Comparing high N and low N, the mean yield reduction was 20% and traits heritabilities were stable. Thus, ISE was mainly dependent on genetic correlation. For grain yield, it was estimated at 0.78. For the other investigated agronomic traits, ISE was between 0.25 and 0.99. The other studies used fewer genotypes. In Sarcevic et al. (2014), 19 varieties were tested and yield reduction was only 10%, promoting high genetic correlations. Moreover, genetic correlations were allowed

Table 2: Efficiency of selection in high N environment for low N environment (indirect selection efficiency – ISE) regarding yield reduction between high and low N trials

Genotypes	Yield reduction (%)	ISE	References
270	35	0.65–0.99	Brancourt-Hulmel et al. (2005)
12-188	27	0.86–1.02	Przystalski et al. (2008)
225	20	0.78	Cormier et al. (2013)
19	10	1.04	Sarcevic et al. (2014)

to exceed 1. In result, ISE for grain yield was high (1.04), as for grain N yield (1.34) and most grain quality rheological parameters (0.81–1.00). Using data sets from seven European countries comparing organic and non-organic cropping systems, Przystalski *et al.* (2008) found an ISE ranging from 0.86 to 1.02 for grain yield (calculated from the published results) under a N stress inducing a mean yield reduction of 27%. However, this result seems overestimated regarding the unbalanced data set and the number of varieties used. Annicchiarico *et al.* (2010) studied three data sets containing 7, 11, and 13 genotypes under two production systems (organic and conventional). Yield reduction ranged from 14% to 28% and ISE ranged from 0.89 to 1.20 for grain yield, but there were no consistent genotype \times production system interactions, and/or heritabilities in organic system were lower than in conventional systems mostly due to higher experimental error.

When data set size is sufficient to properly estimate genetic correlation and N stress is substantial, ISE for grain yield is high, but may not exceed one. Consequently, regarding breeder financial issues, indirect selection is efficient in moderate N stresses, but it does not overpass direct selection in low N conditions. This was already observed in maize (*Zea mays*), for which selection under high N for performance under low N was predicted significantly less efficient than direct selection under low N when the relative yield reduction due to N stress exceeded 43% (Bänziger *et al.* 1997). Concerning varieties recommendation, the approach is different as the goal is not to increase a trait mean value but to advise wheat growers, and hence to predict the top ranking varieties, meaning that we should focus on variety rankings between high N and low N conditions. Here again, to apply results from high N to low N experiments is not an easy task. Indeed, even with a high genetic correlation between high N and low N conditions, the probability to predict the top varieties in low N from high N ranking is low (0.55 for a genetic correlation of 0.8 in the simulation study of Przystalski *et al.* (2008)).

Molecular breeding

Molecular breeding can be defined as the use of molecular information to develop new genotypes. This molecular information can arise at different levels of the metabolic process: from genes through proteins to metabolites. In complex traits such as NUE, several regulation pathways occur at different levels (*e.g.* transcription factor, post-transcriptional modification, allosteric regulation). These pathways depend on N levels (Howarth *et al.* 2008, Ruuska *et al.* 2008, Wan *et al.* 2013), organs (Ruuska *et al.* 2008), genotypes (Mcintyre *et al.* 2011, Tenea *et al.* 2012) and developmental stage (Ruuska *et al.* 2008, Wan *et al.* 2013). In the development of genetically modified crop, this complexity makes promoter choice critical. Reviews of transgenic efforts to improve NUE in plant were published by Pathak *et al.* (2011) and McAllister *et al.* (2012). Using the example of research on alanine aminotransferase (AlaAT), a successful transgenic approach to increase NUE in oil seed rape (Good *et al.* 2007), in rice (Shrawat *et al.* 2008) and currently tested in wheat, the authors concluded that enzymes and proteins other than those involved in primary N uptake and assimilation may be good targets, potentially due to less post-transcriptional controls.

Indeed, it has been believed for a long time that due to their strategic position along the N assimilatory pathway, NR, NiR, GS and GOGAT enzymes were major checkpoints controlling

plant NUE. But, the first results of modifications of these genes have not produced completely relevant NUE phenotypes. However, there is some evidence that increasing NR activity improves NO₂⁻ assimilation in *Arabidopsis* (Takahashi *et al.* 2001). Moreover, it seems that wheat genotypes exhibiting a higher NR activity have a greater potential for N utilization under non-limiting N supply with a well-coordinated system of N uptake and assimilation (Vouillot *et al.* 1996, Anjana *et al.* 2011). Recently, it was reported that overexpression of a tobacco NR gene in wheat increased the seed protein content, without the need for increased N fertilization (Zhao *et al.* 2013). Such an interesting finding could rekindle the possibility of using NR as a breeding target to improve wheat NUE, yield and grain quality.

Indirect evidence of the role of the GS enzyme in the control of NUE was also provided in wheat through correlation studies that suggested that the leaf enzyme activity could be used as a marker to monitor plant N status (Kichey *et al.* 2007). In addition, a number of quantitative trait loci (QTL) related to grain yield and grain protein content colocalizing with structural genes encoding either cytosolic GS1 (Habash *et al.* 2007, Fontaine *et al.* 2009, Guo *et al.* 2012, Gadaleta *et al.* 2014) or plastidic GS2 (Gadaleta *et al.* 2011, Bordes *et al.* 2013) were identified. However, functional validation of these candidate genes will be necessary to demonstrate their impact on wheat productivity (Swarbeck *et al.* 2011).

Following the discovery that in rice mutants deficient in one of the two forms of NADH-GOGAT there was a considerable reduction in spikelet number (see Yamaya and Kusano 2014 for a review), studies on the wheat enzyme were also undertaken. Based on a quantitative genetic study in which colocalization between QTL for NUE and NADH-GOGAT was observed (Quraishi *et al.* 2011), it was proposed that in wheat and in other cereals, this gene could be used to improve grain filling either using genetic manipulation or by selecting the best alleles (Salse *et al.* 2013). In durum wheat, it was also found that there is a strong correlation between NADH-GOGAT gene expression and grain protein content (Nigro *et al.* 2013), thus indicating that unlike in a C4 plant such as maize (Martin *et al.* 2006), it is not cytosolic GS1, but NADH-GOGAT that is one of the major checkpoints controlling NUE in C3 cereals. Such a finding reinforces the current concept that NUE control may be specific, depending not only on the species examined but also on the genetic variability within the species (Hirel *et al.* 2007, Simons *et al.* 2014).

Regarding marker-assisted selection, to deal with N pathway complexity of regulation, the easiest screening might be based on protein or metabolite. Kusano *et al.* (2011) wrote a good review on metabolic approaches focusing on N metabolism. In wheat, Howarth *et al.* (2008) assessed the impact of N supply on amino acid content during senescence. Moreover, various proteomic studies were performed at different growing stages and organs (Bahrman *et al.* 2004a,b, 2005, Altenbach *et al.* 2011, Tétard-Jones *et al.* 2013). Nevertheless, these approaches are limited to the exploration of a narrow genetic diversity (Table 3). In fact, due to affordable cost (time and price), most molecular information available is at the genome level as genetic molecular markers. This information was used in association mapping studies on NUE-related traits (Table 4) mostly using biparental design such as doubled haploids (DH) populations (An *et al.* 2006, Laperche *et al.* 2006a,b, 2007, 2008, Habash *et al.* 2007, Fontaine *et al.* 2009, Li *et al.* 2010, Zheng *et al.* 2010, Bogard *et al.* 2011, 2013) or recombinant inbred line

Table 3: List of 'omics studies' related to nitrogen-use efficiency in wheat

References	Genotypes	N levels	Organs	Stage	Methods	Data points
Proteomic						
Bährman et al. (2004a)	2 (Arche, Réctal)	0; 2; 8; and 20 mg N/plant/day	Leaf	60 days	2D gel electrophoresis	524 spots
Bährman et al. (2004b)		0.5 and 3.0 mm NO ₃ ⁻	Root	2nd node		541 spots
Bährman et al. (2005)	1 (Butte 86)	0 and 30 mg N/plant/DAP	Grain	Maturity		860 spots
Altenbach et al. (2011)	1 (Malacca)	Organic, conventional	Flag leaf	Ear emergence, anthesis, kernel milk stage		54N 111N
Tétard-Jones et al. (2013)				Anthesis, 9 DPA	cDNA microarray	36 000 sequences
Transcriptomic						
Ruuska et al. (2008)	1 (Janz)	1 mM KNO ₃ and 2 mM KNO ₃ + 3 mM Ca(NO ₃) ₂	Lower leaves and stem, flag leaf, penult internode			
Howarth et al. (2008)	1 (Hereward)	48 and 192 kg N/ha	Leaves 2 and 3	Senescence	GeneChip Affymetrix	55 052 transcripts
McIntyre et al. (2011)	8 (Seri × Babax pop)	0; 44; 60 and 172 kg N/ha	Stem	Anthesis		
Tenea et al. (2012)	3 (Tommi, Centenaire, Cubus)	Organic, conventional	Flag leaf	Kernel milk stage		
Wan et al. (2013)	6 (Cordiale, Hereward, Istiabraç, Malacca, Marksman and Xi 19)	100; 200 and 350 kg N/ha	Caryopse	14, 21, 28 and 35 DPA		
Metabolomic						
Howarth et al. (2008)	1 (Hereward)	48 and 192 kg N/ha	Leaves 2 and 3	Senescence	Gas chromatography-mass spectrometry	

Table 4: List of association mapping studies related to nitrogen-use efficiency in wheat

References	Pop.	Genotypes	Origin	Marker	Map (cM)	Env	Year	Site	Treatment	Traits	QTL
An et al. (2006)	DH	120	Hanxuan 10 × Lumai 14	395 (AFLP, SSR, EST)	3904		2	1	LN=HN-150 kg N ha	5	34
Li et al. (2010)	Panel +DH +RIL	260 +120 +142	Core collection Hanxuan 10 × Lumai 14 Xiaoyan 54 × Jing 411	3 TaGS2		1	1	1	LN HN	5	
Guo et al. (2012)	RIL	131	Chuan 35050 × Shamong 483	719 (DARt, SSR, EST)	4008	12	1	1	N, P, K	24	380
Sun et al. (2013)						3	1	1	NO ₃ ⁻ /NH ₄ ⁺ ratio	8	147
Xu et al. (2013)	RIL	182	Xiaoyan 54 × Jing 411	555 (SSR, EST, <i>Gli1</i> loci)		4	2	1	LN HN	14	126
Laperche et al. (2007)	DH	222	Arche × Recital	190 (SSR, GLU-1A/ID, Rht-B1, SPA, Ft-gogat-D1, VRN-A1, B1)	2164	14	2	4	LN=HN-100 kg N ha	18	233
Laperche et al. (2006a)	DH	120			2164	1	1	1		6	45
Laperche et al. (2008)	DH	222			2164	14	2	4	LN=HN-100 kg N ha	4	131
Zheng et al. (2010)	DH	222			2164	12	2	3	LN HN	16	148
Fontaine et al. (2009)	DH	137-221			3285	3	3	1		21	145
Habash et al. (2007)	DH	91	CS × SQ1	449 (SSR + GS loci)	3522	1	1	1		10	138
Garcia-Suarez et al. (2010)	RIL	114	W7984 × Opata85			4	2	1	LN=0; HN=120 kg N ha	7	140
Bogard et al. (2011)	DH	140	Toisonдор × 3CF9107	475 (DARt, SSR, SNP)	2344	10	2	5	LN=(25-50)%HN	2	
Bogard et al. (2013)	3 DH +80 +140	80	Toisonдор × Quebon CF9107 × Quebon	741 (DARt, SSR, SNP)	2510	7	2	3	LN=25%HN	2	89
Bordes et al. (2013)	Panel	196	Toisonдор × CF9107	899 (DARt, SSR, SNP)		12	2	3	LN=HN-(35-120) kg N	8	54
Cormier et al. (2014)	Panel	214	Core collection Commercial varieties	23 603 SNP	3167	8	2	3	LN=HN-100 kg N	28	333

HN, high nitrogen; LN, low nitrogen.

(RIL) populations (Garcia-Suarez *et al.* 2010, Li *et al.* 2010, Guo *et al.* 2012, Sun *et al.* 2013, Xu *et al.* 2013). Three studies covered a broader genetic diversity (Li *et al.* 2010, Bordes *et al.* 2013, Cormier *et al.* 2014) using large association panels. Discovering QTL colocalizing with known N uptake or assimilation enzymes and new QTL, these studies provided novel insights on NUE genetic determinism.

Nevertheless, several difficulties persist in order to implement this knowledge in breeding, as NUE and its related traits appeared highly polygenic and genetic background specific. Thus, several loci with small effects should be pyramided. As the volume of genotyping information is increasing with the recent development of several wheat SNP arrays (90K, Wang *et al.* 2014; 420K, 670K, and 820K), genomic prediction methods may overpass these limitations and facilitate breeding. However, until now, these methods are still at a developmental stage. Indeed, $G \times N$ interactions and more generally $G \times E$ interactions remain major trade-offs in marker-assisted selection aiming to develop new genotypes adapted to a broad range of environments and N levels.

Exploiting heterosis

F1 hybrid wheat cultivars have been regularly registered in Central Europe, which represents more than half of the world's hybrid wheat production (Longin *et al.* 2012). Commercial hybrids may be produced with chemical hybridizing agents, which induce male sterility when applied at the right stage, but also based on photoperiod sensitivity or on cytoplasmic male sterility. Limits to the use of F1 hybrids are the cost of the seed, related to the difficulty to produce them on a regular basis, coupled with the absence of high heterosis for yield.

However, hybrids may show particular characteristics for abiotic stress tolerance and NUE. Limited but consistent best parent heterosis has been reported for grain yield under high yielding conditions, for example +4.3% for 10 hybrids (Borghi *et al.* 1988), +7.3% for 17 hybrids (Brears *et al.* 1988), +3.6% for 430 hybrids (Morgan *et al.* 1989) in experiments conducted in field plots. On average, in Europe, in five studies, Longin *et al.* (2012) reported mid-parent heterosis around 10%, ranging from 3.5% to 15.0%. It was also reported that the hybrids are more stable than pure lines (Mühleisen *et al.* 2014), indicating a higher tolerance to abiotic stresses.

Perezin *et al.* (1998) and Oury *et al.* (1994, 1995) reported either a higher grain protein content of the hybrids for the same yield or the same protein content despite a higher grain yield. These results suggest a higher NUE and N uptake for hybrids compared to pure lines. Some studies also showed that best parent heterosis was higher at low N level than at high N level (Le Gouis and Pluchard 1996, Le Gouis *et al.* 2002). This was, however, not confirmed by Kindred and Gooding (2005) who used four commercial hybrids and observed a significant heterosis only at high N level. Le Gouis *et al.* (2002) observed a best parent heterosis for total N at anthesis and harvest, meaning a better N uptake, while Kindred and Gooding (2004) reported only little heterosis for total above-ground N, but an increased N utilization efficiency. Mid-parent heterosis for N uptake at flowering and maturity could be related to a more efficient root system. Indeed, heterosis was shown for different root characteristics such as root length, root dry matter and root surface area (Kraljevic-Balalic *et al.* 1988, Wang *et al.* 2006).

Conclusion

NUE is complex and is determined by a wide diversity of physiological traits. Consequently, breeding for enhanced NUE can be achieved through selection on several components. However, compensations and regulations are numerous and dependent on the N regimes, genotypes and developmental stage, leading to difficulties to create efficient NUE phenotypes. Nevertheless, 'omics and association studies' provided interesting results allowing to prioritize routes for improvement. Moreover, high-throughput genotyping combined with the development of high-throughput phenotyping methods will accelerate research in a wide diversity of environments and genotypes.

Author Contributions

DG and FC, definition of NUE and rationale for its improvement; JF, root size and morphology; BH, root N transporter systems; YML, interaction with microorganisms; BH, nitrate assimilation; JF, leaf and canopy photosynthesis per unit N; JF, postanthesis N remobilization and senescence dynamics; JF, optimizing grain protein concentration and composition; JF, phenotyping for NUE; and FC and JLG, breeding for NUE; FC and JLG, involved in coordination of contribution and manuscript editing. YML and JLG acknowledge ANR support for project BacterBlé (ANR-14-CE19-0017).

References

- Abbate, P. E., D. H. Andrade, L. Lazaro, J. H. Baraitti, H. G. Beradocco, V. H. Inza, and F. Marturano, 1998: Grain yield in recent Argentine wheat cultivars. *Crop Sci.* **38**, 1203–1209.
- Abenavoli, M. R., C. D. De Santis, M. Sidari, A. Sorgonà, M. Badiani, and G. Cacco, 2001: Influence of coumarin on the net nitrate uptake in durum wheat. *New Phytol.* **150**, 619–627.
- Acereche, M. M., and G. A. Slafer, 2009: Variation of grain nitrogen content in relation with grain yield in old and modern Spanish wheats grown under a wide range of agronomic conditions in a Mediterranean region. *J. Agric. Sci.* **147**, 657–667.
- Allard, V., P. Martre, and J. Le Gouis, 2013: Genetic variability in biomass allocation to roots in wheat is mainly related to crop tillering dynamics and nitrogen status. *Eur. J. Agron.* **46**, 68–76.
- Almario, J., Y. Moëgne-Loccoz, and D. Muller, 2013: Monitoring of the relation between 2,4-diacetylphloroglucinol-producing *Pseudomonas* and *Thielaviopsis basicola* populations by real-time PCR in tobacco black root-rot suppressive and conducive soils. *Soil Biol. Biochem.* **57**, 144–155.
- Altenbach, S. B., C. K. Tanaka, W. J. Hurkman, L. C. Whiteland, W. H. Vensel, and F. M. Dupont, 2011: Differential effects of a post-anthesis fertilizer regimen on the wheat flour proteome determined by quantitative 2-DE. *Proteome Sci.* **4**, 9–46.
- An, D., J. Su, Q. Liu, Y. Zhu, Y. Tong, J. Li, R. Jing, B. Li, and Z. Li, 2006: Mapping QTLs for nitrogen uptake in relation to the early growth of wheat (*Triticum aestivum* L.). *Plant Soil* **284**, 73–84.
- Anjana, S. Umar, Y. P. Abrol and M. Iqbal 2011: Modulation of nitrogen-utilization efficiency in wheat genotypes differing in nitrate reductase activity. *J. Plant Nutr.* **34**, 920–933.
- Andrews, M., J. A. Raven, and P. J. Lea, 2013: Do plants need nitrate? The mechanisms by which nitrogen form affects plants. *Ann. Appl. Biol.* **163**, 174–199.
- Angus, J. F., V. V. S. R. Gupta, G. D. Pitson, and A. J. Good, 2014: Effects of banded ammonia and urea fertiliser on soil properties and the growth and yield of wheat. *Crop Past. Sci.* **65**, 337–352.
- Annicchiarico, P., E. Chiapparino, and M. Perenzin, 2010: Response of common wheat varieties to organic and conventional production

- systems across Italian locations, and implications for selection. *Field Crops Res.* **116**, 230–238.
- Anten, N. P. R., F. Schieving, and M. J. A. F. Werger, 1995: Patterns of light and nitrogen distribution in relation to whole canopy carbon gain in C3 and C4 mono- and dicotyledonous species. *Oecologia* **101**, 504–513.
- Apan, A., R. Kelly, S. Phinn, W. Strong, D. Lester, D. Butler, and A. Robson, 2006: Predicting grain protein content in wheat using hyperspectral sensing of in-season crop canopies and partial least squares regression. *Int. J. Geo. Inf.* **2**, 93–108.
- Aparicio, N., D. Villegas, J. L. Araus, J. Casadesús, and C. Royo, 2002: Relationship between growth traits and spectral reflectance indices in durum wheat. *Crop Sci.* **42**, 1547–1555.
- Araus, J. L., and J. E. Cairns, 2014: Field high-throughput phenotyping: the new crop breeding frontier. *Trends Plant Sci.* **19**, 52–61.
- Araus, J. L., T. Amaro, Y. Zuhair, and M. M. Nachit, 1997: Effect of leaf structure and water status on carbon isotope discrimination in field grown durum wheat. *Plant Cell Environ.* **20**, 1484–1494.
- Araus, J. L., J. Casadesus, and J. Bort, 2001: Recent tools for the screening of physiological traits determining yield. In: M. P. Reynolds (ed.), *Application of Physiology in Wheat Breeding*, 59–77. CIMMYT, Mexico, Mexico.
- Atkin, O. K., D. Bruhn, V. M. Hurry, and M. G. Tjoelker, 2005: The hot and the cold: unravelling the variable response of plant respiration to temperature. *Funct. Plant Biol.* **32**, 87–105.
- Atkinson, J. A., L. U. Wingen, M. Griffiths, M. P. Pound, O. Gaju, M. J. Foulkes, J. Le Gouis, S. Griffiths, M. J. Bennett, J. King, and D. M. Wells, 2015: Phenotyping pipeline reveals major seedling root growth QTL in hexaploid wheat. *J. Exp. Bot.* **66**, 2283–2292.
- Atul-Nayyar, A., C. Hamel, K. Hanson, and J. Germida, 2009: The arbuscular mycorrhizal symbiosis links N mineralization to plant demand. *Mycorrhiza* **19**, 239–246.
- Austin, R. B., C. L. Morgan, M. A. Ford, and S. G. Bhagwat, 1982: Flag leaf photosynthesis of *Triticum aestivum* and related diploid and tetraploid species. *Ann. Bot.* **49**, 177–189.
- Babar, M. A., M. P. Reynolds, M. van Ginkel, A. R. Klatt, W. R. Raun, and M. L. Stone, 2006: Spectral reflectance to estimate genetic variation for in-season biomass, leaf chlorophyll, and canopy temperature in wheat. *Crop Sci.* **46**, 1046–1057.
- Bahrman, N., J. Le Gouis, L. Negroni, L. Amilhat, P. Leroy, A.-L. Lainé, and O. Jaminon, 2004a: Differential protein expression assessed by two-dimensional gel electrophoresis for two wheat varieties grown at four nitrogen levels. *Proteomics* **4**, 709–719.
- Bahrman, N., L. Negroni, O. Jaminon, and J. Le Gouis, 2004b: Wheat leaf proteome analysis using sequence data of proteins separated by two-dimensional electrophoresis. *Proteomics* **4**, 2672–2684.
- Bahrman, N., A. Gouy, F. Devienne-Barret, B. Hirel, F. Vedele, and J. Le Gouis, 2005: Differential change in root protein patterns of two wheat varieties under high and low nitrogen nutrition levels. *Plant Sci.* **168**, 81–87.
- Bai, C., Y. Liang, and M. J. Hawkesford, 2013: Identification of QTLs associated with seedling root traits and their correlation with plant height in wheat. *J. Exp. Bot.* **64**, 1745–1753.
- Baldani, J. I., and V. L. D. Baldani, 2005: History on the biological nitrogen fixation research in graminaceous plants: special emphasis on the Brazilian experience. *An. Acad. Bras. Ciênc.* **77**, 549–579.
- Bänziger, M., F. J. Betran, and H. R. Lafite, 1997: Efficiency of high-nitrogen selection environments for improving maize for low-nitrogen target environments. *Crop Sci.* **37**, 1103–1109.
- Bardon, C., F. Piola, F. Bellvert, F. Z. Haichar, G. Comte, G. Meiffren, T. Pommier, S. Puijalón, N. Tsafack, and F. Poly, 2014: Evidence for biological denitrification inhibition (BDI) by plant secondary metabolites. *New Phytol.* **204**, 62–630.
- Barraclough, P. B., H. Kuhlmann, and A. H. Weir, 1989: The effects of prolonged drought and nitrogen fertiliser on root and shoot growth and water uptake by winter wheat. *J. Agron. Crop Sci.* **163**, 352–360.
- Barraclough, P. B., J. R. Howarth, J. Jones, R. Lopez-Bellido, S. Parmar, C. E. Shepherd, and M. J. Hawkesford, 2010: Nitrogen efficiency of wheat: genotypic and environmental variation and prospects for improvement. *Eur. J. Agron.* **33**, 1–11.
- Barraclough, P. B., R. Lopez-Bellido, and M. J. Hawkesford, 2014: Genotypic variation in the uptake, partitioning and remobilisation of nitrogen during grain-filling in wheat. *Field Crops Res.* **156**, 242–248.
- Beauchamp, E. G., L. W. Kannenberg, and R. B. Hunter, 1976: Nitrogen accumulation and translocation in corn genotypes following silking. *Agron. J.* **68**, 418–422.
- Behl, R. K., S. Ruppel, E. Kothe, and N. Narula, 2012: Wheat × Azotobacter × VA Mycorrhiza interactions towards plant nutrition and growth – a review. *J. Appl. Bot. Food Qual.* **81**, 95–109.
- Berendse, F., and R. Aerts, 1987: Nitrogen use efficiency: a biologically meaningful definition? *Funct. Ecol.* **1**, 293–296.
- Berger, B., B. Parent, and M. Tester, 2010: High-throughput shoot imaging to study drought responses. *J. Exp. Bot.* **61**, 3519–3528.
- Bernard, S. M., A. L. Møller, G. Dionisio, T. Kichey, T. P. Jahn, F. Dubois, M. Baudo, M. S. Lopes, T. Tercé-Laforgue, C. H. Foyer, M. A. Parry, B. G. Forde, J. L. Araus, B. Hirel, J. K. Schjoerring, and D. Z. Habash, 2008: Gene expression, cellular localisation and function of glutamine synthetase isozymes in wheat (*Triticum aestivum* L.). *Plant Mol. Biol.* **67**, 89–105.
- Bertheloot, J., P. Martre, and B. Andrieu, 2008: Dynamics of light and nitrogen distribution during grain filling within wheat canopy. *Plant Physiol.* **148**, 1707–1720.
- Bertheloot, J., P. H. Cournède, and B. Andrieu, 2011: NEMA, a functional-structural model of nitrogen economy within wheat culms after flowering. I. Model description. *Ann. Bot.* **108**, 1085–1096.
- Bertrand, H., C. Plassard, X. Pinchet, B. Touraine, P. Normand, and J. C. Cleyet-Marel, 2000: Stimulation of the ionic transport system in *Brassica napus* by a plant growth-promoting rhizobacterium (*Achromobacter* sp.). *Can. J. Microbiol.* **46**, 229–236.
- Bindraban, P. S., 1999: Impact of canopy nitrogen profile in wheat on growth. *Field Crops Res.* **63**, 63–77.
- Bingham, I., A. Karley, P. White, W. Thomas, and J. Russell, 2012: Analysis of improvements in nitrogen use efficiency associated with 75 years of spring barley breeding. *Eur. J. Agron.* **42**, 49–58.
- Bloom, A. J., M. Burger, B. A. Kimball, and P. Pinter Jr, 2014: Nitrate assimilation is inhibited by elevated CO₂ in field grown wheat. *Nat. Clim. Chang.* **4**, 477–480.
- Blum, A., 2009: Effective use of water (EUW) and not water-use efficiency (WUE) is the target of crop yield improvement under drought stress. *Field Crops Res.* **112**, 119–123.
- Bogard, M., V. Allard, M. Brancourt-Hulmel, E. Heumez, J. M. Machet, M. H. Jeuffroy, P. Gate, P. Martre, and J. Le Gouis, 2010: Deviation from the grain protein concentration–grain yield negative relationship is highly correlated to post-anthesis N uptake in winter wheat. *J. Exp. Bot.* **61**, 4303–4312.
- Bogard, M., M. Jourdan, V. Allard, P. Martre, M. R. Perretant, C. Ravel, E. Heumez, S. Orford, J. Snape, S. Griffiths, O. Gaju, J. Foulkes, and J. Le Gouis, 2011: Anthesis date mainly explained correlations between post-anthesis leaf senescence, grain yield, and grain protein concentration in a winter wheat population segregating for flowering time QTLs. *J. Exp. Bot.* **62**, 3621–3636.
- Bogard, M., V. Allard, P. Martre, E. Heumez, J. W. Snape, S. Griffiths, O. Gaju, J. Foulkes, and J. Le Gouis, 2013: Identifying wheat genomic regions for improving grain protein concentration independently of grain yield using multiple inter-related populations. *Mol. Breed.* **31**, 587–599.
- Boisson, M., K. Mondon, V. Torney, N. Nicot, A. L. Laine, N. Bahrman, A. Gouy, F. Daniel-Vedele, B. Hirel, P. Sourdille, M. Dardevet, C. Ravel, and J. Le Gouis, 2005: Partial sequences of nitrogen metabolism genes in hexaploid wheat. *Theor. Appl. Genet.* **110**, 932–940.
- Bonkowski, M., 2004: Protozoa and plant growth: the microbial loop in soil revisited. *New Phytol.* **162**, 617–631.
- Bordes, J., C. Ravel, J. P. Jaubertie, B. Duperrier, O. Gardet, E. Heumez, A. L. Pissavy, G. Charmet, J. Le Gouis, and F. Balfourrier, 2013: Genomic regions associated with the nitrogen limitation response revealed in a global wheat core collection. *Theor. Appl. Genet.* **126**, 805–822.
- Borghi, B., M. Perenzin, and R. J. Nash, 1988: Agronomic and qualitative characteristics of ten bread wheat hybrids produced using a chemical hybridizing agent. *Euphytica* **39**, 185–194.

- Borras, L., G. A. Slafer, and M. E. Otegui, 2004: Seed dry weight response to source-sink manipulations in wheat, maize and soybean: a quantitative reappraisal. *Field Crops Res.* **86**, 131–146.
- Borrell, A. K., and G. L. Hammer, 2000: Nitrogen dynamics and the physiological basis of stay-green in sorghum. *Crop Sci.* **40**, 1295–1307.
- Bottini, R., F. Cassán, and P. Piccoli, 2004: Gibberellin production by bacteria and its involvement in plant growth promotion and yield increase. *Appl. Microbiol. Biotechnol.* **65**, 497–503.
- Bradley, P. M., and J. T. Morris, 1991: The influence of salinity on the kinetics of uptake in *Spartina alterniflora*. *Oecologia* **85**, 375–380.
- Brancourt-Hulmel, M., G. Doussinault, C. Lecomte, P. Bérard, B. LeBuanec, and M. Trotter, 2003: Genetic improvement of agronomic traits of winter wheat cultivars released in France from 1946 to 1992. *Crop Sci.* **43**, 37–45.
- Brancourt-Hulmel, M., E. Heumez, P. Pluchard, D. Beghin, C. Depatureaux, A. Giraud, and J. Le Gouis, 2005: Indirect versus direct selection of winter wheat for low input or high input levels. *Crop Sci.* **45**, 1427–1431.
- Brazelton, J. N., E. E. Pfeufer, T. A. Sweat, B. B. McSpadden Gardener, and C. Coenen, 2008: 2,4-diacetylphloroglucinol alters plant root development. *Mol. Plant Microbe Interact.* **21**, 1349–1358.
- Brears, T., A. G. Hydon, and J. Bingham, 1988: An assessment of the feasibility of producing F1 and F2 hybrids for the UK. *Proc 7th Int Wheat Genet Symp*, 1057–1062.
- Buchner, P., and M. J. Hawkesford, 2014: Complex phylogeny and gene expression patterns of members of the NITRATE TRANSPORTER1/PEPTIDE TRANSPORTER family (NPF) in wheat. *J. Exp. Bot.* **65**, 5697–57101.
- Buée, M., W. De Boer, F. Martin, L. van Overbeek, and E. Jurkevitch, 2009: The rhizosphere zoo: an overview of plant-associated communities of microorganisms, including phages, bacteria, archaea, and fungi, and of some of their structuring factors. *Plant Soil* **321**, 189–212.
- Cacco, G., E. Attinà, A. Gelsomino, and M. Sidari, 2000: Effect of nitrate and humic substances of different molecular size on kinetic parameters of nitrate uptake in wheat seedlings. *J. Plant Nutr. Soil Sci.* **163**, 313–320.
- Cai, C., X. Q. Zhao, Y. G. Zhu, B. Li, Y. P. Tong, and Z. S. Li, 2007: Regulation of the high-affinity nitrate transport system in wheat roots by exogenous abscisic acid and glutamine. *J. Integr. Plant Biol.* **49**, 1719–1725.
- Calderini, D. F., M. P. Reynolds, and G. A. Slafer, 2006: Source-sink effects on grain weight of bread wheat, durum wheat, and triticale at different locations. *Aust. J. Agric. Res.* **57**, 227–233.
- Carvalho, P., and M. J. Foulkes, 2011: Roots and the uptake of water and nutrients. In: R. A. Meyers (ed.), *Encyclopedia of Sustainability Science and Technology*, 1390–1404. Springer, Heidelberg, Germany, Chapter 195.
- Carvalho, P., S. Azam-Ali, and M. J. Foulkes, 2014: Quantifying relationships between rooting traits and water uptake under drought in Mediterranean barley and durum wheat. *J. Integr. Plant Biol.* **56**, 455–469.
- Cassán, F., D. Perrig, V. Sgroy, O. Masciarelli, C. Penna, and V. Luna, 2009: *Azospirillum brasilense* Az39 and *Bradyrhizobium japonicum* E109, inoculated singly or in combination, promote seed germination and early seedling growth in corn (*Zea mays* L.) and soybean (*Glycine max* L.). *Eur. J. Soil Biol.* **45**, 28–35.
- Causin, H. F., and A. J. Barneix, 1993: Regulation of NH₄⁺ uptake in wheat plant: effect of root ammonium concentration and amino acids. *Plant Soil* **151**, 211–218.
- Chen, J. B., Y. Liang, X. Y. Hu, X. X. Wang, F. Q. Tan, H. Q. Zhang, Z. L. Ren, and P. G. Luo, 2010: Physiological characterization of 'stay green' wheat cultivars during the grain filling stage under field growing conditions. *Acta Physiol. Plant* **32**, 875–882.
- Chen, C. C., G. Q. Han, H. Q. He, and M. Westcott, 2011: Yield, protein, and remobilization of water soluble carbohydrate and nitrogen of three spring wheat cultivars as influenced by nitrogen input. *Agron. J.* **103**, 786–795.
- Cheng, W., D. W. Johnson, and S. Fu, 2003: Rhizosphere effects on decomposition. *Soil Sci. Soc. Am. J.* **67**, 1418–1427.
- Christiansen, M. W., and P. L. Gregersen, 2014: Members of the barley NAC transcription factor gene family show differential co-regulation with senescence-associated genes during senescence of flag leaves. *J. Exp. Bot.* **65**, 4009–4022.
- Christiansen-Weniger, C., A. F. Groneman, and J. A. van Veen, 1992: Associative N₂ fixation and root exudation of organic acids from wheat cultivars of different aluminium tolerance. *Plant Soil* **139**, 167–174.
- Christopher, J. T., A. M. Manschadi, G. L. Hammer, and A. K. Borell, 2008: Developmental and physiological traits associated high yield and stay-green phenotype in wheat. *Aust. J. Agric. Res.* **59**, 354–364.
- Coelho, M. R. R., I. E. Marriel, S. N. Jenkins, C. V. Lanyon, L. Seldin, and A. G. O'Donnell, 2009: Molecular detection and quantification of nifH gene sequences in the rhizosphere of sorghum (*Sorghum bicolor*) sown with two levels of nitrogen fertilizer. *Appl. Soil Ecol.* **42**, 48–53.
- Cohan, J. P., 2009: Prix des engrais azotés: quels impacts sur les céréales? *Perspectives Agricoles* **352**, 18–22.
- Cohen, A. C., R. Bottini, and P. N. Piccoli, 2008: *Azospirillum brasilense* Sp 245 produces ABA in chemically-defined culture medium and increases ABA content in arabidopsis plants. *Plant Growth Regul.* **54**, 97–103.
- Combes-Meynet, E., J. F. Pothier, Y. Moëne-Loccoz, and C. Prigent-Combare, 2011: The *Pseudomonas* secondary metabolite 2,4-diacetylphloroglucinol is a signal inducing rhizoplane expression of *Azospirillum* genes involved in plant-growth promotion. *Mol. Plant Microbe Interact.* **24**, 271–284.
- Cormier, F., S. Faure, P. Dubreuil, E. Heumez, K. Beauchêne, S. Lafarge, S. Praud, and J. Le Gouis, 2013: A multi-environmental study of recent breeding progress on nitrogen use efficiency in wheat (*Triticum aestivum* L.). *Theor. Appl. Genet.* **126**, 3035–3048.
- Cormier, F., J. Le Gouis, P. Dubreuil, S. Lafarge, and S. Praud, 2014: A genome-wide identification of chromosomal regions determining nitrogen use efficiency components in wheat (*Triticum aestivum* L.). *Theor. Appl. Genet.* **127**, 2679–2693.
- Couillerot, O., E. Combes-Meynet, J. F. Pothier, F. Bellvert, E. Challita, M. A. Poirier, R. Rohr, G. Comte, Y. Moëne-Loccoz, and C. Prigent-Combare, 2011: The role of the antimicrobial compound 2,4-diacetylphloroglucinol in the impact of biocontrol *Pseudomonas fluorescens* F113 on *Azospirillum brasilense* phyto-stimulators. *Microbiology* **157**, 1694–1705.
- Crawford, N. M., and A. D. M. Glass, 1998: Molecular and physiological aspects of nitrate uptake in plants. *Trends Plant Sci.* **3**, 389–395.
- Creus, C. M., M. Graziano, E. M. Casanovas, M. A. Pereyra, M. Simon-tacchi, S. Puntarulo, C. A. Barassi, and L. Lamattina, 2005: Nitric oxide is involved in the *Azospirillum brasilense*-induced lateral root formation in tomato. *Planta* **221**, 297–303.
- Criddle, R. S., M. R. Ward, and R. C. Huffaker, 1988: Nitrogen uptake by wheat seedlings, interactive effects of four nitrogen sources: NO₃⁻, NO₂⁻, NH₄⁺, and urea. *Plant Physiol.* **86**, 166–175.
- Critchley, C. S., 2001: A Physiological Explanation for the Canopy Nitrogen Requirement of Wheat. PhD Thesis. University of Nottingham, UK.
- Curzi, M. J., C. M. Ribaud, G. D. Trincherro, J. A. Cura, and E. A. Pagano, 2008: Changes in the content of organic and amino acids and ethylene production of rice plants in response to the inoculation with *Herbaspirillum seropedicae*. *J. Plant Interact.* **3**, 163–173.
- Dechorgnat, J., C. T. Nguyen, P. Armengaud, M. J. Jossier, E. Diatloff, S. Filleur, and F. Daniel-Vedele, 2011: From the soil to the seeds: along journey of nitrate in plants. *J. Exp. Bot.* **62**, 1349–1359.
- Den Herder, G., G. Van Isterdael, T. Beekman, and I. De Smet, 2010: The roots of a new green revolution. *Trends Plant Sci.* **15**, 600–607.
- Derkx, A. P., S. Orford, S. Griffiths, M. J. Foulkes, and M. J. Hawkesford, 2012: Identification of differentially senescing mutants of wheat and impacts on yield, biomass and nitrogen partitioning. *J. Integr. Plant Biol.* **54**, 555–566.
- Dobbelaere, S., A. Croonenborghs, A. Thys, A. Vande Broek, and J. Vanderleyden, 1999: Phyto-stimulatory effect of *Azospirillum brasili-*

- lense* wild type and mutant strains altered in IAA production on wheat. *Plant Soil* **212**, 153–162.
- Dreccer, M., A. Schapendonk, G. Slafer, and R. Rabbinge, 2000: Comparative response of wheat and oilseed rape to nitrogen supply: absorption and utilisation efficiency of radiation and nitrogen during the reproductive stages determining yield. *Plant Soil* **220**, 189–205.
- Dubois, F., T. Tercé-Laforgue, M. B. Gonzalez-Moro, M. B. Estavillo, R. Sangwan, A. Gallais, and B. Hirel, 2003: Glutamate dehydrogenase in plants: is there a new story for an old enzyme? *Plant Physiol. Biochem.* **41**, 565–576.
- Ehdaie, B., 1995: Variation in water-use efficiency and its components in wheat. II. Pot and field experiments. *Crop Sci.* **35**, 1617–1626.
- Ehdaie, B., and J. G. Waines, 1993: Variation in water-use efficiency and its components in wheat. I. Well-watered pot experiment. *Crop Sci.* **33**, 294–299.
- Ehdaie, B., and J. G. Waines, 1997: Growth and evapotranspiration efficiency in landrace and dwarf spring wheats. *J. Genet. Breed.* **51**, 201–209.
- Ehdaie, B. and J. G. Waines 2003: 1RS translocation increases root biomass in Veery-type wheat isogenic lines and associates with grain yield. In: N. E. Pogna, M. Romano, E. A. Pogna, G. Galterio (ed.), *Proceedings of the 10th International Wheat Genetics Symposium*, 693–695. ISC: Paestum, Rome.
- Ehdaie, B., R. W. Whitkus, and J. G. Waines, 2003: Root biomass, water-use efficiency, and performance of wheat-rye translocations of chromosomes 1 and 2 in spring bread wheat ‘Pavon’. *Crop Sci.* **43**, 710–717.
- Ehdaie, B., A. E. Hall, G. D. Farquhar, H. T. Nguyen, and J. G. Waines, 1991: Water-use efficiency and carbon isotope discrimination in wheat. *Crop Sci.* **31**, 1282–1288.
- Eitel, U. H., T. S. Magney, L. A. Vierling, T. T. Brown, and D. R. Huggins, 2014: LiDAR based biomass and crop nitrogen estimates for rapid, non-destructive assessment of wheat nitrogen status. *Field Crops Res.* **159**, 21–32.
- Evans, J. R., 1983: Nitrogen and photosynthesis in the flag leaf of wheat (*Triticum aestivum* L.). *Plant Physiol.* **72**, 297–302.
- Fageria, N. K., V. C. Baligar, and Y. C. Li, 2008: The role of nutrient efficient plants in improving crop yields in the twenty first century. *J. Plant Nutr.* **31**, 1121–1157.
- Falconer, D., and T. Mackay, 1996: *Introduction to Quantitative Genetics*, 4th edn. Longman Scientific & Technical, New York.
- Feil, B., 1997: The inverse yield-protein relationships in cereals: possibilities and limitations for genetically improving the grain protein yield. *Trends Agron* **1**, 103–119.
- Fester, T., W. Maier, and D. Strack, 1999: Accumulation of secondary compounds in barley and wheat roots in response to inoculation with an arbuscular mycorrhizal fungus and co-inoculation with rhizosphere bacteria. *Mycorrhiza* **8**, 241–246.
- Field, C., 1983: Allocating leaf nitrogen for the maximization of carbon gain: leaf age as a control on the allocation program. *Oecologia* **56**, 341–347.
- Fiorani, F., and U. Schurr, 2013: Future scenarios for plant phenotyping. *Annu. Rev. Plant Biol.* **64**, 267–291.
- Fontaine, J. X., C. Ravel, K. Pageau, E. Heumez, F. Dubois, B. Hirel, and J. Le Gouis, 2009: A quantitative genetic study for elucidating the contribution of glutamine synthetase, glutamate dehydrogenase and other nitrogen-related physiological traits to the agronomic performance of common wheat. *Theor. Appl. Genet.* **119**, 645–662.
- Fontaine, J. X., T. Tercé-Laforgue, P. Armengaud, G. Clément, J. P. Renou, S. Pelletier, M. Catterou, M. Azzopardi, Y. Gibon, P. J. Lea, B. Hirel, and F. Dubois, 2012: Characterization of a NADH-dependent glutamate dehydrogenase mutant of *Arabidopsis* demonstrates the key role of this enzyme in root carbon and nitrogen metabolism. *Plant Cell* **24**, 4044–4065.
- Ford, K. E., P. J. Gregory, M. J. Gooding, and S. Pepler, 2006: Genotype and fungicide effects on late-season root growth of winter wheat. *Plant Soil* **284**, 33–44.
- Forde, B. J., and P. J. Lea, 2007: Glutamate in plants: metabolism, regulation, and signalling. *J. Exp. Bot.* **58**, 2339–2358.
- Foulkes, M. J., and E. H. Murchie, 2011: Optimising canopy physiology traits to improve the nutrient-utilisation efficiency of crops. In: M. Hawkesford, and P. Barraclough (eds), *The Molecular Basis of Nutrient Use Efficiency in Crops*, 65–82. Wiley-Blackwell, Chichester, West Sussex, Hoboken, NJ.
- Foulkes, M. J., R. Sylvester-Bradley, and R. K. Scott, 1998: Evidence for differences between winter wheat cultivars in acquisition of soil mineral nitrogen and uptake and utilisation of applied fertiliser nitrogen. *J. Agric. Sci.* **130**, 29–44.
- Foulkes, M. J., M. J. Hawkesford, P. B. Barraclough, M. J. Holdsworth, S. Kerr, S. Kightley, and P. R. Shewry, 2009: Identifying traits to improve the nitrogen economy of wheat: recent advances and future prospects. *Field Crops Res.* **114**, 329–342.
- Freeman, K. W., W. R. Raun, G. V. Johnson, R. W. Mullen, M. L. Stone, and J. B. Solie, 2007: Late-season prediction of wheat grain yield and grain protein analysis. *Commun. Soil Sci. Plant Anal.* **34**, 1837–1852.
- Friedrich, J. W., and L. E. Schrader, 1979: N deprivation in maize during grain-filling. II. Remobilisation of 15N and 35S and the relationship between N and S accumulation. *Agron. J.* **71**, 466–472.
- Furbank, R. T., and M. Tester, 2011: Phenomics—technologies to relieve the phenotyping bottleneck. *Trends Plant Sci.* **16**, 635–644.
- Gadaleta, A., D. Nigro, A. Giancaspro, and A. Blanco, 2011: The glutamine synthetase (GS2) genes in relation to grain protein content of durum wheat. *Funct. Integra. Genomics* **11**, 665–670.
- Gadaleta, A., D. Nigro, I. Marcotuli, A. Giancaspro, S. L. Giove, and A. Blanco, 2014: Isolation and characterization of cytosolic glutamine synthetase (*GSe*) genes and association with grain protein content in durum wheat. *Crop Past. Sci.* **65**, 38–45.
- Gaju, O., V. Allard, P. Martre, J. W. Snape, E. Heumez, J. Le Gouis, D. Moreau, M. Bogard, S. Griffiths, S. Orford, S. Hubbart, and M. J. Foulkes, 2011: Identification of traits to improve the nitrogen-use efficiency of wheat genotypes. *Field Crops Res.* **123**, 139–152.
- Gaju, O., V. Allard, P. Martre, J. Le Gouis, D. Moreau, M. Bogard, S. Hubbart, and M. J. Foulkes, 2014: Nitrogen partitioning and remobilization in relation to leaf senescence, grain yield and grain N concentration in wheat cultivars. *Field. Crop. Res.* **155**, 213–223.
- Garcia-Suarez, J. V., M. S. Roder, and J. L. Diaz de León, 2010: Identification of QTLs and associated molecular markers of agronomic traits in wheat (*Triticum aestivum* L.) under two conditions of nitrogen fertilization. *Cereal Res. Commun.* **38**, 459–470.
- Garnett, T., V. Conn, and B. Kaiser, 2009: Root based approach to improving nitrogen use efficiency in plants. *Plant Cell Environ.* **32**, 1272–1283.
- Gaur, V. S., U. S. Singh, A. K. Gupta, and A. Kumar, 2012: Understanding the differential nitrogen sensing mechanism in rice genotypes through the expression analysis of high and low affinity ammonium transporter genes. *Mol. Biol. Rep.* **39**, 2233–2241.
- Germida, J., and S. Siciliano, 2001: Taxonomic diversity of bacteria associated with the roots of modern, recent and ancient wheat cultivars. *Biol. Fertil. Soils* **33**, 410–415.
- Gioeffi, E., A. de Neergaard, and J. K. Schjoerring, 2012: Interactions between uptake of amino acids and inorganic nitrogen in wheat plants. *Biogeosci.* **9**, 1509–1518.
- Girin, T., L. C. David, C. Chardin, R. Sibout, A. Krapp, S. Ferrario-Mery, and F. Daniel-Vedele, 2014: Brachypodium: a promising hub between model species and cereals. *J. Exp. Bot.* **65**, 5683–5696.
- Giunta, F., M. Rosella, and M. Deidda, 2002: SPAD readings and associated leaf traits in durum wheat, barley and triticale cultivars. *Euphytica* **125**, 197–205.
- Glass, A. D. M., 2009: Nitrate uptake by plant roots. *Botany* **87**, 659–667.
- Glick, B. R., 2005: Modulation of plant ethylene levels by the bacterial enzyme ACC deaminase. *FEMS Microbiol. Lett.* **251**, 1–7.
- Good, A. G., A. K. Shrawat, and D. G. Muench, 2004: Can less yield more? Is reducing nutrient input into the environment compatible with maintaining crop production? *Trends Plant Sci.* **9**, 597–605.

- Good, A. G., S. J. Johnson, M. De Pauw, R. T. Carroll, N. Savidov, J. Vidmar, Z. Lu, G. Taylor, and V. Stroehrer, 2007: Engineering nitrogen use efficiency with alanine aminotransferase. *Can. J. Bot.* **85**, 252—262.
- Gooding, M. J., and W. P. Davies, 1992: Foliar urea fertilization of cereals: a review. *Fertil. Res.* **32**, 209—222.
- Gooding, M. J., M. Addisu, R. K. Uppal, J. W. Snape, and H. E. Jones, 2012: Effect of wheat dwarfing genes on nitrogen-use efficiency. *J. Agric. Sci.* **150**, 3—22.
- Goyal, S. S., and R. C. Huffaker, 1986: The uptake of NO_3^- , NO_2^- , and NH_4^+ by intact wheat (*Triticum aestivum*) seedlings. *Plant Physiol.* **82**, 1051—1056.
- Graham, J. H., and R. G. Linderman, 1980: Ethylene production by ectomycorrhizal fungi, *Fusarium oxysporum* f. sp. pini, and by aseptically synthesized ectomycorrhizae and *Fusarium*-infected Douglas-fir roots. *Can. J. Microbiol.* **26**, 1340—1347.
- Gregory, P. J., and S. C. Brown, 1989: Root growth, water use and yield of crops in dry environments: what characters are desirable? *Aspects Appl. Biol.* **22**, 234—243.
- Gregory, P. J., D. J. Hutchison, D. B. Read, P. M. Jennesson, W. B. Gilboy, and E. J. Morton, 2003: Non-invasive imaging of roots with high resolution X-ray micro-tomography. *Plant Soil* **255**, 351—359.
- Gu, R., F. Duan, X. An, F. Zhang, N. von Wirèn, and L. Yuan, 2013: Characterization of the AMT-mediated high affinity ammonium uptake in roots of maize (*Zea mays* L.). *Plant Cell Physiol.* **54**, 1515—1524.
- Guarda, G., S. Padovan, and G. Delogu, 2004: Grain yield, nitrogen-use efficiency and baking quality of old and modern Italian bread-wheat cultivars grown at different nitrogen levels. *Eur. J. Agron.* **21**, 181—192.
- Guo, Y., F. M. Kong, Y. F. Xu, Y. Zhao, X. Liang, Y. Y. Wang, D. G. An, and S. S. Li, 2012: QTL mapping for seedling traits in wheat grown under varying concentrations of N, P and K nutrients. *Theor. Appl. Genet.* **124**, 851—865.
- Gutierrez, M., M. P. Reynolds, W. R. Raun, M. L. Stone, and A. R. Klatt, 2010a: Spectral water indices for assessing yield in elite bread wheat genotypes under well-irrigated, water-stressed, and high-temperature conditions. *Crop Sci.* **50**, 197—214.
- Gutierrez, M., M. P. Reynolds, and A. R. Klatt, 2010b: Association of water spectral indices with plant and soil water relations in contrasting wheat genotypes. *J. Exp. Bot.* **61**, 329—3303.
- Gutierrez-Rodriguez, M., M. P. Reynolds, J. A. Escalante-Estrada, and M. T. Rodriguez-Gonzalez, 2004: Association between canopy reflectance indices and yield and physiological traits in bread wheat under drought and well-irrigated conditions. *Aust. J. Agric. Res.* **55**, 1139—1147.
- Habash, D. Z., S. Bernard, J. Schondelmaier, J. Weyen, and S. A. Quarrie, 2007: The genetics of nitrogen use in hexaploid wheat: N utilisation, development and yield. *Theor. Appl. Genet.* **114**, 403—419.
- Hakwesford, M. J., 2014: Reducing the reliance on nitrogen fertilizer for wheat production. *J. Cereal Sci.* **59**, 276—283.
- Hall, A. J., and R. A. Richards, 2013: Prognosis for genetic improvement of yield potential and water-limited yield of major grain crops. *Field Crops Res.* **143**, 18—33.
- Hamada, A., M. Nitta, S. Nasuda, K. Kato, M. Fujita, H. Matsunaka, and Y. Okumoto, 2012: Novel QTLs for growth angle of seminal roots in wheat (*Triticum aestivum* L.). *Plant Soil* **354**, 395—405.
- Hargreaves, C. E., P. J. Gregory, and A. G. Bengough, 2009: Measuring root traits in barley (*Hordeum vulgare* ssp. *vulgare* and ssp. *spontaneum*) seedlings using gel chambers, soil sacs and X-ray microtomography. *Plant Soil* **316**, 285—297.
- Hawkins, H. G., and E. George, 2001: Reduces ^{15}N -nitrogen transport through arbuscular hyphae to *Triticum aestivum* supplied with ammonium vs. nitrate nutrition. *Ann. Bot.* **87**, 303—311.
- Herold, M. B., E. M. Baggs, and T. J. Daniell, 2012: Fungal and bacterial denitrification are differently affected by long-term pH amendment and cultivation of arable soil. *Soil Biol. Biochem.* **54**, 25—35.
- Hetrick, B. A. D., G. W. T. Wilson, B. S. Gill, and T. S. Cox, 1995: Chromosome location of mycorrhizal responsive genes in wheat. *Can. J. Bot.* **73**, 891—897.
- Hirel, B., J. Le Gouis, B. Ney, and A. Gallais, 2007: The challenge of improving nitrogen use efficiency in crop plants: towards a more central role for genetic variability and quantitative genetics within integrated approaches. *J. Exp. Bot.* **58**, 2369—2387.
- Hirose, T., 1971: Nitrogen turnover and dry matter production of a *Solidago altissima* population. *Jpn. J. Ecol.* **21**, 18—32.
- Hirose, T., 2011: Nitrogen use efficiency revisited. *Oecologia* **166**, 863—867.
- Hirose, T., and M. J. A. Werger, 1987: Maximizing daily canopy photosynthesis with respect to the leaf nitrogen allocation pattern in the canopy. *Oecologia* **72**, 520—526.
- Hoad, S. P., G. Russell, M. E. Lucas, and I. J. Bingham, 2001: The management of wheat, barley and oat root systems. In: D. L. Sparks (ed.), *Advances in Agronomy*, 193—246. Elsevier Academic Press Inc, San Diego.
- Hochholdinger, F., and R. Tuberosa, 2009: Genetic and genomic dissection of maize root development and architecture. *Curr. Opin. Plant Biol.* **12**, 172—177.
- Hooda, P. S., A. C. Edwards, H. A. Anderson, and A. Miller, 2000: A review of water quality concerns in livestock farming areas. *Sci. Tot. Environ.* **250**, 143—167.
- Hosoi, F., and K. Omasa, 2009: Estimating vertical plant area density profile and growth parameters of a wheat canopy at different growth stages using three-dimensional portable lidar imaging. *ISPRS J. Photogramm. Remote Sens.* **64**, 151—158.
- Howarth, J. R., S. Parmar, J. Jones, C. Shepherd, D. I. Corol, A. M. Galster, N. D. Hawkins, S. J. Miller, J. M. Baker, P. J. Verrier, J. L. Ward, M. H. Beale, P. B. Barraclough, and M. J. Hawkesford, 2008: Co-ordinated expression of amino acid metabolism in response to N and S deficiency during wheat grain filling. *J. Exp. Bot.* **59**, 3675—3689.
- Hsu, S.-F., and D. H. Buckley, 2009: Evidence for the functional significance of diazotroph community structure in soil. *ISME J.* **3**, 124—136.
- Huang, C. Y., H. Kuchel, J. Edwards, S. Hall, B. Parent, P. E. Herdina, D. M. Hartley, P. Langridge, and A. C. McKay, 2013: A DNA-based method for studying root responses to drought in field-grown wheat genotypes. *Sci. Rep.* **3**, 3194.
- Hund, A., N. Ruta, and M. Liedgens, 2009: Rooting depth and water use efficiency of tropical maize inbred lines, differing in drought tolerance. *Plant Soil* **318**, 311—325.
- Hungria, M., R. J. Campo, E. M. Souza, and F. O. Pedrosa, 2010: Inoculation with selected strains of *Azospirillum brasilense* and *A. lipoferum* improves yields of maize and wheat in Brazil. *Plant Soil* **331**, 413—425.
- Hurd, E., 1964: Root study of three wheat varieties and their resistance to drought and damage by soil cracking. *Can. J. Plant Sci.* **44**, 240—248.
- Iniguez, A. L., Y. Dong, and E. W. Triplett, 2004: Nitrogen fixation in wheat provided by *Klebsiella pneumoniae* 342. *Mol. Plant Microbe Interact.* **17**, 1078—1085.
- Jarvis, S., N. Hutchings, F. Brentrup, J. E. Olesen, and K. W. van de Hoek, 2011: Nitrogen flows in farming systems across Europe. In: B. Grizzetti (ed.), *The European Nitrogen Assessment. Sources, Effects and Policy Perspectives*, 21—28. Cambridge University Press, Exeter, UK.
- Jeuffroy, M. H., B. Ney, and A. Ourry, 2002: Integrated physiological and agronomic modelling of N capture and use within the plant. *J. Exp. Bot.* **53**, 809—823.
- Joshi, A. K., M. Kumari, V. P. Singh, C. M. Reddy, S. Kumar, J. Rane, and R. Chand, 2007: Stay green trait: variation, inheritance and its association with spot blotch resistance in spring wheat (*Triticum aestivum* L.). *Euphytica* **153**, 59—71.
- Kaiser, W. M., E. Planchet, and S. Rümer, 2011: Nitrate reductase and nitric oxide. In: C. H. Foyer, and H. Zhang (eds), *Annual Plant Reviews, Nitrogen Metabolism in Plants in the Post-genomic Era*, 127—146. Wiley-Blackwell, Chichester.
- Kapulnik, Y., Y. Okon, and Y. Henis, 1987: Yield response of spring wheat cultivars (*Triticum aestivum* and *T. turgidum*) to inoculation

- with *Azospirillum brasilense* under field conditions. *Biol. Fertil. Soil* **4**, 27–35.
- Karamos, R. E., K. Hanson, and F. C. Stevenson, 2014: Nitrogen form, time and rate of application, and nitrification inhibitor effects on crop production. *Can. J. Plant Sci.* **94**, 425–432.
- Kibite, S., and L. E. Evans, 1984: Causes of negative correlations between grain yield and grain protein concentration in common wheat. *Euphytica* **33**, 801–810.
- Kichey, T., J. Le Gouis, B. Hirel, and F. Dubois, 2005: Evolution of the cellular and subcellular localization of glutamine synthetase and glutamate dehydrogenase during flag leaf senescence in wheat (*Triticum aestivum* L.). *Plant Cell Physiol.* **46**, 964–974.
- Kichey, T., B. Hirel, E. Heumez, F. Dubois, and J. Le Gouis, 2007: In winter wheat (*Triticum aestivum* L.), post-anthesis nitrogen uptake and remobilisation to the grain correlates with agronomic traits and nitrogen physiological markers. *Field Crops Res.* **102**, 22–32.
- Kindred, D. R., and M. J. Gooding, 2004: Heterotic and seed rate effects on nitrogen efficiencies in wheat. *J. Agric. Sci.* **142**, 639–657.
- Kindred, D. R., and M. J. Gooding, 2005: Heterosis for yield and its physiological determinants in wheat. *Euphytica* **142**, 149–159.
- Kindred, D. R., T. M. O. Verhoeven, R. M. Weightman, J. S. Swanston, R. C. Agu, J. M. Brosnan, and R. Sylvester-Bradley, 2008: Effects of variety and fertiliser nitrogen on alcohol yield, grain yield, starch and protein content, and protein composition of winter wheat. *J. Cereal Sci.* **48**, 46–57.
- Kong, L., F. Wang, L. López-bellido, J. M. Garcia-Mina, and J. Si, 2013: Agronomic improvement through the genetic and physiological regulation of nitrogen uptake in wheat (*Triticum aestivum* L.). *Plant Biotech. Rep.* **7**, 129–139.
- Köpke, U., 1979: Ein Vergleich von Feldmethoden zur Bestimmung des Wurzelwachstums landwirtschaftlicher Kulturpflanzen. Doctoral Thesis. University of Göttingen.
- Körschens, M., E. Albert, M. Armbruster, D. Barkusky, M. Baumecker, L. Behle-Schalk, R. Bischoff, Z. Čergan, F. Ellmer, F. Herbst, S. Hoffmann, B. Hofmann, T. Kismányoky, J. Kubat, E. Kunzova, C. Lopez-Fando, I. Merbach, W. Merbach, M. T. Pardor, J. Rogasik, J. Rühlmann, H. Spiegel, E. Schulz, A. Tajnsek, Z. Toth, H. Wegener, and W. Zorn, 2013: Effect of mineral and organic fertilization on crop yield, nitrogen uptake, carbon and nitrogen balances, as well as soil organic carbon content and dynamics: results from 20 European long-term field experiments of the twenty-first century. *Arch. Agron. Soil Sci.* **59**, 1017–1040.
- Kraljevic-Balalic, M., R. Kastori, and M. Vojvodic, 1988: Inheritance of total root area, length and dry weight in F1 wheat crosses. *Genetika* **20**, 229–234.
- Kull, O., 2002: Acclimation of photosynthesis in canopies: models and limitations. *Oecologia* **133**, 267–279.
- Kusano, M., A. Fukushima, H. Redestig, and K. Saito, 2011: Metabolomic approaches toward understanding nitrogen metabolism in plants. *J. Exp. Bot.* **62**, 1439–1453.
- Labboun, S., T. Tercé-Laforgue, A. Roscher, M. Bedu, F. M. Restivo, C. N. Velanis, D. S. Skopelitis, P. N. Moshou, K. A. Roubelakis-Angelakis, A. Suzuki, and B. Hirel, 2009: Resolving the role of plant glutamate dehydrogenase: I. In vivo real time nuclear magnetic resonance spectroscopy experiments. *Plant Cell Physiol.* **50**, 1761–1773.
- Lammerts van Bueren, E. T., S. S. Jones, L. Tamm, K. M. Murphy, J. R. Myers, C. Leifert, and M. M. Messmer, 2011: The need to breed crop varieties suitable for organic farming, using wheat, tomato and broccoli as examples: a review. *NJAS-Wagen. J. Life Sci.* **58**, 193–205.
- Laperche, A., F. Devienne-Barret, O. Maury, J. Le Gouis, and B. Ney, 2006a: A simplified conceptual model of carbon/nitrogen functioning for QTL analysis of wheat adaptation to nitrogen deficiency. *Theor. Appl. Genet.* **113**, 1131–1146.
- Laperche, A., M. Brancourt-Hulmel, E. Heumez, O. Gardet, and J. Le Gouis, 2006b: Estimation of genetic parameters of a DH wheat population grown at different N stress levels characterized by probe genotypes. *Theor. Appl. Genet.* **112**, 797–807.
- Laperche, A., M. Brancourt-Hulmel, E. Heumez, O. Gardet, E. Hanocq, F. Devienne-Barret, and J. Le Gouis, 2007: Using genotype \times nitrogen interaction variables to evaluate the QTL involved in wheat tolerance to nitrogen constraints. *Theor. Appl. Genet.* **115**, 399–415.
- Laperche, A., J. Le Gouis, E. Hanocq, and M. Brancourt-Hulmel, 2008: Modelling nitrogen stress with probe genotypes to assess genetic parameters and genetic determinism of winter wheat tolerance to nitrogen constraint. *Euphytica* **161**, 259–271.
- Le Gouis, J., and P. Pluchard, 1996: Genetic variation for nitrogen use efficiency in winter wheat (*Triticum aestivum* L.). *Euphytica* **92**, 221–224.
- Le Gouis, J., B. Béghin, E. Heumez, and P. Pluchard, 2000: Genetic differences for nitrogen uptake and nitrogen utilisation efficiencies in winter wheat. *Eur. J. Agron.* **12**, 163–173.
- Le Gouis, J., D. Béghin, E. Heumez, and P. Pluchard, 2002: Diallel analysis of winter wheat at two nitrogen levels. *Crop Sci.* **42**, 1129–1134.
- Lea, P. J., and R. A. Azevedo, 2007: Nitrogen use efficiency. 2. Amino acid metabolism. *Ann. Appl. Biol.* **151**, 269–275.
- Lea, P. J., and B. J. Miñlin, 2011: Nitrogen assimilation and its relevance to crop improvement. In: H. Zhang (ed.), *Annual Plant Reviews, Nitrogen Metabolism in Plants in the Post-genomic Era*, 1–40. Wiley-Blackwell, Chichester.
- Lefsky, M. A., W. B. Cohen, G. G. Parker, and D. J. Harding, 2002: Lidar remote sensing for ecosystem studies. *Bioscience* **52**, 19–30.
- Lelong, C. C. D., P. Burger, G. Jubelin, B. Roux, S. Labbe, and F. Baret, 2008: Assessment of unmanned aerial vehicles imagery for quantitative monitoring of wheat crop in small plots. *Sensors* **8**, 3557–3585.
- Lemaire, G., E. Oosterom, J. Van Sheehy, M. H. Jeuffroy, A. Massignam, and L. Rossat, 2007: Is crop N demand more closely related to dry matter accumulation or leaf area expansion during vegetative growth? *Field Crops Res.* **100**, 91–106.
- Léran, S., K. Varala, J. C. Boyer, M. Chiurazzi, N. Crawford, F. Daniel-Vedele, L. David, R. Dickstein, E. Fernandez, B. Forde, W. Gassmann, D. Geiger, A. Gojon, J. M. Gong, B. A. Halkier, J. M. Harris, R. Hedrich, A. M. Limami, D. Rentsch, M. Seo, L. F. Tsay, M. Zhang, G. Coruzzi, and B. Lacombe, 2014: A unified nomenclature of NITRATE TRANSPORTER 1/PEPTIDE TRANSPORTER family members in plants. *Trends Plant Sci.* **19**, 5–9.
- Li, X. P., X. Q. Zhao, X. He, G. Y. Zhao, B. Li, D. C. Liu, A. M. Zhang, X. Y. Zhang, Y. P. Tong, and Z. S. Li, 2010: Haplotype analysis of the genes encoding glutamine synthetase plastic isoforms and their association with nitrogen-use- and yield-related traits in bread wheat. *New Phytol.* **189**, 449–458.
- Lizana, X. C., and D. F. Calderini, 2013: Yield and grain quality of wheat in response to increased temperatures at key periods for grain number and grain weight determination: considerations for the climatic change scenarios of Chile. *J. Agric. Sci.* **151**, 209–221.
- Lobet, G., L. Pages, and X. Draye, 2011: A novel image-analysis toolbox enabling quantitative analysis of root system architecture. *Plant Physiol.* **157**, 29–39.
- Lobos, G. A., I. Matus, A. Rodriguez, S. Romero-Bravo, J. L. Araus, and A. del Pozo, 2014: Wheat genotypic variability in grain yield and carbon isotope discrimination under Mediterranean conditions assessed by spectral reflectance. *J. Integr. Plant Biol.* **56**, 470–479.
- Long, S. P., X. G. Zhu, S. L. Naidu, and D. R. Ort, 2006: Can improvement in photosynthesis increase crop yields? *Plant Cell Environ.* **29**, 315–330.
- Longin, C. F. H., J. Mühleisen, H. P. Maurer, H. Zhang, M. Gowda, and J. C. Reif, 2012: Hybrid breeding in autogamous cereals. *Theor. Appl. Genet.* **125**, 1087–1096.
- Lontoc-Roy, M., P. Dutilleul, S. O. Prasher, L. W. Han, T. Brouillet, and D. L. Smith, 2006: Advances in the acquisition and analysis of CT scan data to isolate a crop root system from the soil medium and quantify root system complexity in 3-D space. *Geoderma* **137**, 231–241.
- Lopes, M. S., and M. P. Reynolds, 2012: Stay-green in spring wheat can be determined by spectral reflectance measurements (normalized difference vegetation index) independently from phenology. *J. Exp. Bot.* **63**, 3789–3798.
- López-Castañeda, C., R. A. Richards, G. D. Farquhar, and R. E. Williamson, 1996: Seed and seedling characteristics contributing to varia-

- tion in early vigor among temperate cereals. *Crop Sci.* **36**, 1257–1266.
- Loqué, D., and N. von Wirén, 2004: Regulatory levels for the transport of ammonium in plant roots. *J. Exp. Bot.* **55**, 1293–1305.
- Ludewig, U., B. Neuhäuser, and M. Dynowski, 2007: Molecular mechanisms of ammonium transport and accumulation in plants. *FEBS Lett.* **581**, 2301–2308.
- Lynch, J., 1995: Root architecture and plant productivity. *Plant Physiol.* **109**, 7–13.
- Lynch, J. P., 2007: Roots of the second green revolution. *Aust. J. Bot.* **55**, 493–512.
- Ma, Z., T. C. Walk, A. Marcus, and J. P. Lynch, 2001: Morphological synergism in root hair length, density, initiation and geometry for phosphorus acquisition in *Arabidopsis thaliana*: a modeling approach. *Plant Soil* **236**, 221–235.
- MacFall, J. S., and G. A. Johnson, 2012: Plants, seeds, roots, and soils as applications of magnetic resonance microscopy. In: R. K. Harris, and R. E. Wasylshen (eds), *Encyclopedia of NMR*, Vol. 6, 3403–3409. John Wiley & Sons, Chichester, UK.
- Mairhofer, S., S. Zappala, S. Tracy, C. Sturrock, M. J. Bennett, S. J. Mooney, and T. P. Pridmore, 2013: Recovering complete plant root system architectures from soil via X-ray mu-computed tomography. *Plant Methods* **9**, 1–7.
- Maketon, C., A. M. Fortuna, and P. A. Okubara, 2012: Cultivar-dependent transcript accumulation in wheat roots colonized by *Pseudomonas fluorescens* Q8r1-96 wild type and mutant strains. *Biol. Control* **60**, 216–224.
- Malhi, S. S., and R. L. Lemke, 2013: Effectiveness of seedrow-placed N with polymer-coated and NBPT-treated urea for canola and wheat. *J. Plant Nutr.* **36**, 2205–2224.
- Manschadi, A. M., J. Christopher, P. de Voil, and G. L. Hammer, 2006: The role of root architectural traits in adaptation of wheat to water-limited environments. *Funct. Plant Biol.* **33**, 823–837.
- Manschadi, A. M., J. T. Christopher, G. L. Hammer, and P. de Voil, 2010: Experimental and modelling studies of drought-adaptive root architectural traits in wheat (*Triticum aestivum* L.). *Plant Biosyst.* **144**, 458–462.
- Manske, G. G. B., and P. L. G. Vlek, 2002: Root architecture-wheat as a model plant. In: Y. Waisel, A. Eshel, and U. Kafkafi (eds), *Plant Roots: The Hidden Half*, 3rd edn, 249–259. Marcel Dekker Inc., New York.
- Manske, G. G. B., R. K. Behl, A. B. Lutger, and P. L. G. Vlek, 2000: Enhancement of mycorrhizal infection, nutrient efficiency and plant growth by Azotobacter in wheat: evidence of varietal effects. In: N. Narula (ed.), *Azotobacter in Sustainable Agriculture*, 136–147. CBS Publishers, New Delhi, India.
- Manske, G. G. B., J. I. Ortiz-Monasterio, and P. L. D. Vlek, 2001: Techniques for measuring genetic diversity in roots. In: M. P. Reynolds, J. I. Ortiz-Monasterio, and A. McNab (eds), *Application of Physiology in Wheat Breeding*, 208–240. CIMMYT, D.F. Mexico.
- Mantelin, S., and B. Touraine, 2004: Plant growth promoting bacteria and nitrate availability: impacts on root development and nitrate uptake. *J. Exp. Bot.* **394**, 27–34.
- Mantelin, S., G. Desbrosses, M. Larcher, T. J. Tranbarger, J. C. Cleyet-Marel, and B. Touraine, 2006: Nitrate-dependent control of root architecture and N nutrition are altered by a plant growth-promoting *Phyllobacterium* sp. *Planta* **223**, 591–603.
- Martin, A., J. Lee, T. Kichey, D. Gerentes, M. Zivy, C. Tatou, T. Baliau, B. Valot, M. Davanture, F. Dubois, T. Tercé-Laforgue, M. Coque, A. Gallais, M. B. Gonzalez-Moro, L. Bethencourt, I. Quilleré, D. Z. Habash, P. J. Lea, A. Charcosset, P. Perez, A. Murigneux, H. Sakakibara, K. J. Edwards, and B. Hirel, 2006: Two cytosolic glutamine synthetase isoforms of maize (*Zea mays* L.) are specifically involved in the control of grain production. *The Plant Cell* **18**, 3252–3274.
- Marshner, H., 1995: *Mineral Nutrition of Higher Plants*. London Academic Press, London.
- Martre, P., J. R. Porter, P. D. Jamieson, and E. Triboi, 2003: Modeling grain nitrogen accumulation and protein composition to understand the Sink/Source regulations of nitrogen remobilization for wheat. *Plant Physiol.* **133**, 1959–1967.
- Martre, P., P. D. Jamieson, M. A. Semenov, R. F. Zyskowski, J. R. Porter, and E. Triboi, 2006: Modelling protein content and composition in relation to crop nitrogen dynamics for wheat. *Eur. J. Agron.* **25**, 138–154.
- Mathesius, U., 2009: Comparative proteomic studies of root-microbe interactions. *J. Proteomics* **72**, 353–366.
- Mazzola, M., D. L. Funnell, and J. M. Raaijmakers, 2004: Wheat cultivar-specific selection of 2,4-diacetylphloroglucinol-producing fluorescent *Pseudomonas* species from resident soil populations. *Microb. Ecol.* **48**, 338–348.
- McAllister, C. H., P. H. Beatty, and A. G. Good, 2012: Engineering nitrogen use efficient crop plants: the current status. *Plant Biotechnol. J.* **10**, 1011–1025.
- McCullough, D. E., and L. A. Hunt, 1993: Mature tissue and crop canopy respiratory characteristics of rye, triticale and wheat. *Ann. Bot.* **72**, 269–282.
- Mcintyre, C. L., R. E. Casu, A. Rattey, M. F. Dreccer, J. W. Kam, A. F. van Herwaarden, R. Shorter, and G. P. Xue, 2011: Linked gene networks involved in nitrogen and carbon metabolism and levels of water-soluble carbohydrate accumulation in wheat stems. *Funct. Integr. Genomics* **11**, 585–597.
- Metzner, R., A. Eggert, D. van Dusschoten, D. Pflugfelder, S. Gerth, U. Schurr, N. Uhlmann, and S. Jahnke, 2015: Direct comparison of MRI and X-ray CT technologies for 3D imaging of root systems in soil: potential and challenges for root trait quantification. *Plant Methods* **11**, 1–11.
- Meynard, J. M., 1987: L'analyse de l'élaboration du rendement dans les essais de fertilisation azotée. *Perspectives Agricoles* **115**, 76–83.
- Miller, A. J., and S. J. Smith, 1996: Nitrate transport and compartmentation in cereal root cells. *J. Exp. Bot.* **47**, 843–854.
- Miller, A. J., X. Fan, M. Orsel, S. J. Smith, and D. M. Wells, 2007: Nitrate transport and signaling. *J. Exp. Bot.* **58**, 2297–2306.
- Moënnelocoz, Y., P. Mavingui, C. Combes, P. Normand, and C. Steinberg, 2014: Microorganisms and biotic interactions. In: J. C. Bertrand, P. Caumette, P. Lebaron, and P. Normand (eds), *Environmental Microbiology: Fundamentals and Applications*. Springer, Dordrecht, The Netherlands (In Press).
- Molina-Favero, C., C. M. Creus, M. Simontacchi, S. Puntarulo, and L. Lamattina, 2008: Aerobic nitric oxide production by *Azospirillum brasilense* Sp245 and its influence on root architecture in tomato. *Mol. Plant Microbe Interact.* **21**, 1001–1009.
- Moll, R. H., E. J. Kamprath, and W. A. Jackson, 1982: Analysis and interpretation of factors which contribute to efficiency of nitrogen utilization. *Agronomy* **74**, 562–564.
- Monaghan, J. M., J. W. Snape, A. J. S. Chojecki, and P. S. Kettlewell, 2001: The use of grain protein deviation for identifying wheat cultivars with high grain protein concentration and yield. *Euphytica* **122**, 309–317.
- Monneveux, P., P. H. Zaidi, and C. Sanchez, 2005: Population density and low nitrogen affects yield-associated traits in tropical maize. *Crop Sci.* **45**, 535–545.
- Mooney, S. J., T. P. Pridmore, J. Helliwell, and M. J. Bennett, 2012: Developing X-ray computed tomography to non-invasively image 3-D root systems architecture in soil. *Plant Soil* **352**, 1–22.
- Moreau, D., V. Allard, O. Gaju, J. Le Gouis, M. J. Foulkes, and P. Martre, 2012: Acclimation of leaf nitrogen to vertical light gradient at anthesis in wheat is a whole-plant process that scales with the size of the canopy. *Plant Physiol.* **160**, 1479–1490.
- Morgan, C. L., R. B. Austin, M. A. Ford, J. Bingham, W. J. Angus, and S. Chowdhury, 1989: An evaluation of F1 hybrid winter wheat genotypes produced a chemical hybridizing agent. *J. Agric. Sci. Camb.* **112**, 143–149.
- Moubayidin, L., R. Di Mambro, and S. Sabatini, 2009: Cytokinin-auxin crosstalk. *Trends Plant Sci.* **14**, 557–562.
- Mühleisen, J., H. P. Piepho, H. P. Maurer, C. F. H. Longin, and J. C. Reif, 2014: Yield stability of hybrids versus lines in wheat, barley and triticale. *Theor. Appl. Genet.* **127**, 309–316.

- Munier-Jolain, N., and C. Salon, 2005: Are the carbon costs of seed production related to the quantitative and qualitative performance? An appraisal for legumes and other crops. *Plant Cell Environ.* **28**, 1388—1395.
- Murchie, E. H., and T. Lawson, 2013: Chlorophyll fluorescence analysis: a guide to good practice and understanding some new applications. *J. Exp. Bot.* **64**, 3983—3998.
- Murchie, E. H., M. Pinto, and P. Horton, 2009: Agriculture and the new challenges for photosynthesis research. *New Phytol.* **181**, 532—552.
- Muurinen, S., G. A. Slafer, and P. Peltonen Sainio, 2006: Breeding effects on nitrogen use efficiency of spring cereals under northern conditions. *Crop Sci.* **46**, 561—568.
- Nacry, P., E. Bouguyon, and A. Gojon, 2013: Nitrogen acquisition by roots: physiological and developmental mechanisms ensuring plant adaptation to fluctuating resources. *Plant Soil* **370**, 1—29.
- Nagel, K. A., A. Putz, F. Gilmer, K. Heinz, A. Fischbach, J. Pfeifer, M. Faget, S. Blossfeld, M. Ernst, C. Dimaki, B. Kastenholz, A. K. Kleintert, A. Galinski, H. Scharr, F. Fiorani, and U. Schurr, 2012: GROWSCREEN-Rhizo is a novel phenotyping robot enabling simultaneous measurements of root and shoot growth for plants grown in soil-filled rhizotrons. *Funct. Plant Biol.* **39**, 891—904.
- Naruoka, Y., J. D. Sherman, S. P. Lanning, N. K. Blake, J. M. Martin, and L. E. Talbert, 2012: Genetic analysis of green leaf duration in spring wheat. *Crop Sci.* **52**, 99—109.
- Nasholm, T., K. Kielland, and U. Ganeteg, 2009: Uptake of organic nitrogen by plants. *New Phytol.* **182**, 31—48.
- Neiverth, A., S. Delai, D. M. Garcia, K. Saatkamp, E. M. de Souza, F. de Oliveira Pedrosa, V. F. Guimarães, M. F. dos Santos, E. C. G. Vendruscolo, and A. C. T. da Costa, 2014: Performance of different wheat genotypes inoculated with the plant growth promoting bacterium *Herbaspirillum seropedicae*. *Eur. J. Soil Biol.* **64**, 1—5.
- Nelson, D. R., and P. M. Mele, 2006: The impact of crop residue amendments and lime on microbial community structure and nitrogen-fixing bacteria in the wheat rhizosphere. *Soil Res.* **44**, 319—329.
- Nguyen, C., 2003: Rhizodeposition of organic C by plants: mechanisms and controls. *Agronomy* **23**, 375—396.
- Nieder, R., D. K. Benbi, and H. W. Scherer, 2011: Fixation and defixation of ammonium in soils: a review. *Biol. Fertil. Soils* **47**, 1—14.
- Nigro, D., Y. Q. Gu, N. Huo, I. Marcotuli, A. Blanco, A. Gadaleta, and O. D. Anderson, 2013: Structural analysis of the wheat genes encoding NADH-dependent glutamine-2-oxoglutarate amidotransferases and correlation with grain protein content. *Plos One* **8**, e73751.
- Olivares-Villegas, J. J., M. P. Reynolds, and G. K. McDonald, 2007: Drought-adaptive attributes in the Seri/Babax hexaploid wheat population. *Funct. Plant Biol.* **34**, 189—203.
- Omasa, K., F. Hosoi, and A. Konishi, 2007: 3D lidar imaging for detecting and understanding plant responses and canopy structure. *J. Exp. Bot.* **58**, 881—898.
- Ortiz, R., H. J. Braun, J. Crossa, J. H. Crouch, G. Davenport, J. Dixon, S. Dreisigacker, E. Duveiller, Z. He, J. Huerta, A. K. Joshi, M. Kishii, P. Kosina, Y. Manes, M. Mezzalama, A. Morgounov, J. Murakami, J. Nicol, G. Ortiz Ferrara, I. Ortiz-Monasterio, T. S. Payne, R. J. Pena, M. P. Reynolds, K. D. Sayre, R. C. Sharma, R. P. Singh, J. Wang, M. Warburton, H. Wu, and M. Iwanaga, 2008: Wheat genetic resources enhancement by the International Maize and Wheat Improvement Center (CIMMYT). *Genet. Resour. Crop Evol.* **55**, 1095—1140.
- Ortiz-Castro, R., H. A. Contreras-Cornejo, L. Macías-Rodríguez, and J. López-Bucio, 2009: The role of microbial signals in plant growth and development. *Plant Signal Behav.* **4**, 701—712.
- Ortiz-Monasterio, I., K. D. Sayre, S. Rajaram, and M. McMahon, 1997: Genetic progress in wheat yield and nitrogen use efficiency under four N rates. *Crop Sci.* **37**, 898—904.
- O'Toole, J. C., and W. L. Bland, 1987: Genotypic variation in crop plant-root systems. *Adv. Agron.* **41**, 91—145.
- Oury, F.-X., and C. Godin, 2007: Yield and grain protein concentration in bread wheat: how to use the negative relationship between the two characters to identify favourable genotypes? *Euphytica* **157**, 45—57.
- Oury, F.-X., P. Brabant, P. Pluchard, P. Bérard, and M. Rousset, 1994: Une étude de la qualité des blés hybrides à travers différents tests technologiques. *Agronomy* **14**, 377—385.
- Oury, F.-X., E. Tribou, P. Bérard, J. L. Ollier, and M. Rousset, 1995: Etude des flux de carbone et d'azote chez des blés hybrides et leurs parents, pendant la période de remplissage du grain. *Agronomy* **15**, 193—204.
- Oury, F.-X., P. Bérard, M. Brancourt-Hulmel, C. Depatureaux, G. Doussinault, N. Galic, A. Giraud, E. Heumez, C. Lecomte, P. Pluchard, B. Rolland, M. Rousset, and M. Trottet, 2003: Yield and grain protein concentration in bread wheat: a review and a study of multi-annual data from a French breeding program. *J. Genet. Breed.* **57**, 59—68.
- Pace, G. M., and P. R. McClure, 1986: Comparison of nitrate uptake kinetic parameters across maize inbred lines. *J. Plant Nutr.* **8**, 1095—1111.
- Parry, M. A. J., P. J. Andralojc, R. A. C. Mitchell, P. J. Madgwick, and A. J. Keys, 2003: Manipulation of rubisco: its amount, activity, function and regulation. *J. Exp. Bot.* **54**, 1321—1333.
- Parry, M. A. J., M. Reynolds, M. E. Salvucci, C. Raines, P. J. Andralojc, X. G. Zhu, G. D. Price, A. G. Condon, and R. Furbank, 2011: Raising yield potential of wheat: (II) increasing photosynthetic capacity and efficiency. *J. Exp. Bot.* **62**, 453—468.
- Pask, A. J. D., 2009: Optimising nitrogen storage in wheat canopies for genetic reduction in fertiliser nitrogen inputs. PhD Thesis. University of Nottingham, UK.
- Pask, A. J. D., R. Sylvester-Bradley, P. D. Jamieson, and M. J. Foulkes, 2012: Quantifying how wheat crops accumulate and use N during growth. *Field Crops Res.* **126**, 104—118.
- Passioura, J., 1977: Grain yield, harvest index, and water use of wheat. *J. Aust. Inst. Agric. Sci.* **43**, 117—120.
- Passioura, J. B., 2006: The perils of pot experiments. *Funct. Plant Biol.* **33**, 1075—1079.
- Passioura, J. B., 2010: Scaling up: the essence of effective agricultural research. *Funct. Plant Biol.* **37**, 585—591.
- Pathak, R. R., S. Lochab, and N. Raghuram, 2011: Plant systems | Improving plant nitrogen-use efficiency. In: M. Moo-Young (ed.), *Comprehensive Biotechnology*, 2nd edn, Vol. 4, 209—218. Elsevier, Oxford.
- Perezin, M., M. Corbellini, M. Accerbi, P. Vaccino, and B. Borghi, 1998: Bread wheat: F1 hybrid performance and parental diversity estimates using molecular markers. *Euphytica* **100**, 273—279.
- Perin, L., L. Martínez-Aguilar, R. Castro-González, Estrada-de los Santos P., T. Cabellos-Avelar, H. V. Guedes, V. M. Reis, and J. Caballero-Mellado, 2006: Diazotrophic Burkholderia species associated with field-grown maize and sugarcane. *Appl. Environ. Microbiol.* **72**, 3103—3110.
- Phillips, D. A., T. C. Fox, M. D. King, T. V. Bhuvanewari, and L. R. Teuber, 2004: Microbial products trigger amino acid exudation from plant roots. *Plant Physiol.* **136**, 2887—2894.
- Plett, D., J. Toubia, T. Garnett, M. Tester, B. N. Kaiser, and U. Baumann, 2010: Dichotomy in the NRT gene family of dicots and grass species. *PLoS One* **5**, e15289.
- Polomski, J., and N. Kuhn, 2002: Root research methods. In: Y. Waisel, A. Eshel, and U. Kafkafi (eds), *Plant Roots: The Hidden Half*, 3rd edn, 300—306. Marcel Dekker Inc., New York.
- Poorter, H., J. Bühler, D. van Dusschoten, J. Climent, and J. A. Postma, 2012: Pot size matters: a meta-analysis of the effects of rooting volume on plant growth. *Funct. Plant Biol.* **39**, 839—850.
- Pothier, J. F., C. Prigent-Combaret, J. Haurat, Y. Moëgne-Loccoz, and F. Wisniewski-Dyé, 2008: Duplication of plasmid-borne nitrite reductase gene nirK in the wheat-associated plant growth-promoting rhizobacterium *Azospirillum brasilense* Sp245. *Mol. Plant Microbe Interact.* **21**, 831—842.
- Prasad, P. V. V., P. Q. Craufurd, and R. J. Summerfield, 1999: Fruit number in relation to pollen production and viability in groundnut exposed to short episodes of heat stress. *Ann. Bot.* **84**, 381—386.
- Price, A. H., J. Townend, M. P. Jones, A. Audebert, and B. Courtois, 2002: Mapping QTLs associated with drought avoidance in upland rice grown in the Philippines and West Africa. *Plant Mol. Biol.* **48**, 683—695.
- Prigent-Combaret, C., D. Blaha, J. F. Pothier, L. Vial, M. A. Poirier, F. Wisniewski-Dyé, and Y. Moëgne-Loccoz, 2008: Physical organization

- and phylogenetic analysis of *acdR* as leucine-responsive regulator of the 1-aminocyclopropane-1-carboxylate deaminase gene *acdS* in phyto-beneficial *Azospirillum lipoferum* 4B and other Proteobacteria. *FEMS Microbiol. Ecol.* **65**, 202–219.
- Przystalski, M., A. Osman, E. M. Thiemt, B. Rolland, L. Ericsson, H. Østergård, L. Levy, M. Wolfe, A. Büschse, H.-P. Piepho, and P. Krajewski, 2008: Comparing the performance of cereals varieties in organic and non-organic cropping systems in different European countries. *Euphytica* **163**, 417–433.
- Quraishi, U. M., M. Abrouk, F. Murat, C. Pont, S. Foucrier, G. Demai-zieres, C. Confolent, N. Rivière, G. Charmet, E. Paux, A. Murigenux, L. Guerreiro, S. Lafarge, J. Le Gouis, C. Feuillet, and G. Salse, 2011: Cross-genome map based dissection of a nitrogen use efficiency ortho-meta QTL in bread wheat unravels concerted cereal genome evolution. *Plant J.* **65**, 745–756.
- Ravel, C., P. Martre, I. Romeuf, M. Dardevet, R. El-Malki, J. Bordes, N. Duchateau, D. Brunel, F. Balfourier, and G. Charmet, 2009: Nucleo-tide polymorphism in the wheat transcriptional activator *Spa* influences its pattern of expression and has pleiotropic effects on grain protein composition, dough viscoelasticity, and grain hardness. *Plant Physiol.* **151**, 2133–2144.
- Rawluk, C. D. L., G. J. Racz, and C. A. Grant, 2000: Uptake of foliar or soil application of 15N-labelled urea solution at anthesis and its effect on wheat grain yield and protein. *Can. J. Plant Sci.* **80**, 331–334.
- Reardon, C. L., H. T. Gollany, and S. B. Wuest, 2014: Diazotroph community structure and abundance in wheat–fallow and wheat–pea crop rotations. *Soil Biol. Biochem.* **69**, 406–412.
- Rebetzke, G. J., and R. A. Richards, 1999: Genetic improvement of early vigour in wheat. *Aust. J. Agric. Res.* **50**, 291–301.
- Reynolds, M. P., M. Van Ginkel, and J. M. Ribaut, 2000: Avenues for genetic modification of radiation use efficiency in wheat. *J. Exp. Bot.* **51**, 459–473.
- Reynolds, M. P., F. Dreccer, and R. Trethowan, 2007: Drought-adaptive traits derived from wheat wild relatives and landraces. *J. Exp. Bot.* **58**, 177–186.
- Reynolds, M. P., Y. Manes, A. Izanloo, and P. Langridge, 2009: Phenotyping for physiological breeding and gene discovery in wheat. *Ann. Appl. Biol.* **155**, 309–320.
- Richard, C. A. I., L. T. Hickey, S. Fletcher, R. Jennings, K. Chenu, and J. T. Christopher, 2015: High-throughput phenotyping of seminal root traits in wheat. *Plant Methods* **11**, 1–13.
- Richardson, A. E., J. M. Baréa, A. M. McNeill, and C. Prigent-Com-baret, 2009: Acquisition of phosphorus and nitrogen in the rhizosphere and plant growth promotion by microorganisms. *Plant Soil* **321**, 305–339.
- Robertson, G. P., and P. M. Vitousek, 2009: Nitrogen in agriculture: bal-ancing the cost of an essential resource. *Annu. Rev. Environ. Res.* **34**, 97–125.
- Robinson, D., 2001: Root proliferation, nitrate inflow and their carbon costs during nitrogen capture by competing plants in patchy soil. *Plant Soil* **232**, 41–50.
- Romer, C., K. Bürling, M. Hunsche, T. Rumpf, G. Noga, and L. Plümer, 2011: Robust fitting of fluorescence spectra for pre-symptomatic wheat leaf rust detection with support vector machines. *Comput. Electron. Agric.* **79**, 180–188.
- Ruuska, S. A., D. C. Lewis, G. Kennedy, R. T. Furbank, C. L. D. Jenk-ins, and L. M. Tabe, 2008: Large scale transcriptome analysis of the effects of nitrogen nutrition on accumulation of stem carbohydrate reserves in reproductive stage wheat. *Plant Mol. Biol.* **66**, 15–32.
- Sadras, V. O., and G. Lemaire, 2014: Quantifying crop nitrogen status for comparisons of agronomic practices and genotypes. *Field Crops Res.* **164**, 54–64.
- Sadras, V. O., and R. A. Richards, 2014: Improvement of crop yield in dry environments: benchmarks, levels of organisation and the role of nitrogen. *J. Exp. Bot.* **65**, 1981–1995.
- Saint Pierre, C., J. Crossa, Y. Manes, and M. P. Reynolds, 2010: Gene action of canopy temperature in bread wheat under diverse environ-ments. *Theor. Appl. Genet.* **120**, 1107–1117.
- Sakakibara, Y., H. Kimura, A. Iwamura, T. Saitoh, T. Ikegami, G. Kur-isu, and T. Hase, 2012: A new structural insight into differential inter-action of cyanobacterial and plant ferredoxins with nitrite reductase as revealed by NMR and X-ray crystallographic studies. *J. Biochem.* **151**, 483–492.
- Salse, J., U. M. Quraishi, C. Pont, F. Murat, J. Le Gouis, and S. Lafarge, 2013: Grain Filling of a Plant Through the Modulation of NADH-Glu-tamate Synthase. US patent 20130047300 A1.
- Sarcevic, H., K. Jukic, I. Ikić, and A. Lovric, 2014: Estimation of quanti-tative genetic parameters for grain yield and quality in winter wheat under high and low nitrogen fertilization. *Euphytica* **199**, 57–67.
- Schneider, C. A., W. S. Rasband, and K. W. Eliceiri, 2012: NIH image to ImageJ: 25 years of image analysis. *Nat. Methods* **9**, 671–675.
- Semenov, M. A., P. D. Jamieson, and P. Martre, 2007: Deconvoluting nitrogen use efficiency in wheat: a simulation study. *Eur. J. Agron.* **26**, 283–294.
- Sétif, P., M. Hirasawa, N. Cassan, B. Lagoutte, J. N. Tripathy, and D. B. Knaff, 2009: New insights into the catalytic cycle of plant nitrite reductase. Electron transfer kinetics and charge storage. *Biochemistry* **48**, 2828–2838.
- Sharma, S., S. Xu, B. Ehdai, A. Hoops, T. J. Close, A. J. Lukaszewski, and J. G. Waines, 2011: Dissection of QTL effects for root traits using a chromosome arm-specific mapping population in bread wheat. *Theor. Appl. Genet.* **122**, 759–769.
- Shearman, V. J., R. Sylvester-Bradley, and M. J. Foulkes, 2005: Physio-logical processes associated with wheat yield progress in the UK. *Crop Sci.* **45**, 175–185.
- Shewry, P. R., and N. G. Halford, 2002: Cereal seed storage proteins: structures, properties and role in grain utilisation. *J. Exp. Bot.* **53**, 947–958.
- Shrawat, A. K., R. T. Carroll, M. DePauw, G. J. Taylor, and A. G. Good, 2008: Genetic engineering of improved nitrogen use efficiency in rice by the tissue-specific expression of alanine aminotransferase. *Plant Biotechnol. J.* **6**, 337–345.
- Siddiqi, M. Y., A. D. M. Glass, T. J. Ruth, and T. W. Rufty, 1990: Stud-ies of the uptake of nitrate in barley. *Plant Physiol.* **93**, 1426–1432.
- Silva, S. A., F. I. F. de Carvalho, V. R. Caetano, A. C. Oliveira, J. L. M. Coimbra, N. J. S. Vasconcelos, and C. Lorencetti, 2000: Genetic basis of stay-green trait in bread wheat. *J. New Seeds* **2**, 55–68.
- Simmonds, N. W., 1995: The relation between yield and protein in cereal grain. *J. Sci. Food Agric.* **67**, 309.
- Simons, M., R. Saha, L. Guillard, G. Clément, P. Armengaud, R. Cañas, C. D. Maranas, P. J. Lea, and B. Hirel, 2014: Nitrogen use efficiency in maize (*Zea mays* L.): from omics studies to metabolic modelling. *J. Exp. Bot.* **65**, 5657–5671.
- Sinclair, T. R., and J. Amir, 1992: A model to assess nitrogen limitations on the growth and yield of spring wheat. *Field Crops Res.* **30**, 63–78.
- Sinclair, T. R., and T. Horie, 1989: Leaf nitrogen, photosynthesis, and crop radiation use efficiency: a review. *Crop Sci.* **29**, 90–98.
- Søgaard, R., M. Alstertfjord, N. MacAulay, and T. Zeuthen, 2009: Ammonium ion transport by the AMT/Rh homolog TaAMT1;1 is stimulated by acidic pH. *Pflügers Arch.* **458**, 733–743.
- Srivastava, S., V. Chaudhry, A. Mishra, P. S. Chauhan, A. Rehman, A. Yadav, N. Tuteja, and C. S. Nautiyal, 2012: Gene expression profiling through microarray analysis in *Arabidopsis thaliana* colonized by *Pseudomonas putida* MTCC5279, a plant growth promoting rhizobac-terium. *Plant Signal Behav.* **7**, 235–245.
- Subbarao, G. V., T. Ban, M. Kishii, O. Ito, H. Samejima, H. Y. Wang, S. J. Pearce, S. Gopalakrishnan, K. Nakahara, A. K. M. Zakir Hossain, H. Tsujimoto, and W. L. Berry, 2007: Can biological nitrification inhibition (BNI) genes from perennial *Leymus racemosus* (Triticeae) combat nitrification in wheat farming? *Plant Soil* **299**, 55–64.
- Sun, J. J., Y. Guo, G. Z. Zhang, M. G. Gao, G. H. Zhang, F. M. Kong, Y. Zhao, and S. S. Li, 2013: QTL mapping for seedling traits under different nitrogen forms in wheat. *Euphytica* **191**, 317–331.
- Suzuki, A., and D. B. Knaff, 2005: Glutamate synthase: structural, mech-anistic and regulatory properties, and role in the amino acid metabo-lism. *Photosynth. Res.* **83**, 191–217.

- Sylvester-Bradley, R., and D. R. Kindred, 2009: Analysing nitrogen responses of cereals to prioritize routes to the improvement of nitrogen use efficiency. *J. Exp. Bot.* **60**, 1939–1951.
- Sylvester-Bradley, R., D. T. Stokes, R. K. Scott, and V. B. A. Willington, 1990: A physiological analysis of the diminishing responses of winter wheat to applied nitrogen. 2. Evidence. *Aspects Appl. Biol.* **25**, 289–300.
- Swarbreck, S. M., M. Defoin-Platel, M. Hindle, M. Saqi, and D.Z. Habash, 2011: New perspectives on glutamine synthetase in grasses. *J. Exp. Bot.* 1511–1522.
- Takahashi, M., Y. Sasaki, I. Shoji, and S. Morikawa, 2001: Nitrite reductase gene enrichment improves assimilation of NO₂ in Arabidopsis. *Plant Physiol.* **126**, 731–741.
- Tardieu, F., 2013: Plant response to environmental conditions: assessing potential production, water demand, and negative effects of water deficit. *Front. Physiol.* **4**, 17.
- Tenea, G. N., F. Cordeiro Raposo, and A. Maquet, 2012: Comparative transcriptome profiling in winter wheat grown under different agricultural practices. *J. Agric. Food Chem.* **60**, 10970–10978.
- Tercé-Laforgue, T., M. Bedu, C. Dargel-Graffin, F. Dubois, Y. Gibon, F. M. Restivo, and B. Hirel, 2013: Resolving the role of plant glutamate dehydrogenase: II. Physiological characterization of plants overexpressing individually or simultaneously the two enzyme subunits. *Plant Cell Physiol.* **54**, 1634–1647.
- Tester, M., and P. Langridge, 2010: Breeding technologies to increase crop production in a changing world. *Science* **327**, 818–822.
- Tétard-Jones, C., P. N. Shotton, L. Rempelos, J. Cooper, M. Eyre, C. H. Orr, C. Leifert, and A. M. R. Gatehouse, 2013: Quantitative proteomics to study the response of wheat to contrasting fertilisation regimes. *Mol. Breed.* **31**, 379–393.
- Thomas, H., and C. M. Smart, 1993: Crops that stay green. *Ann. Appl. Biol.* **123**, 193–219.
- Thomsen, H. C., D. Erikson, I. S. Møller, and J. K. Schoerring, 2014: Cytosolic glutamine synthetase: a target for improvement of crop nitrogen use efficiency. *Trends Plant Sci.* **19**, 656–663.
- Thorne, G. N., W. Pearman, W. Day, and A. D. Todd, 1988: Estimation of radiation interception by winter wheat from measurements of leaf area. *J. Agric. Sci. Camb.* **110**, 101–108.
- Trachsel, S., S. Kaeppler, K. Brown, and J. Lynch, 2011: Shovelomics: high throughput phenotyping of maize (*Zea mays* L.) root architecture in the field. *Plant Soil* **341**, 75–87.
- Triboi, E., and J. Ollier, 1991: Kinetic and role of carbon and nitrogen stored in stem on 21 wheat genotypes. *Agronomy* **11**, 239–246.
- Uauy, C., A. Distelfeld, T. Fahima, A. Blechl, and J. Dubcovsky, 2006: A NAC gene regulating senescence improves grain protein, zinc, and iron content in wheat. *Science* **314**, 1298–1301.
- Upadhyay, S. K., D. P. Singh, and R. Saikia, 2009: Genetic diversity of plant growth promoting rhizobacteria isolated from rhizospheric soil of wheat under saline condition. *Curr. Microbiol.* **59**, 489–496.
- Vamerali, T., M. Bandiera, and G. Mosca, 2012: Minirhizotrons in modern root studies. In: S. Mancuso (ed.), *Measuring Roots*, 341–362. Springer-Verlag, Berlin Heidelberg, Berlin.
- Van Oosterom, E. J., A. K. Borrell, S. C. Chapman, I. J. Broad, and G. L. Hammer, 2010a: Functional dynamics of the nitrogen balance of sorghum: I. N demand of vegetative plant parts. *Field Crops Res.* **115**, 19–28.
- Van Oosterom, E. J., S. C. Chapman, A. K. Borrell, I. J. Broad, and G. L. Hammer, 2010b: Functional dynamics of the nitrogen balance of sorghum: II. Grain filling period. *Field Crops Res.* **115**, 29–38.
- Venieraki, A., M. Dimou, P. Pergalis, I. Kefalogianni, I. Chatzipavlidis, and P. Katinakis, 2011: The genetic diversity of culturable nitrogen-fixing bacteria in the rhizosphere of wheat. *Microb. Ecol.* **61**, 277–285.
- Veresoglou, S. D., and G. Menexes, 2010: Impact of inoculation with *Azospirillum* spp. on growth properties and seed yield of wheat: a meta-analysis of studies in the ISI Web of Science from 1981 to 2008. *Plant Soil* **337**, 469–480.
- Verma, V., M. J. Foulkes, P. Caligari, R. Sylvester-Bradley, and J. Snape, 2004: Mapping quantitative trait loci for flag leaf senescence as a yield determinant in winter wheat under optimal and drought-stressed environments. *Euphytica* **135**, 255–263.
- Von Wirén, N., and M. Merrick, 2004: Regulation and function of ammonium carriers in bacteria, fungi and plants. *Top. Curr. Genet.* **9**, 95–120.
- Von Wirén, N., S. Gazzarini, and W. B. Frommer, 1997: Regulation of mineral uptake in plants. *Plant Soil* **196**, 191–199.
- Vouilliot, M. O., J. M. Machet, and J. M. Meynard, 1996: Relationship between the amount of reduced nitrogen accumulated in winter wheat shoots and the activity of nitrate reductase measured in situ. *Eur. J. Agron.* **5**, 227–236.
- Walk, T., R. Jaramillo, and J. P. Lynch, 2006: Architectural tradeoffs between adventitious and basal roots for phosphorus acquisition. *Plant Soil* **279**, 347–366.
- Walker, V., O. Couillerot, A. Von Felten, F. Bellvert, J. Jansa, M. Maurhofer, R. Bally, Y. Moëne-Loccoz, and G. Comte, 2012: Variation of secondary metabolite levels in maize seedling roots induced by inoculation with *Azospirillum*, *Pseudomonas* and *Glomus* consortium under field conditions. *Plant Soil* **356**, 151–163.
- Wan, Y., P. R. Shewry, and M. J. Hawkesford, 2013: A novel family of γ -gliadin genes are highly regulated by nitrogen supply in developing wheat grain. *J. Exp. Bot.* **64**, 161–168.
- Wang, M. Y., M. Y. Siddiqi, T. J. Ruth, and A. D. M. Glass, 1993: Ammonium uptake by rice roots (II. Kinetics of $^{13}\text{NH}_4^+$ influx across the plasmalemma). *Plant Physiol.* **103**, 1259–1267.
- Wang, Z. K., Z. F. Ni, H. L. Wu, X. L. Nie, and Q. X. Sun, 2006: Heterosis in root development and differential gene expression between hybrids and their parental inbreds in wheat (*Triticum aestivum* L.). *Theor. Appl. Genet.* **113**, 1283–1294.
- Wang, Y. Y., D. Wong, K. Forrest, A. Allen, S. Chao, B. E. Huang, M. Maccaferri, S. Salvi, S. G. Milner, L. Cattivelli, A. M. Mastrangelo, A. Whan, S. Stephen, G. Barker, R. Wieseke, J. Plieske, International Wheat Genome Sequencing Consortium, M. Lillemo, D. Mather, R. Appels, R. Dolferus, G. Brown-Guedira, A. Korol, A. R. Akhunova, C. Feuillet, J. Salse, M. Morgante, C. Pozniak, M. C. Luo, J. Dvorak, M. Morell, J. Dubcovsky, M. Ganal, R. Tuberosa, C. Lawley, I. Mikoulitch, C. Cavanagh, K. J. Edwards, M. Hayden and E. Akhunov 2014: Characterization of polyploid wheat genomic diversity using a high-density 90 000 single nucleotide polymorphism array. *Plant Biotechnol J* **12**, 787–796.
- Wang, Y. Y., P. K. Hsu, and Y. F. Tsay, 2012a: Uptake, allocation and signaling of nitrate. *Trends Plant Sci.* **17**, 458–467.
- Wang, W. H., B. Köhler, F. Q. Cao, G. W. Liu, Y. Y. Gong, S. Sheng, Q. C. Song, X. Y. Cheng, T. Garnett, M. Okamoto, R. Qin, B. Mueller-Rober, M. Tester, and L. H. Liu, 2012b: Rice DUR3 mediates high-affinity urea transport and plays an effective role in improvement of urea acquisition and utilisation when expressed in *Arabidopsis*. *New Phytol.* **193**, 432–444.
- Wasson, A. P., G. J. Rebetzke, J. A. Kirkegaard, J. Christopher, R. A. Richards, and M. Watt, 2014: Soil coring at multiple field environments can directly quantify variation in deep root traits to select wheat genotypes for breeding. *J. Exp. Bot.* **65**, 6231–6249.
- White, J. W., P. Andrade-Sanchez, M. A. Gore, K. F. Bronson, T. A. Coffelt, M. M. Conley, K. A. Feldmann, A. N. French, J. T. Heun, D. J. Hunsaker, M. A. Jenks, B. A. Kimball, R. L. Roth, R. J. Strand, K. R. Thorp, G. W. Wall, and G. Wang, 2012: Field-based phenomics for plant genetics research. *Field Crops Res.* **133**, 101–112.
- Witte, C. P., 2011: Urea metabolism in plants. *Plant Sci.* **180**, 431–438.
- Wojciechowski, T., M. J. Gooding, L. Ramsay, and P. J. Gregory, 2009: The effects of dwarfing genes on seedling root growth of wheat. *J. Exp. Bot.* **60**, 2565–2573.
- Wu, H., T. Haig, J. Pratley, D. Lemerle, and M. An, 2001: Allelochemicals in wheat (*Triticum aestivum* L.): cultivar difference in the exudation of phenolic acids. *J. Agric. Food Chem.* **49**, 3742–3745.
- Xu, G., X. Fan, and T. Miller, 2012: Plant nitrogen assimilation and use efficiency. *Annu. Rev. Plant Biol.* **63**, 153–182.
- Xu, Y., R. Wang, Y. Tong, H. Zhao, Q. Xie, D. Liu, A. Zhang, B. Li, H. Xu, and D. An, 2013: Mapping QTL for yield and nitrogen-related traits in wheat: influence of nitrogen and phosphorus fertilization on QTL expression. *Theor. Appl. Genet.* **127**, 59–72.

- Yamaya, T., and M. Kusano, 2014: Evidence supporting distinct functions of three cytosolic glutamine synthetases and two NADH-glutamate synthases in rice. *J. Exp. Bot.* **65**, 5519—5525.
- Yin, L. P., P. Li, B. Wen, D. Taylor, and J. O. Berry, 2007: Characterization of a high-affinity nitrate system transporter gene (*TaNRT2.1*) from wheat roots and its evolutionary relationship to other *NRT2* genes. *Plant Sci.* **172**, 621—631.
- Zhang, C., and J. M. Kovacs, 2012: The application of small unmanned aerial systems for precision agriculture: a review. *Precision Agric.* **13**, 693—712.
- Zheng, B. S., J. Le Gouis, M. Leflon, W. Y. Rong, A. Laperche, and M. Brancourt-Hulmel, 2010: Using probe genotypes to dissect QTL × environment interactions for grain yield components in winter wheat. *Theor. Appl. Genet.* **121**, 1501—1517.
- Zhao, X. Q., Z. H. Nie, and X. G. Xiao, 2013: Over-expression of a tobacco nitrate reductase gene in wheat (*Triticum aestivum L.*) increases seed protein content and weight without augmenting nitrogen supply. *Plos One* **8**, e74678.
- Zhu, X. G., S. P. Long, and D. R. Ort, 2010: Improving photosynthetic efficiency for greater yield. *Annu. Rev. Plant Biol.* **61**, 235—261.