**Mixing varieties mitigates early root competition in wheat under water and nutrient limitation**

**Running title: mixing varieties mitigates root competition in wheat**

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# Highlight

Wheat varieties with high root projected area in pure stands experience a strong relaxation of belowground competition in mixtures at the seedling stage under resource-limited conditions.

# Abstract

Competition between plants can lead to a Tragedy of the Commons (TOCs) where over-investments into resource harvesting organs reduce collective performance. Mixing different crop varieties could resolve such TOCs and thus maintain high productivity while increasing within field diversity because varieties might have different resource requirements (niche complementarity effect) or because the most competitive varieties benefit from being mixed with weaker competitors (selection effect). So far, most studies on varietal mixtures have focused on the aboveground compartment, and relatively little is known about belowground competition due to difficulties in accessing root traits. In the present study, we grew durum wheat (*Triticum turgidum* ssp. *durum*) varietal mixtures in a high-throughput root phenotyping platform to characterize early-stage belowground competition between varieties. We grew 36 varieties in pure stands and in 54 binary mixtures under both controlled conditions (R+) and water and nutrient limitation (R-). Seedlings in mixed stands produced less biomass than predicted from their pure stands in R-, which mainly resulted from a negative complementarity effect. About 50% of this biomass reduction was explained by the average projected area of the root systems of the two varieties in pure stands. Instead of a negative interaction between varieties, our results indicate that this negative complementarity effect reflected a relaxation of competition in mixed stands: varieties with high root projected area were strong competitors that over-invested in belowground organs in pure stands. They benefited from having, on average, a weaker competitor than themselves in mixed stands and thus disengaged from the arms race for biomass accumulation. Our results suggest that root area is a promising breeding targets to reduce intra-specific competition and a key trait to consider for mixture assembly.

# Keywords

Agroecology, arms race, competitive hierarchy, high-throughput root phenotyping, niche complementarity, relative yield, root projected area, tragedy of the commons, varietal mixtures, wheat

# Abbreviations

CE: complementarity effects; RY: Relative Yield; RYT: Relative Yield Total; SE: selection effect

# Introduction

Competition for resources is a fundamental determinant of plant phenotypes and plant community dynamics (Tilman, 2020). A plant's survival, growth and reproduction can be reduced by highly competitive neighbours that absorb and use resources more quickly and/or more efficiently. To deal with such situations, plants have evolved various mechanisms to detect the presence of neighbours and/or the early exhaustion of resources, and to react by becoming more efficient at capturing resources or more conservative with their own resources (Pierik *et al.*, 2013). For example, plants can anticipate light competition by detecting changes in the red:far-red ratios of reflected and transmitted light on the leaves of their neighbours (Ballaré *et al.*, 1990). These changes in light quality in turn trigger a series of phenotypic changes, known as the shade avoidance syndrome, which ultimately lead to more vertical growth in order to out-compete neighbours, e.g., increased plant height or hyponastia of leaves (Ballaré and Pierik, 2017). Similarly, competition for belowground resources (water or nutrients) can lead to root proliferation in the presence of a competitor (Robinson *et al.*, 1999; Gersani *et al.*, 2001), which can be triggered either by early detection of resource depletion, or by the detection of chemical markers from the competitors (Schenk, 2006; Pierik *et al.*, 2013).

While such responses primarily evolved to maximize individual plant fitness under competition, they can lead to a competitive arms race between individuals, and ultimately decrease fitness at the scale of the group, which is known as a Tragedy of the Commons (TOCs, Hardin, 1968). This reduction in collective performance results from two effects: resources allocated to competitive organs are diverted from reproduction, and all individuals suffer from an intense pressure on the resources from their neighbours. Such trajectories have important implications for agriculture, as intense competition between adjacent plants from the same species can reduce yield per unit area (Anten and Vermeulen, 2016). This was notoriously identified by agronomists and plant breeders in the context of the Green Revolution: intra-specific competition, especially for light, becomes a strong determinant of yield in a typical high density cereal cropping system with low weed pressure and high fertilizer and pesticide inputs (Donald, 1963, 1968; Jennings and de Jesus, 1968). This observation led to the emergence of a new paradigm for plant breeding based on the idea that selection should target varieties with weak competitive abilities, because such varieties can be grown at high density without wasting resources into competition (Donald, 1968). The major yield gains achieved with the introduction of dwarfing genes contributed to validate this paradigm as these genes mainly reduced above ground plant stature and, *de facto*, the intensity of intra specific competition (Donald, 1968; Jennings and Herrera, 1968).

Transitioning towards low-input farming practices, notably by reducing the use of fertilizers, will reduce the amount of nutrients readily available for plants, and as such, will exacerbate the relative effect of belowground compared to aboveground intra-specific competition. When plants compete for soil resources, game theory models predict that individuals will over-invest in root biomass, i.e., they will continue allocating biomass in the roots even when the cost of the root system starts outweighing the benefits associated with the increased access to soil resources, leading to a Tragedy of the Commons (Hardin, 1968; Zhang *et al.*, 1999; Gersani *et al.*, 2001; Anten and Vermeulen, 2016). Multiple empirical evidences support this prediction: overinvestment in roots in response to competition has been shown to reduce final aboveground biomass in wheat (Zhu *et al.*, 2019) and soybean (Gersani *et al.*, 2001). Topsoil root production also negatively correlates with grain yields in oats and barley (Vain *et al.*, 2023). Thus, resolving belowground TOC might be key to maintain high yields under low input farming practices.

Belowground TOCs could be resolved by conducting direct selection on root architectural and morphological traits, e.g., by selecting smaller root systems with narrower angles as early proposed by Donald (1968). Direct selection on the size of resource-foraging organs in the aboveground compartment was very efficient to increase yield in the past, as exemplified with dwarfing genes. However, because they are much less visible, root traits received less explicit attention (Anten and Vermeulen, 2016). Even with modern phenotyping tools, direct selection on root traits might be challenging and costly, and we only have little information on how these traits respond to selection (Kuijken *et al.*, 2015). Alternatively, one could use the principles that prevent the evolution of TOCs in natural ecosystems, notably group selection and kin selection, and apply them in plant breeding to select crops that have less competitive (or more cooperative) root systems, which is the core idea of Darwinian Agriculture and Evolutionary Agroecology (Denison *et al.*, 2003; Weiner *et al.*, 2017). Theoretical models suggest that these evolutionary principles can be used to avoid TOCs and to select more cooperative crops (Montazeaud *et al.*, 2020; Biernaskie, 2022). However, they are not straightforward to implement in practice, and they rely on high genetic relatedness between individuals, meaning that they produce varieties in which individuals are genetically homogeneous. Both ecological and agronomic research, in contrast, suggest that there are multiple benefits to increase genetic diversity within crop stands. For example, mixing different varieties in the same field can be very efficient at limiting pathogen spreads and disease severity (Wolfe, 1985; Mundt *et al.*, 1995; Zhu *et al.*, 2000; Finckh and Wolfe, 2006), and, on average, varietal mixtures yield 2-5% more than expected on the basis of their pure stand components, which is known as overyielding (Kiær *et al.*, 2009; Borg *et al.*, 2018; Reiss and Drinkwater, 2018; Beillouin *et al.*, 2021).

Reducing intra-specific competition for resources while increasing genetic diversity in the field could thus be the most optimal way to take advantage of intra-specific plant-plant interactions in agriculture. Two ecological mechanisms are known to reduce competition in diversified plant communities: the niche complementarity effect and the selection effect (Loreau and Hector, 2001). The niche complementarity effect results from differences in ecological niches between species that have different resource requirements and hence experience less competition (MacArthur and Levins, 1967), which ultimately translates into a higher biomass production in mixture (e.g., Roscher et al. 2008; Mueller et al. 2013). In natural plant communities, rooting depth differences between species are believed to be a major driver of belowground complementarity effects (Parrish and Bazzaz, 1976; Mueller *et al.*, 2013). While rooting depth differences have never been associated with complementarity effects in varietal mixtures (Montazeaud *et al.*, 2018), complementarity spatial root distribution can improve water and nutrient uptake in more complex crop assemblages that associate species with contrasted root architectures (Postma and Lynch, 2012; Schmutz and Schöb, 2023). In addition to complementarity effects, selection effects can generate overyielding by favouring species that are the most productive. Through positive selection effects, these species are even more productive in the mixture than in the pure stands, i.e., they are “selected” by the mixture, which they rapidly dominate (Loreau and Hector, 2001). For example, competitive species can benefit from relaxed competition in mixture because the mixture allows them to escape an arms race with themselves. If the dominant species gains more yield or biomass than the sub-dominant loses, it can generate overyielding. Such an effect has for example been shown to contribute to overyielding in tree communities (Schmid and Niklaus, 2017; Williams *et al.*, 2017) and in inter-specific crop mixtures (Li *et al.*, 2018). Selection effects can be driven by belowground traits conferring dominance to particular plant types, e.g., in grassland communities grown under dry conditions, overyielding is driven by the dominance of deep-rooting species (Bakker *et al.*, 2019).

Belowground TOCs could thus be resolved by increasing plant diversity in the field, which could promote ecological effects such as complementarity and selection effects. In natural plant communities, these effects are heavily dependent on the level of resources available for the plants. For example, complementarity effects are on average stronger under low nutrient conditions in grasslands (Craven *et al.*, 2016), which aligns with the more general observation that positive plant-plant interactions tend to be stronger under harsher environments (i.e., the stress-gradient hypothesis, Bertness and Callaway, 1994; Maestre *et al.*, 2009). These observations suggest that varietal mixtures could hold interesting promises for future agriculture, providing not only adaptations to input reductions but also to environmental stresses such as drought. However, we still know very little about the ecological mechanisms at play in varietal mixtures, especially belowground, and how they are affected by resource availability (Borg *et al.*, 2018).

In the present study, we investigated the potential of varietal mixtures to reduce intra-specific belowground competition at the seedling stage in durum wheat (*Triticum turgidum* ssp*. durum*). We used a panel of 36 varieties previously shown to exhibit contrasted responses to combined water and nitrogen limitation, and grew them in monogenotypic pots and binary mixtures under highly controlled climate condition in a high throughput root phenotyping platform under both non-limiting and limiting water and nutrient conditions. We hypothesized that (i) root responses to neighbours are already expressed at the seedling stage, (ii) such responses are more important under resource limited conditions, (iii) overinvestment in biomass at the seedling stage reflects a response to neighbour competition (iv) varietal mixtures can mitigate such responses either through complementarity or selection effects

# Material and Methods

## Plant material

This study made use of field data collected on a diversity panel of 250 durum wheat genotypes, which was assembled during the EU Project SolACE (<https://www.solace-eu.net/>) to analyse wheat responses to combined water and nitrogen limitations (Collet, 2022). This panel comprised genotypes from four different collections (Collet, 2022) (i) “CREA”, with Italian cultivars, worldwide cultivars, and breeding lines selected by CREA (Consiglio per la Ricercar in agricoltura e l’analisi dell’Economia Agraria, Italy); (ii) “EPO”, an highly diverse collection of fixed lines derived from an evolutionary pre-breeding population (David et al 2014); (iii) “GPDUR”, with old and modern cultivars from various geographic areas including Western Europe; (iv) “UNIBO”, a diversity panel comprising genotypes from pre-breeding programs, elite lines, and representative genotypes of several worldwide breeding programs since the 1970s. Based on both field and platform data, a subset of 36 genotypes exhibiting contrasted yield responses to resource availability (i.e., ranging from stable to unstable yields) was selected by the European consortium to perform further experiments. Information on the 36 genotypes can be found in Supplementary Table 1.

## Experimental design

Based on the 36 genotypes, we designed a set of 54 binary mixtures selected at random, with each genotype observed in three different mixtures (Supplementary Table 2). Pure stands (here referring to groups of a single genotype, n = 36) and mixtures (here referring to groups of two genotypes, n = 54) were grown in RhizoTubes® (Jeudy *et al.*, 2016), transparent pots designed for high-throughput root phenotyping (Figure 1a & 1b), with six plants per RhizoTube® placed ~ 9 cm apart. The six plants had the same genotype in pure stands, whereas two genotypes were grown in alternate positions in the mixtures (Figure 1c). The 36 pure stands and the 54 mixtures were grown under combined water and nutrient limitation (R- treatment) or under optimal growth conditions (R+ treatment). All pure stands and mixtures were replicated three times within each treatment following a randomized complete block design within treatment, leading to a total of 540 RhizoTubes® (Figure 1c). In addition, six RhizoTubes® per experimental block per treatment (i.e., 36 RhizoTubes® in total) were grown with the commercial variety ANVERGUR and were used as controls to check for environmental heterogeneity in the greenhouse.

## Growth conditions

Seeds were first disinfected with a solution of 6 g/L of active chlorine (4 tablets/L of a standard commercial chlorine) in which they were immersed, agitated for 15 min, and finally rinsed 10 times with sterile water on the 22nd of June 2019. They were then soaked overnight, and sown into Petri dishes on the 23rd. They stayed at 4°C during 24h before being transplanted on the into the RhizoTubes® on the 24th. RhizoTubes® have a diameter of 17 cm and a depth of 49.5 cm (Jeudy *et al.*, 2016). They were filled with a 25:75 mixture of sand (Biot B4, Silices et Refractaires de la Méditerranée) and perlite. Temperatures were maintained around 20-25°C, relative humidity around 70-80%, and photoperiod was set to 16h, with an average PAR of 330 µmol.m-².s-1 during the day. Seedlings were daily provided with a liquid nutrient solution that contained water, N, P, K and all micronutrients required for plant growth (Supplementary Table 3). The water content of each RhizoTube® was monitored each day, and the amounts of nutrient solution were adjusted to maintain the RhizoTubes® at 100% of their water storage capacity (Supplementary Figure 1). In the R- treatment, the provision of nutritive solution was stopped on June 28th (four days after seedling transfer), causing the water content to decrease, ultimately reaching 55% of the full storage capacity by the end of the experiment (Supplementary Figure 1). Plants were harvested between the 16th and the 19th of July, i.e., about three weeks after transplantation, and were at the beginning of the tillering stage.

## Phenotyping

Root traits were measured for each RhizoTube® based on image analysis as described in Jeudy *et al.*, (2016). We used images taken on the 15th of July, i.e., as close as possible to harvest in order to (i) have sufficiently developed root systems, (ii) be sure that the root systems from adjacent plants were sufficiently close to interact, (iii) synchronize as much as possible root trait measurements and biomass measurements in order to increase the chance to detect causal relationships between them. At this date however, the roots of the different plants were overlapping in most RhizoTube®, and the image processing algorithm was not able to isolate the root systems of individual plants. Instead, we thus aggregated root traits at the level of the RhizoTube® as a whole. Three root traits could be computed following this aggregation: root depth, corresponding to the distance between the top of the RhizoTube® and the deepest root pixel; root length, the total length of roots detected on the image; and root area, the 2D projected area of the total root system. Root area combines information on both root length and root diameter. We did not consider root depth in our analyses because root tips reached the bottom of the RhizoTubes® in most cases, leading to highly left-skewed trait distribution and very low trait variability.

We also measured a set of aboveground plant traits in order to evaluate the relative importance of the belowground vs aboveground compartment in explaining mixture biomass. At harvest, we extracted plants from the RhizoTubes®. Because the aboveground organs were clearly separated between the neighbouring plants, we could separate individual plants by carefully and manually disentangling their root systems. Then, contrary to root traits measured via image analysis, we were able to measure aboveground and biomass traits at the level of individual plants. For each plant, we counted the number of leaves on the main tiller (hereafter “# leaves”) and the total number of tillers (hereafter “# tillers”). Above and belowground biomass were then separated for each plant and dried before weighing to determine shoot biomass, root biomass, root:shoot ratio, and total biomass. Leaf nitrogen content (hereafter “leaf N”) was measured with Near-Infrared Spectrometry (NIRS). We measured one NIR spectrum per leaf per plant in each RhizoTube® (i.e., six spectrum per RhizoTube®) using the Fieldspec 2500© (Analytical Spectral Devices, Inc. (ASD), Boulder, CO, USA) spectrometer. NIRS measurements were done one day before the harvest (i.e., on the 15th for the Rhizotubes harvested on the 16th, on the 16th for the RhizoTubes® harvested on the 17th, etc). NIR spectra were converted into nitrogen content using the calibration described in Ecarnot *et al.* (2013).

## Statistical analysis

We performed all statistical analyses with R v. 4.3.2 (R Core Team, 2019).

We first tested the effect of the treatment (R+ *vs* R-) on the different traits and biomass components (above and belowground) using only pure stand data summed per Rhizotube® (except leaf N which was averaged per Rhizotube®). We used mixed linear models with a given trait or biomass component as the response variable, treatment as a fixed effect, and genotype identity as a random intercept and random treatment slope. We also included two covariates as fixed effects: block, and harvest date or measurement date (except for root traits which were all measured on the same day). We assessed the significance of the fixed effects with standard analyses of variance and *F* statistics computed with Kenward-Roger's approximations for the degrees of freedom (Supplementary Table 4). We fitted the mixed model with the *lmer()* function (package *lme4*), and checked significance with the *anova()* function (package *lmerTest*).

To compare the relative biomass of mixed *vs* pure stands, we computed the Relative Yields (RYs, de Wit and van den Bergh 1965) of the varieties in mixed stands for each biomass component (aboveground, belowground, and total biomass):

(1) ,

Where is the Relative Yield of the variety *i* grown in mixture with the variety *j* in the treatment *k*, is the biomass (aboveground, belowground, or total biomass) of the variety *i* grown in mixture with the variety *j* in the treatment *k* and, and is the pure stands reference biomass of the variety *i* in treatment *k*. As described above, we harvested the experiment over four consecutive days because the experiment was too big to be harvested within a single day (i.e., 3240 plants in total). To avoid confounding effects between harvest date and other factors, notably treatment (R+ *vs* R-) and spatial blocks, we harvested one quarter of each block within each treatment each day (Figure 1d). This means that, within each block\*treatment combination, the Rhizotubes® had four different harvest dates. As a consequence, it was not possible to compute RY and compare pure and mixed stands within treatment\*block combinations, because for a given mixture, the harvest date could be different between the mixture and the two pure stand components. Instead, we first separated our dataset between the pure and mixed stands. Then, we summed the biomass of all plants of the same genotype within each RhizoTube® (i.e., 6 plants in pure stands, 3 plants in mixed stands). We used the pure stands dataset to compute pure stands reference biomass. To do so, we fitted a linear mixed model with biomass as the response variable, harvest date, block, and treatment as fixed effects, and variety identity as a random effect (here we included only the random effect of the variety on the intercept, as adding the random effect on the treatment slope led to singular models due to very low variance on the slope). We then summed the Best Linear Unbiased Predictor (BLUP) of each variety with the estimated fixed effect of the treatment (R+ or R-) to obtain the pure stands reference biomass values adjusted for the effects of block and harvest date within each treatment (i.e., ). For mixed stands, we also fitted a linear mixed model with each variety biomass as the response variable, harvest date, block, and treatment as fixed effects, and variety pair identity as a random effect on the intercept and on the treatment slope. Pair identity was constructed as the concatenation of the identity of the focal and neighbour variety, such that variety 1 and variety 2 in a mixed stand had pair identities variety1-variety2, and variety2-variety1, respectively. This allowed us to get one BLUP value for each variety within each variety combination, whereas using the same pair identity for both components of the mixture (e.g., variety1-variety2 for both) would have yielded a single value for the two components. We then summed the BLUP value of each variety (intercept in the R+ treatment, intercept + slope in the R- treatment) with the estimated fixed effect of the treatment (R+ or R-) and so we got one biomass value for each variety within each variety combination that was adjusted for the effects of the block and harvest dates within each treatment (i.e., ). We then divided these mixed stand values by the pure stands reference values to obtain RYs for each variety within each mixture following formula (1). Under the null hypothesis that the variety produced equal amount of biomass in mixed than in pure stands, RY = 0.5 because there are half the number of plants of a variety in mixed stands (n = 3) compared to pure stands (n=6). RY > 0.5 means that the variety produced more biomass in mixed than in pure stands, and RY < 0.5 means that the variety produced less biomass in mixed than in pure stands.

In a second step, we summed the RYs of the two varieties in the mixed stand to obtain the Relative Yield Total (RYT, de Wit and van den Bergh 1965) of the mixture:

(2) ,

Where is the Relative Yield Total of the mixture containing varieties *i* and *j* in treatment *k*. RYT = 1 means that the mixture as a whole produced similar amount of biomass than expected from the productivity of the varieties grown in pure stands, whereas RYT > 1 means that the mixture produced more biomass than expected, and RYT < 1 means that the mixture produced less biomass than expected.

For each mixture within each treatment, we then computed complementarity and selection effects (CE and SE, respectively) following the additive partitioning proposed by Loreau and Hector (2001):

(3)

Where is the Net Biodiversity Effect (highly correlated to RYT), is the observed biomass of the mixture, is the expected biomass of the mixture based on the pure stand biomasses and mixture proportions, is the number of components in the mixture (here ), is the difference between the observed Relative Yield of the mixture and the expected Relative Yield of the mixture (i.e., simply its proportion seeded, here expected RY = 0.5), and is the pure stand biomass. We computed CE and SE using the *apm()* function from the *bef* package (<https://github.com/BenjaminDelory/bef>).

We then compared RYT, CE, and SE between the R+ and R- treatment using a linear mixed model with RYT, CE, or SE as the response variable, treatment as a fixed effect, and varietal mixture identity (i.e., non-oriented concatenation of the names of the two varieties grown in mixture) as a random effect on the intercept. We assessed the significance of the fixed effects as detailed above (Supplementary Tables 5 and 6). Finally, we checked whether RYTs significantly differed from 1 and CE and SE from 0 within each treatment using two-sided *t*-tests.

To assess whether the trait composition (above and belowground traits) of the mixture affected varietal interactions, we used traits measured in pure stands to predict mixed stands RYTs, CE, and SE. This approach is based on the hypothesis that pure stand traits are the information available to agronomists and plant breeders when designing varietal mixtures. First, we computed reference trait values for pure stands that we corrected for design effects and measurement dates. We applied the same methodology for # leaves, # tillers, leaf N, root length, and root projected area. As described above, we fitted a linear mixed model with pure stand trait as the response variable, block, measurement date, and treatment as fixed effects, and varietal identity as a random effect. Varietal identity random effect was specified both on the intercept and the treatment slope, except for # leaves where adding the random slope led to singular models due to very low variance on the slope. We then computed pure stands reference trait values as the sum of the BLUP of each variety (intercept in the R+ treatment, intercept + slope in the R- treatment when random slope was specified) with the estimated fixed effect of the treatment (R+ or R-). Then, for each mixed stand, we computed both the average and the absolute trait difference between the two varieties using the pure stands reference trait values. Finally, we fitted a linear model with RYT, CE, or SE as the dependent variable and all trait averages and all trait differences as independent variables (*lm()* function from the *stats* package). We standardized all dependent and independent variables (*μ* = 0, *σ* = 1) and ran a backward model selection (*glmulti()* function from the *glmulti* package). We used the second-order Akaike Information Criterion (AICC, Sugiura 1978) to rank the models and performed model-averaging inference based on the top 10 models using the *coef()* function (*glmulti* package). We report parameter estimates and their 95% unconditional confidence interval computed as ±1.96 unconditional sampling standard deviation, variable importance, and adjusted R-squared averaged over the top 10 models (Burnham and Anderson, 2002). Detailed information on the top 10 models is available in Supplementary Tables 7 and 8.

Finally, to further investigate the ecological mechanisms behind the significant relationships between RYT and trait composition, specifically root area, we assessed the relationship between pure stand biomass and pure stand root area, and between RYs and pure stand root area using simple linear regressions between these variables within each treatment. We used trait and biomass values adjusted for block effects and measurement date effects as explained above, such that we had one value per variety per treatment. We also checked the relationship between RYs and the hierarchical distance in root area between the variety and its neighbour in pure stands. Hierarchical distance was the difference between the focal root area and the neighbour root area, divided by the focal root area (i.e., positive values mean that the focal had higher root area that its neighbour, and *vice versa*). Finally, we tested whether root area plasticity affected RYT in the two treatments. We computed root area plasticity as the difference between the average root area of the pure stands of the two varieties and the observed root area of their mixture, divided by the average of the pure stands. (i.e., positive values mean that root area increased in the mixed relative to the pure stands, and *vice versa*).

# Results

## Effect of resource availability on plant growth and traits

The limitation of water and nutrients strongly reduced total plant biomass in pure stands (1947.35 mg in the R- treatment vs 2364.71 in the R+ treatment, *F*1,87.77 = 144.49, *p* < 0.001,Figure 2a). Such biomass reduction was accompanied by a reallocation of resources from the aboveground to the belowground compartment: while plants produced less above-ground biomass (Figure 2b), fewer leaves (Figure 2d), and fewer tillers (Figure 2e), they produced higher root biomass (Figure 2c), longer roots (Figure 2h), and had higher root areas (Figure 2i) in the R- treatment. Consequently, the root:shoot ratio increased from 0.48 in the R+ treatment to 0.82 in the R- treatment (+71%, F1,87.78 = 3966.58, *p* < 0.001, Figure 2g). Leaf nitrogen concentration also increased in the R- treatment (3.32 vs 2.95%, F1,87.19 = 525.03, *p* < 0.001, Figure 2f).

## Relative biomass of mixtures

RYTs were significantly different between the R+ and R- treatments for all biomass components (Figure 3 and Supplementary Table 5). In the R+ treatment, the biomass production of the mixtures did not significantly differ from the biomass expected from their pure stand components (average RYT for total biomass = 0.99, *t*53 = -0.46, *p* = 0.0.6473, Figure 3a; average RYT for shoot biomass = 1.00, *t*53 = -0.05, *p* = 0.9632, Figure 3b; average RYT for root biomass = 0.99, *t*53 = -0.75, *p* = 0.4568, Figure 3c). In contrast, in the R- treatment, mixtures produced significantly less biomass than expected from the biomass of their components grown in pure stands (average RYT for total biomass = 0.92, *t*53 = -6.18, *p* < 0.001, Figure 3a; average RYT for shoot biomass = 0.94, *t*53 = -4.29, *p* < 0.001, Figure 3b; average RYT for root biomass = 0.94, *t*53 = -6.83, *p* < 0.001, Figure 3c).

## Ecological effects underlying the relative biomass of the mixtures

Complementarity and selection effects were both significantly smaller in the R- than in the R+ treatment for all biomass components, except selection effects on root biomass that were not significantly different between the two treatments (Supplementary Table 6). In the R+ treatment, complementarity and selection effects were not significantly different from 0 for aboveground biomass and total biomass, and selection effects were significantly negative for root biomass (Figure 4). In the R- treatment, in contrasts, both complementarity and selection effects were significantly negative for all biomass components (Figure 4). Complementarity effects were overall stronger than selection effects, e.g., for total biomass, mean complementarity effect = -57.90 ± 148.35 mg, mean selection effect = -3.80 ± 15.76 mg (mean ± s.d.).

## Effect of trait composition on mixture biomass

RYTs were highly variable in both treatments (Figure 3). The trait composition of the mixtures poorly explained RYT variability in total biomass observed in the R+ treatment (Figure 5a, average adjusted R² over the top ten models = 0.10). In contrast, trait composition explained up to 49% of RYT variation in the R- treatment (Figure 5b). Most of this variability was explained by the average root area of the two varieties grown in mixture (R² = 47% in a model with average root area as the single explanatory variable), which had a negative effect on RYT (Figure 5b, Supplementary Table 7): mixing two genotypes with higher average root area in pure stands resulted in a decrease in biomass production in mixture. We obtained similar results when performing the analysis on shoot biomass alone (Supplementary Figure 2a and 2b, Supplementary Table 7). Traits had higher explanatory power on root biomass RYT in the R+ treatment (Supplementary Figure 2c, average adjusted R² over the top ten models = 0.34), with strong negative effects of average leaf number and average root area. In the R- treatment, however, as for the other biomass components, average root area was the main explanatory trait with a negative effect on RYT (Supplementary Figure 2d).

The negative relationship between average root area and RYT was mostly driven by a negative relationship between average root area and complementarity effects: mixing two varieties with high root areas in pure stands reduced biomass production for both varieties in the mixture (Supplementary Figure 3 a and b, Supplementary Table 7). The selection effect was mostly explained by the difference in root area between the varieties: the variety with the highest biomass production in pure stands tended to lose more biomass in mixture when it was grown with a variety that had a very different root area in pure stands. (Supplementary Figure 3 c and d, Supplementary Table 8).

## Relationship between root area and mixture biomass

Interpreting seedling biomass as a proxy for plant performance and final yield, we could conclude that there was a global negative interference between varieties under limiting conditions, and that varieties with higher root areas in pure stands had more negative interactions in mixtures, e.g., were more competitive to each other than varieties with low root areas, resulting in a negative complementarity effect. However, it is difficult to explain why such varieties were not also highly competitive with themselves in pure stands: by construction, varieties with the highest root area are more likely to be paired with neighbours with lower rather than higher root area than themselves in mixtures, and thus to experience reduced belowground competition in mixed stands. An alternative interpretation of our results is that seedling biomass is a better indicator of individual plant competitiveness than of final yield, and that it might actually trade-off with final grain production under conditions where resources are limited and intraspecific competition is an important determinant of yields. In line with this hypothesis, Colombo *et al.* (2022) found that seedling biomass measured on the same phenotyping platform was negatively correlated with grain yields using a large dataset of 715 bread wheat varieties and 200 durum wheat varieties grown in 42 contrasting environments. Then, negative RYTs could reflect a relaxation of competition in mixed compared to pure stands, rather than a negative interaction between varieties. Varieties with high root area in pure stands would be highly competitive varieties that reach such trait values through root proliferation in response to their neighbour in pure stands, which would himself be very competitive. Such strong investment into competition would in turn results in an overinvestment in biomass to outgrow the neighbour. Those varieties, when grown in mixtures, are more likely to be paired with varieties that are less competitive, leading to relaxed competition and to a disengagement from the “arms race” resulting in lower root area and lower biomass. If the root area of the most competitive variety goes below the root area of the less competitive variety, this would lead to a synergistic effect where the less competitive variety also disengage from the arms race.

We tested this hypothesis by examining the relationships between the traits of the varieties in pure stands and their individual biomass and biomass responses to mixture cultivation. We found that there was a strong positive relationship between the total biomass of the pure stands and their root area (Figure 5a). This relationship was stronger in the R- treatment (Figure 5a, Pearson’s *R* = 0.87, slope = 0.079 mg.mm-2, *p* < 0.001) than in the R+ treatment (Pearson’s *R* = 0.74, slope = 0.0446 mg.mm-2, *p* < 0.001). Consistent with our hypothesis, varieties with the highest root areas in pure stands and the highest hierarchical distances in root area with their neighbours were the ones with the strongest biomass reduction in mixed stands in the R- treatment (Figure 5b, Pearson’s *R* = -0.70, *p* < 0.001; Figure 5c, Pearson’s *R* = -0.51, *p* < 0.001). At the opposite, varieties which had lower root areas than their neighbours (i.e., negative hierarchical distance to their neighbour on Figure 5c) produced more biomass in mixture than in pure stands (RY > 0.5). This effect was not symmetrical: for a similar hierarchical distance, varieties which were lower in the hierarchy gained less biomass than the biomass loss observed for varieties placed higher in the hierarchy (e.g., at hierarchical distance = -0.2, estimated RY = 0.53 while at hierarchical distance = 0.2, estimated RY = 0.40, Figure 5c). This asymmetry might explain the negative selection effect observed in the R- treatment. Also, when the hierarchical distance was negative but close to 0 (>-0.1), the varieties still produced less biomass in mixture than in pure stands. This might explain the stronger negative complementarity effect observed when both varieties had high root areas (and thus a small phenotypic difference): both the most competitive variety (positive hierarchical distance on root area) and the less competitive variety (negative hierarchical distance on root area) lost biomass compared to pure stands. None of these relationships were significant in the R+ treatment (Figures 5b and 5c). Finally, the strongest biomass reductions occurred in mixtures where the observed root area was lower than the root area predicted from the pure stands, i.e., where phenotypic plasticity led to reduced root area (Figure 5d). Again, the relationship between RYT and root area plasticity was stronger in the R- treatment (Pearson’s *R* = 0.80, *p* <0.001,slope = 1.93 %-1) than in the R+ treatment (Pearson’s *R* = 0.54, *p* <0.001,slope = 0.91 %-1). We obtained identical results when doing these analyses on shoot and root biomass separately, except that the differences between the R+ and R- treatments were less marked for root biomass (Supplementary Figures 4 & 5). Altogether, these results support the idea that low RYTs in the R- treatment resulted from relaxed belowground competition in mixed relative to pure stands.

# Discussion

## Shift in root allocation under water and nutrient limitation

Wheat seedling growth was strongly affected by the limitation of water and nutrients in our experiment. Resource limitation triggered an overall reduction in biomass, along with a shift in biomass allocation from the aboveground to the belowground compartment. This result is in line with the optimal allocation theory, which states that plants prioritize allocation to increase their uptake of the most limiting resources (Bloom *et al.*, 1985; Weiner, 2004). In our case, the high allocation to roots suggests that belowground resource limitations were much stronger than aboveground resource limitations, a pattern consistent with what we intended to induce with our experimental protocol. In wheat, plasticity of the root-to-shoot ratio and high reallocation to roots have been shown to be advantageous under drought stress (Bacher *et al.*, 2021, 2022). Allocating carbon to the roots enhances access to water through deeper, longer, and more branched roots, which in turns helps maintain high stomatal conductance and physiological activity. We can thus hypothesize that higher root allocation in response to water and nutrient limitation reflected an adaptive response of the varieties.

## Biomass reduction in mixed relative to pure stands reflects a relaxation of competition

On average, mixture biomass was not significantly different from pure stand biomass under optimal growth conditions, indicating that there was no significant effect of interactions between varieties. However, when water and nitrogen were limiting, mixtures produced significantly less biomass than expected from their pure stand components, which was mainly explained by a negative complementarity effect and, to a lesser extent, by a negative selection effect. At first glance, and if we interpret seedling biomass as a good proxy for final plant biomass, this result contradicts ecological theories and many experimental and observational studies on non-domesticated species where plant diversity effects are generally found to be more positive under harsher environments (Bertness and Callaway, 1994; Craven *et al.*, 2016). Under this line of interpretation, we have to explain how a relatively large number of varieties with divergent evolutionary histories and contrasted phenotypes would on average always perform better when surrounded by genetic clones than by genetically distant neighbours. Only a mechanism like kin discrimination could explain such behaviour, but kin discrimination has never been reported in wheat, and its existence in plants is still debated (Pennisi, 2019; Anten and Chen, 2021). A more parsimonious interpretation is that water and nutrient limitation triggered an arms race between plants of highly competitive varieties in pure stands, which manifested through root proliferation and ultimately overinvestment in both below and aboveground biomass. According to previous study on root responses to the presence of competitor plants, such proliferation could have been triggered either by a direct perception of the presence of a competitive neighbour through the detection of chemical cues in the rhizosphere, or by the perception of resource depletion caused by the neighbour (Schenk, 2006; Pierik *et al.*, 2013). Such highly competitive varieties experienced reduced competition in mixed stands and thus disengaged from this competitive arms race and produced less biomass. When the difference in root area between two varieties was relatively small and they both had high root areas in pure stands (resulting in high average root area), the relaxation of competition was synergistic: the reduction in root area of the most competitive variety led to a lower root area than that of the neighbour in pure stands, leading to a simultaneous decrease in competition intensity for the neighbour, and finally to a negative complementarity effect. In our case, a “negative” effect is seen as a reduction of competition intensity which translates into a reduction of biomass. This interpretation is based on the hypothesis that the biomass of a three-week old wheat seedling in a stand is a better indicator of the competitiveness of the plant than of its future grain production. In cereals such as wheat, early seedling growth and vigour are traditionally targeted by plant breeders as a favourable traits for competitiveness against weeds (Lemerle *et al.*, 1996; Bertholdsson, 2005; Hendriks *et al.*, 2022). However, in the absence of weeds and in a context were intraspecific plant-plant interactions become a strong determinant of yield per unit area, favouring competitive seedling might actually decrease yields because seedlings competitiveness would essentially be directed towards themselves. In line with this interpretation, seedling biomass measured in the same platform and under similar growth conditions was found to negatively correlate with grain yields measure in the field over a wide range of environments (Colombo *et al.*, 2022).

## No evidence for niche complementarity driven by trait differences between seedlings

While we found strong complementarity effects between varieties under resource limitation, these were mostly driven by average trait values in pure stands, and we found no evidence of complementarity effects that would be driven by trait differences between varieties. This could be explained by the fact that functional differences between varieties were not large enough 3-weeks after sowing to generate complementarity effects. A second hypothesis is that we did not measure the “right” traits to detect complementarity effects, notably belowground. Our phenotyping method did not allow us to access traits such as root diameter or root tissue density. Other traits could not be computed due to root overlapping between adjacent plants (e.g., root angle) or to the reduced size of the Rhizotube® (e.g., root depth). However, such traits have rarely been found to associated with complementarity effects in ecological studies (Fort *et al.*, 2014; Bakker *et al.*, 2018). Previous studies in rice varietal mixtures also failed to find evidence of belowground niche complementarity driven by differences in morphological and architectural root traits such as rooting depth, root diameter, or specific root length (Montazeaud *et al.*, 2018). Overall, this study confirm that root trait differences alone are less likely to generate complementarity effects in varietal mixtures than they are for example in intercropping where differences in root foraging strategies between species can be more significant (Zhang *et al.*, 2014; Homulle *et al.*, 2022; Schmutz and Schöb, 2023).

## Root area as the main driver of competitive hierarchy

We identified root area as the main driver of plant biomass and mixing effects in our experiment. The average root area of the two varieties in pure stands could explain up to 50% of RYT variability under resource-limiting conditions. A higher root area in pure stands was associated with a greater biomass reduction in mixture, especially when the mixture partner had a lower root area. These results support the idea of an early-stage belowground competitive hierarchy between varieties (Kunstler *et al.*, 2012), where higher root area is associated with higher competitive ability. In line with these results, root functional traits associated with root foraging and absorption potential have already been shown to shape early-stage competitive hierarchies between grassland species (Fort *et al.*, 2014; Ravenek *et al.*, 2016; Wagg *et al.*, 2017). The very high explanatory power of root area found in our study might be explained by the fact that this trait integrates several functional dimensions of the root system that are classically captured by distinct traits (e.g., root length density, specific root length, or root diameter).

## Root plasticity contributes to mixing effects

We found that root area in mixed stands deviated from root area observed in pure stands, indicating a plastic response of the root system to neighbour genotype identity. On average, root area decreased in mixed relative to pure stands, and the stronger the decrease, the lower the RYT especially in the R- treatment. In accordance with ecological theory, our results thus support the view that phenotypic plasticity contributes to mitigate competition intensity in diverse plant communities (Callaway *et al.*, 2003; Schiffers *et al.*, 2011; Burns and Strauss, 2012). In varietal mixtures, previous studies have already shown that plasticity in aboveground traits such as plant height, specific leaf area, or canopy cover contribute to overyielding, notably by increasing trait divergence between varieties (Kong and Zhao, 2023; Tschurr *et al.*, 2023; Su *et al.*, 2024). Contrary to these studies where plasticity was associated with positive overyieldings on final grain production, we here show that plastic root changes may contribute to mixture performance by decreasing biomass production at the seedling stage, which could ultimately translate into higher yields through reduced early stage competition between seedlings. We also show that plasticity does not only contribute to mixture performance by increasing phenotypic differences between varieties, but also by displacing the average trait value of the varieties.

## Practical implications for plant breeding

Crop performance, including grain yield, is affected by trade-offs between individual competitiveness and group performance. As early pointed out by plant breeders (Donald, 1968), and more recently revisited with the concepts of Darwinian Agriculture, or Evolutionary Agroecology, these trade-offs can hold promising opportunities to increase productivity, notably by reversing past selection for individual competitiveness (Denison *et al.*, 2003; Weiner, 2019). This can be achieved either by selecting on group performance, i.e., selecting on population yield (Montazeaud *et al.*, 2020), or by targeting key traits related to competitive ability. Our study suggests that selecting genotypes with reduced root area in pure stands and reduced root area proliferation in presence of neighbours could be a way to reduce competition intensity between seedlings, which could then translate into higher yields. This result aligns with classical prediction of game theory models: investment in root biomass beyond the payoff point where soil resource absorption compensate the cost of the root system only happens at cost for neighbouring plants, leading to a Tragedy of the Commons (Hardin, 1968; Gersani *et al.*, 2001; Anten and Vermeulen, 2016). Interestingly, modern wheat varieties that have been subject to selection for increased population yield for many generations display reduced root biomass at the seedling stage (Colombo *et al.*, 2022), and reduced root proliferation in presence of a neighbour compared to old landraces (Zhu *et al.*, 2019). In oat and barley, excessive growth of the root system in the topsoil is also associated with yield reductions (Vain *et al.*, 2023).

Beyond direct selection on root traits in pure stand varieties, which could be challenging to implement, mixing varieties could be another solution to resolve belowground TOCs. This solution would allow to benefit from other known positive effects of genetic diversity at the same time (e.g., improved disease control, Wolfe, 1985; Mundt *et al.*, 1995; Zhu *et al.*, 2000; Finckh and Wolfe, 2006)). Our study suggests that highly competitive varieties could benefit from relaxed belowground competition in varietal mixtures, which could translate into overyielding. Conveniently, the choice of the varieties could be guided by their root projected area measured in pure stands. Of course, the effect of relaxed competition at the seedling stage on final grain yield would still need to be validated in field trials. In our particular experimental set-up, previous studies have already shown that the biomass of the seedling measured in the phenotyping platform after three weeks of growth was negatively correlated with grain yields measured on the same varieties in the field (Colombo *et al.* 2022), suggesting that higher seedling biomass is indeed detrimental for final yields in comparable conditions. This means that promoting phenotypic differences between varieties is not the only way to reduce competition and may only work for some traits, such as phenological traits (Fletcher *et al.*, 2019; Lowry *et al.*, 2020) or traits related to light interception (Su *et al.*, 2024).

# Supplementary Data

**Supplementary Table 1:** List of the 36 wheat varieties used in the experiment

**Supplementary Table 2:** List of the 54 binary mixtures used in the experiment

**Supplementary Table 3:** Description of the nutrient solution

**Supplementary Table 4:** Analysis of Variance (ANOVA) of biomass components and traits in pure stands to test the treatment effect

**Supplementary Table 5:** Analysis of Variance (ANOVA) to test the effect of the treatment on RYTs

**Supplementary Table 6:** Analysis of Variance (ANOVA) to test the effect of the treatment on complementarity effects (CE) and selection effects (SE)

**Supplementary Table 7:** Ten best fitting models between RYTs on aboveground, belowground, and total biomass and mixture trait composition

**Supplementary Table 8:** Ten best fitting models between complementarity effects (CE) and selection effects (SE) measured on total biomass and mixture trait composition

**Supplementary Figure 1:** RhizoTubes® monitoring

**Supplementary Figure 2:** Relationships between the trait composition of the mixtures and their above and belowground RYTs

**Supplementary Figure 3:** Relationships between the trait composition of the mixtures and complementarity effects (CE) and selection effects (SE) measured on total biomass

**Supplementary Figure 4:** bivariate plots illustrating the interaction between root area, resource availability and shoot biomass

**Supplementary Figure 5:** bivariate plots illustrating the interaction between root area, resource availability and root biomass

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# Author contributions

Conception of the research and design of the experiment: C. J., C. S, H. F., P. R.

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Harvest and trait measurements: H. F., L. M. C., M. E., P. R.

Data analysis: G. M.

Redaction of the manuscript: G. M. with inputs from all authors.

# Conflict of interest

The authors declare no conflict of interest.

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# Data availability

Data and code used for analysis are available at https://doi.org/10.5281/zenodo.14163518.

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# Figure legends

**Figure 1: Experimental design.** (**a**) and (**b**) close-up views on RhizoTubes® showing wheat seedlings and their roots. (**c**) Spatial distribution of the seedlings within the RhizoTubes® in both pure (up) and mixed (bottom) stands. Different colours represent different genotypes. (**d**) Schematic representation of the experiment, each dark square representing a RhizoTube®. The green squares are the control RhizoTubes® and are all grown with the same wheat variety to check environmental heterogeneity.

**Figure 2: Effect of resource limitation on plant growth and traits.** Comparison of total biomass (**a**), shoot biomass (**b**), root biomass (**c**), number of leaves (**d**), number of tillers (**e**), leaf nitrogen concentration (**f**), root:shoot ratio (**g**), root length (**h**), and root area (**i**) between the R+ (blue) and the R- (red) treatments. Only pure stand data were used, and trait values were summed per Rhizotube® (except for leaf N for which we averaged trait values per Rhizotube®). Points and error bars represent the mean ± standard deviation. The number of observations in each treatment is reported below each violin plot. Symbols above the plots represent the significance of the treatment effect (\*: *p* < 0.05, \*\*: *p* < 0.01, \*\*\*: *p* < 0.001, complete analysis of variance is reported in Supplementary Table 4).

**Figure 3: Effect of resource limitation on interactions between varieties.** Comparison of Relative Yield Total (RYT) indices on total biomass (**a**), shoot biomass (**b**), and root biomass (**c**) between the R+ (blue) and the R- (red) treatments. Points and error bars represent the mean ± standard deviation. The number of observations in each treatment is reported below each violin plot. Symbols above violins represent the significance of a two-sided *t*-test testing if the mean RYT within treatment is significantly different from 1 (\*\*\*: *p* < 0.001). ANOVAs testing the significance of treatment effect on RYTs are reported in Supplementary Table 5.

**Figure 4: Effect of resource limitation on complementarity and selection effects.** Comparison of complementarity effects (CE) and selection effects (SE) on total biomass (**a**, **b**), shoot biomass (**c**, **d**), and root biomass (**e**, **f**) between the R+ (blue) and the R- (red) treatments. Points and error bars represent the mean ± standard deviation. The number of observations in each treatment is reported below each violin plot. Symbols above violins represent the significance of a two-sided *t*-test testing if the mean biodiversity effect within treatment is significantly different from 0 (\*\*\*: *p* < 0.001, \*\*: *p* < 0.01). ANOVAs testing the significance of treatment effect on biodiversity effects are reported in Supplementary Table 6.

**Figure 5: Relationships between the trait composition of the mixtures and their performance.** Standardized effects of traits on mixture RYTs measured on total biomass in the R+ treatment (**a**), and R- treatment (**b**). Backward model selection was performed on a full model with RYT as the response variable and all trait means and differences as explanatory variables. Based on AICC, the top-ten models were retained to compute model-averaged estimates reported on the left side of the panels with their 95% unconditional confidence intervals (Supplementary Table 7). Empty symbols represent trait differences and filled symbols represent trait means. The relative importance of the variables are reported on the right side of the panels and can be interpreted as the probability that the variable appears in the best model. Hatched bars represent trait differences and filled bars represent trait means. Colours refer to the type of traits, with aboveground traits and belowground traits represented in green and brown, respectively. Adjusted R-squared averaged across the top-ten models () are also reported.

**Figure 6: Interactions between root area, resource availability, and biomass. (a)** relationship between the total biomass of the pure stands and their root area (n = 36 per treatment), **(b)** relationship between RY computed on total biomass and root area measured in pure stands (n = 108 per treatment), **(c)** relationship between RY computed on total biomass and the hierarchical distance on root area, i.e., the difference between the root area of the focal and the root area of the neighbour, both measured in pure stands (n = 108 per treatment), **(d)** relationship between RYT computed on total biomass and root area plasticity, i.e., the difference between the expected (based on pure stands) and the observed root area (n = 54 per treatment). Pearson correlation coefficients (*R*) and *p-*values (*p*) refer to simple linear models fitted independently in the R+ (blue, circle) and R- (red, triangles) treatments.

# Legends for Supplementary Materials

**Supplementary Table 1: Variety information.**

**Supplementary Table 2: List of the 54 binary mixtures.**

**Supplementary Table 3: Description of the nutrient solution.**

**Supplementary Table 4: Analysis of Variance (ANOVA) of biomass components and traits in pure stands.** Pure stand data was summed per Rhizotube® (except leaf N which was averaged per Rhizotube®). We used Type III analysis of Variance using the Kenward-Roger’s method on mixed models where the identity of the variety was used as a random effect on both the intercept and the slope of the treatment effect (R+ vs R- treatment). For each fixed effects, we report the sum of squares (“Sum Sq”), the mean squares (“Mean Sq”), the numerator degrees of freedom (“NumDF”), the denominator degrees of freedom (“DenDF”), the value of the *F* statistic (“F value”), and the *p*-value (“Pr(>F)”).

**Supplementary Table 5: Analysis of Variance (ANOVA) of RYTs.** Type III analysis of Variance using the Kenward-Roger’s method on mixed models where the identity of the genotypic pair (concatenation of the identity of the two genotypes in a RhizoTube®) was used as a random effect on the intercept. We report the fixed effect of the treatment with the sum of squares (“Sum Sq”), the mean squares (“Mean Sq”), the numerator degrees of freedom (“NumDF”), the denominator degrees of freedom (“DenDF”), the value of the *F* statistic (“F value”), and the *p*-value (“Pr(>F)”).

**Supplementary Table 6: Analysis of Variance (ANOVA) of complementarity and selection effects (CE and SE, respectively).** Type III analysis of Variance using the Kenward-Roger’s method on mixed models where the identity of the genotypic pair (concatenation of the identity of the two genotypes in a RhizoTube®) was used as a random effect on the intercept. We report the fixed effect of the treatment with the sum of squares (“Sum Sq”), the mean squares (“Mean Sq”), the numerator degrees of freedom (“NumDF”), the denominator degrees of freedom (“DenDF”), the value of the *F* statistic (“F value”), and the *p*-value (“Pr(>F)”).

**Supplementary Table 7: Ten best fitting models between RYT on aboveground, belowground, and total biomass and mixture trait composition.** The top-ten models are ranked according to their AICc. ∆AICc (“delta\_AICc”), model weights (“weight”), and adjusted R-squared (“R2\_adj”). The “avg” and “diff” suffixes refer to trait averages and trait differences, respectively.

**Supplementary Table 8: Ten best fitting models between CE and SE computed on total biomass and mixture trait composition.** The top-ten models are ranked according to their AICc. ∆AICc (“delta\_AICc”), model weights (“weight”), and adjusted R-squared (“R2\_adj”). The “avg” and “diff” suffixes refer to trait averages and trait differences, respectively.

**Supplementary Figure 1: RhizoTubes® monitoring.** Measurements of nutrient solution inputs (**a**) and water status (**b**) of the RhizoTubes® in the R+ treatment (blue) and the R- treatment (red) over the course of the experiment. Values are averaged over all RhizoTubes®. Seedlings were transferred in the RhizoTubes on the 24th of June, and plants were harvested from the 16thto the 19th of July 2019.

**Supplementary Figure 2: Relationships between the trait composition of the mixtures and their above and belowground RYTs.** Standardized effects of traits on mixture RYTs measured on above- (**a** and **b**) and below- (**c** and **d**) ground biomass in the R+ treatment (**a** and **c**) and R- treatment (**b** and **d**). Backward model selection was performed on a full model with RYT as the response variable and all trait means and differences as explanatory variables. Based on AICC, the top-ten models were retained to compute model-averaged estimates reported on the left side of the panels with their 95% unconditional confidence intervals (Supplementary Table 7). Empty symbols represent trait differences and filled symbols represent trait means. The relative importance of the variables are reported on the right side of the panels and can be interpreted as the probability that the variable appears in the best model. Hatched bars represent trait differences and filled bars represent trait means. Colours refer to the type of traits, with aboveground traits and belowground traits represented in green and brown, respectively. Adjusted R-squared averaged across the top-ten models () are also reported.

**Supplementary Figure 3: Relationships between the trait composition of the mixtures and complementarity and selection effects (CE and SE, respectively).** Standardized effects of traits on mixture CE (**a** and **b**) and SE (**c** and **d**) computed on total biomass in the R+ treatment (**a** and **c**) and R- treatment (**b** and **d**). Backward model selection was performed on a full model with CE (or SE) as the response variable and all trait means and differences as explanatory variables. Based on AICC, the top-ten models were retained to compute model-averaged estimates reported on the left side of the panels with their 95% unconditional confidence intervals (Supplementary Table 8). Empty symbols represent trait differences and filled symbols represent trait means. The relative importance of the variables are reported on the right side of the panels and can be interpreted as the probability that the variable appears in the best model. Hatched bars represent trait differences and filled bars represent trait means. Colours refer to the type of traits, with aboveground traits and belowground traits represented in green and brown, respectively. Adjusted R-squared averaged across the top-ten models () are also reported.

**Supplementary Figure 4: Interactions between root area, resource availability, and shoot biomass. (a)** relationship between the shoot biomass of the pure stands and their root area (n = 36 per treatment), **(b)** relationship between RY computed on shoot biomass and root area measured in pure stands (n = 108 per treatment), **(c)** relationship between RY computed on shoot biomass and the hierarchical distance on root area, i.e., the difference between the root area of the focal and the root area of the neighbour, both measured in pure stands (n = 108 per treatment), **(d)** relationship between RYT computed on shoot biomass and root area plasticity, i.e., the difference between the expected (based on pure stands) and the observed root area (n = 54 per treatment). Pearson correlation coefficients (*R*) and *p-*values (*p*) refer to simple linear models fitted independently in the R+ (blue, circle) and R- (red, triangles) treatments.

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