New Phytologist Supporting Information
Belowground competition favors character convergence but not character displacement in root traits
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Trait name	**Functional Class**	**Description**	**Trait Code**	**PC Contribution (%)**
Accumulated width*	Topology	Percentage of width accumulation at 10-90 % depth	D10-D90	PC1: 7.00-10.69 %
Skeleton width	Architecture	Width calculated from the medial axis of the root system.	SKL WIDTH	PC2: 7.50 %
Skeleton depth	Architecture	Depth calculated from the medial axis of the root system.	SKL DEPTH	PC2: 10.84 %
Maximum soil tissue angle	Architecture	Maximum soil tissue angle measured over all root tips.	STA MAX	PC4: 6.94 %
Maximum width of the root system	Architecture	Maximum root system width measured from first to last horizontal foreground pixel.	WIDTH MAX	PC2: 7.53 %
Maximum root tissue angle	Architecture	Maximum root tissue angle measured over all root tip paths.	RTA MAX	PC2: 9.02 %
Root top angle range	Architecture	Range of root tissue angles present in the root system.	RTA RANGE	PC4: 5.73 %

Spatial root distribution X	Architecture	Spatial distribution of the root shape in the x-axis. This is the x component of the vector pointing from the center of the bounding box of the root shape to the center of mass of the root shape.	RDISTR X	PC2: 0.22 %
Spatial root distribution Y	Architecture	Spatial distribution of the root shape in the y-axis. This is the x component of the vector pointing from the center of the bounding box of the root shape to the center of mass of the root shape.	RDISTR Y	PC2: 8.01 %
Adventitious root angle	Architecture	Adventitious root angle estimated from the paths detected in the number of adventitious roots.	ADVT ANG	PC2: 4.83 %
Basal root angle	Architecture	Basal root angles estimated from the paths detected in the number of basal roots.	BASAL ANG	PC2: 6.61 %
50 percent drop	Architecture	Depth value where 50% of the root tip paths emerged from the central path.	DROP 50	PC2: 10.85 %
Projected root area	Size	Number of foreground pixels belonging to the root system.	AREA	PC3: 13.49 %
Skeleton nodes	Morphology	Nodes calculated from the medial axis of the root system.	SKL_NODES	PC4: 8.25 %

Stem diameter	Morphology	Stem diameter derived from medial axis.	DIA STM	PC3: 2.31 %
Simple stem diameter	Morphology	Simple stem diameter calculated in root estimator for shovelomics	DIA STM SIMPLE	PC2: 11.51 %
Average root density	Morphology	Ratio of foreground to background pixels within	AVG DENSITY	PC4: 1.43 %
Mean tip diameter	Morphology	Mean tip diameter estimated from the medial circle at the tips.	TD AVG	PC4: 14. 53 %
Root tip count	Morphology	Overall number of tips detected in the image	RTP COUNT	PC3: 9.37 %
Number of Adventitious	Morphology	Number of root tip paths emerging from root segment 1.	ADVT COUNT	PC4: 3.47 %
Number of basal roots	Morphology	Number of basal roots estimated as emerging root tip bundles from root segment 2.	BASAL COUNT	PC4: 5.64 %
Basal root angle	Architecture	Basal root angles estimated from the paths detected in the number of basal roots.	BASAL ANG	PC2: 6.61 %
Hypocotyl diameter	Morphology	Hypocotyl diameter estimated over detected hypocotyl region as the average diameters of medial circles.	HYP DIA	PC4: 8.46 %

Tap root diameter	Morphology	Tap root diameter estimated over detected taproot region as the average diameters of medial circles.	TAP DIA	PC4: 10.97 %
Maximum diameter at 90-100% percent depth	Morphology	Maximum diameter found in the interval of 90-100% rooting depth	MAX DIA 90	PC4: 9.42 %

Table S1 lists the full root trait name and its corresponding abbreviated name ('Code') assigned by DIRT software for the 33 traits that were analyzed in the study. Each root trait was cataloged into four functional trait classes indicated within parenthesis *a priori*. We report the PC axis where a given individual root trait contributed the most variance and report its percent contribution to that axis ('PC Contribution'). Traits with '*' indicate multiple traits and a corresponding range in their percent (%) contribution to a given PC axis.

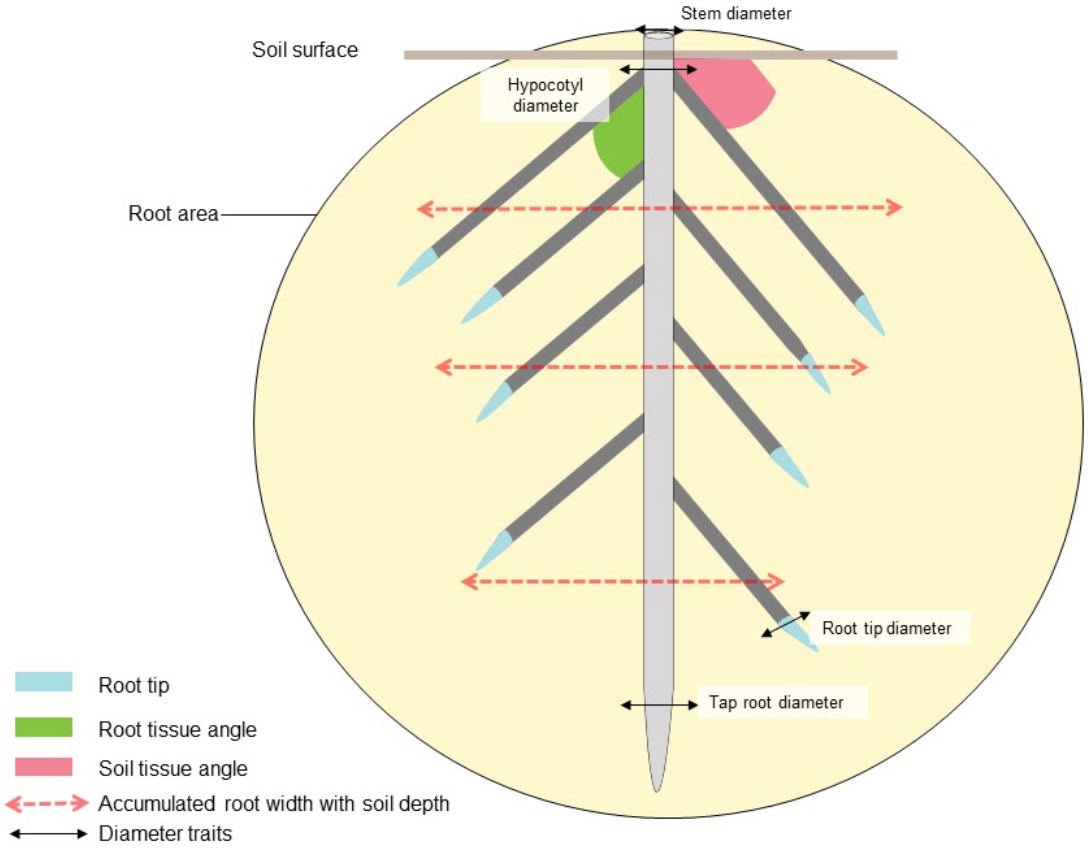


Fig. S1 A sketch for the root traits captured by DIRT. Root area represents the 'AREA' trait, estimated as the total number of pixels of the root system as indicated by a light yellow circle encapsulating the entire sampled root system. Accumulated root width with soil depth is captured with the two-way dashed light red arrows ('D%'; Table S1). Different diameter traits are indicated with two-way solid black arrows including, tap root diameter ('TAP_DIA'), root tip diameter ('TD_AVG'; Table S1), stem diameter ('DIA_STEM'; Table S1) and hypocotyl diameter ('HYP_DIA'; Table S1). Root tips are colored in light blue, and an example of soil root tissue angle and root tissue angle are shown by the pink and green shaded regions, respectively.

Trait	Selection gradient		*F-values*
	Alone	Competition	Treatment × Trait
Root topology (PC1)	0.05 ± 0.04 (.27)	0.01 ± 0.11 (.92)	0.04 (.85)
Root architecture (PC2)	-0.002 ± 0.05 (.97)	0.08 ± 0.07 (.28)	0.50 (.51)
Root morphology (PC4)	0.12^ ± 0.06 (.10)	**-0.17 ± 0.07 (.03)**	**5.33 (.03)**

Table S2 Results of linear selection gradient for root topology (PC1), architecture (PC2), and morphology (PC4), for each Treatment is presented with their respective linear regression slopes (β), its corresponding ± 1 standard error and *p-value* in parentheses. *F-values* and their corresponding *p-values* from ANCOVA are also shown to indicate the effect of Treatment on the pattern of selection for each trait (Treatment × Trait). Bolded values indicate a *p-value* < 0.05 and '^' indicates a marginally significant *p-value* = 0.10.

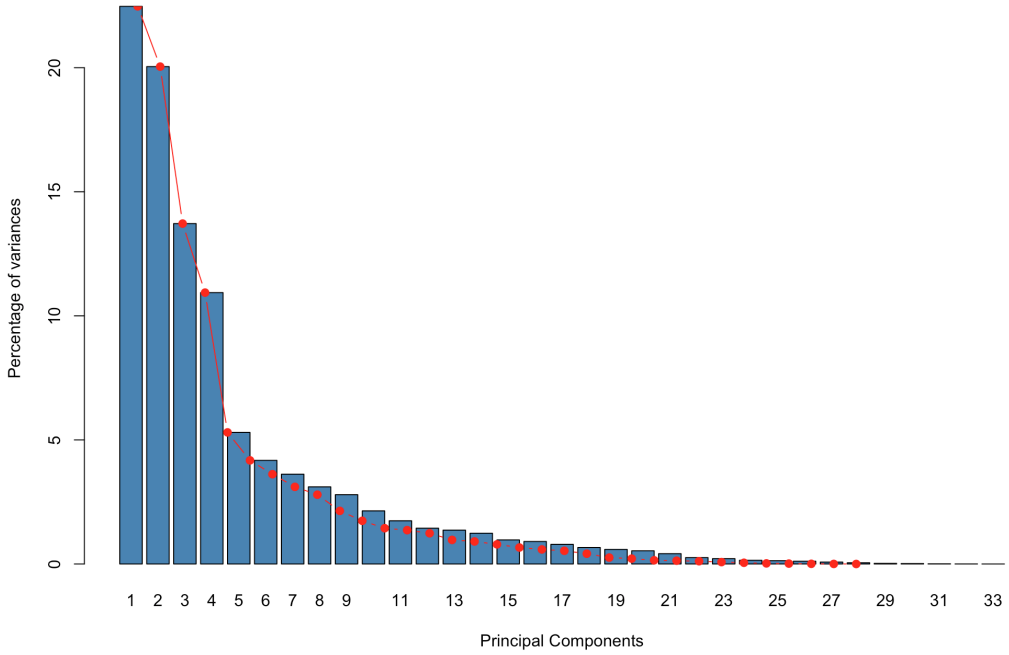


Fig. S2 Scree plot demonstrating the percentage of variance explained by each principal component computed on the correlation matrix of the transformed root traits after the removal of Block effects. The first four principal components contribute to more than 10.0% of the total variation.

Traits	*F-statistics*		χ^2
Trait description	Block DF = 3	Treatment DF = 1	Maternal Line DF = 1
Skeleton nodes (morphology)	**130.59 (<.001)**	2.13 (.15)	0.47 (.50)
Maximum diameter at 90-100% percent depth (morphology)	**1011.34 (<.001)**	1.62 (.20)	<0.001 (.99)
Average root density (morphology)	**113.94 (<.001)**	0.02 (.88)	0.13 (.72)
Mean tip diameter (morphology)	**1208.57 (<.001)**	2.09 (.15)	<0.001 (.99)
Root tip count (morphology)	**13.60 (<.001)**	1.31 (.25)	1.66 (.20)
Soil tissue angle range (architecture)	**5.70 (.001)**	2.78 (.10)	**4.66 (.03)**
Maximum soil tissue angle (architecture)	**7.33 (<.001)**	2.36 (.13)	**5.17 (.02)**
Root top angle range (architecture)	2.29 (.08)	1.82 (0.18)	**4.22 (.04)**
Number of Adventitious roots (morphology)	**1.29 (.28)**	0.01 (0.91)	<0.001 (.99)
Hypocotyl diameter (morphology)	**1116.61 (<.001)**	3.47 (.06)^	<0.001 (.99)
Tap root diameter (morphology)	**840.17 (<.001)**	0.52 (.47)	<0.001 (.99)

Table S3 Results for post hoc linear mixed model analysis on a subset of individual root traits. *F-values* and their corresponding *p-values* from ANOVA are also shown to indicate the effect of Block and Treatment on original root traits. Bolded values indicate a *p-value* < 0.05 and ^ indicates *p-value* < 0.07.

Root trait	Competitor DF = 5	Combination Pairing DF = 54
Root topology (PC1)	1.55 (.17)	1.33 ^ (.07)
Root architecture (PC2)	2.09^ (.07)	**1.38 (.04)**
Root size (PC3)	**2.55 (.03)**	**1.75 (.001)**
Root morphology (PC4)	0.65 (.66)	**1.47 (.02)**

Table S4 Supplementary results for linear model ANOVA on root topology, architecture and morphology to evaluate the effect of Competitor and Combination Pairing on root architecture standardized for Block effects. Root trait was treated as the response variable and Competitor and Combination Pairing were fixed effects, we ran separate models for each root trait (root topology, architecture, size and morphology), respectively. *F-values* and their corresponding *p-values* are shown to indicate the effect of Combination Pairing and Treatment on root architecture. Bolded values indicate a *p-value* < 0.05.

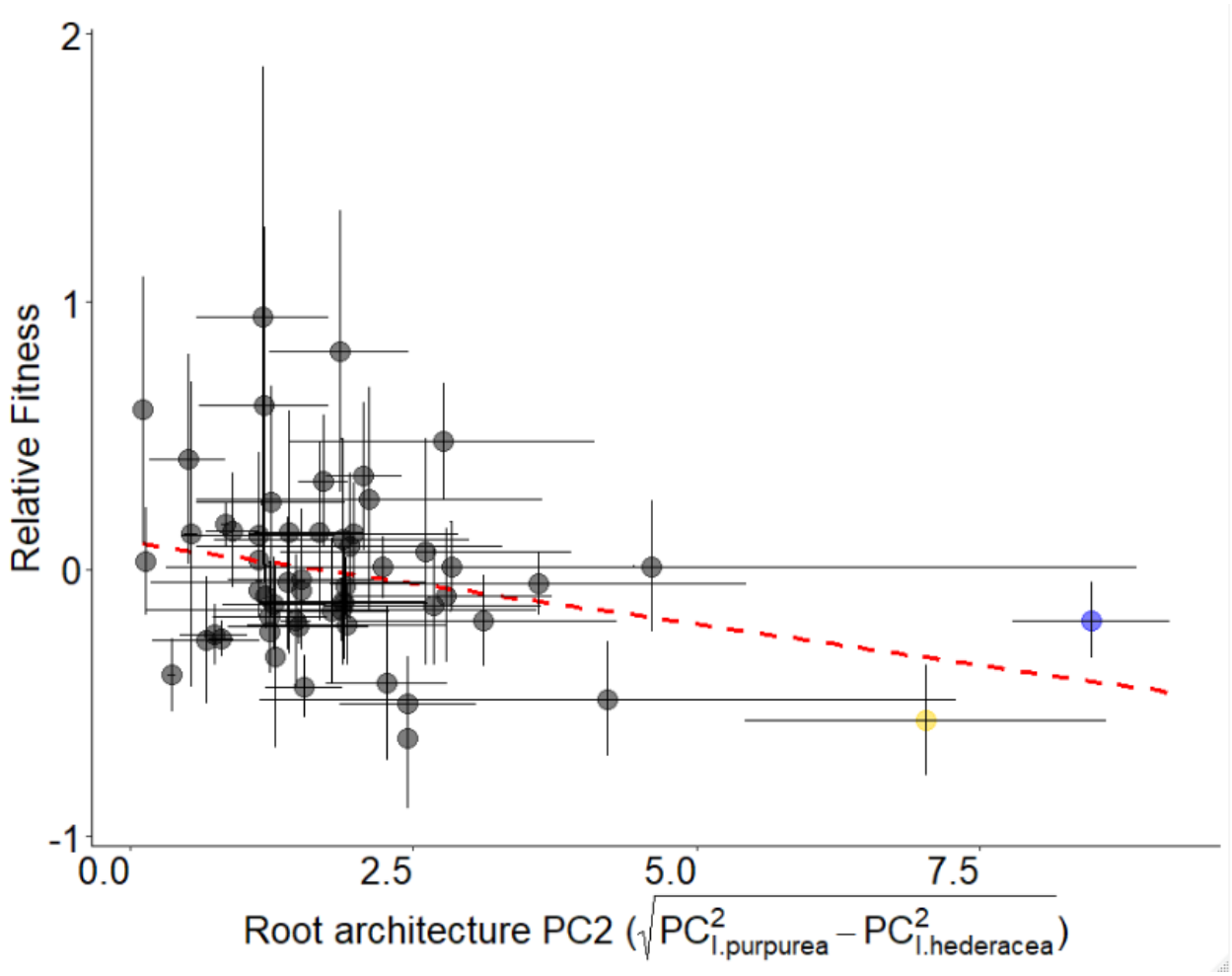


Fig. S3 Negative relationship (β = -0.06 ± 0.03, *p-value* = 0.04; Table 3) between phenotypic distance of root architecture (PC2) and standardized relative fitness for *I. purpurea* when in competition with *I. hederacea*. The phenotypic distance of root architecture was calculated as the Euclidean distance in PC2 between competing pairs of *I. purpurea* and *I. hederacea* after the removal of Block effects, and then averaged by maternal line and species by maternal line combination type. Each point represents two to eight biological replicates. For each point, error bars were drawn based on observed values of relative fitness (Y-axis) and root architecture (X-axis) for a given maternal line within competition treatment, respectively. **Colored points (yellow and blue) indicate two outliers that were maintained in our final analysis because of their low intraspecific variation.**

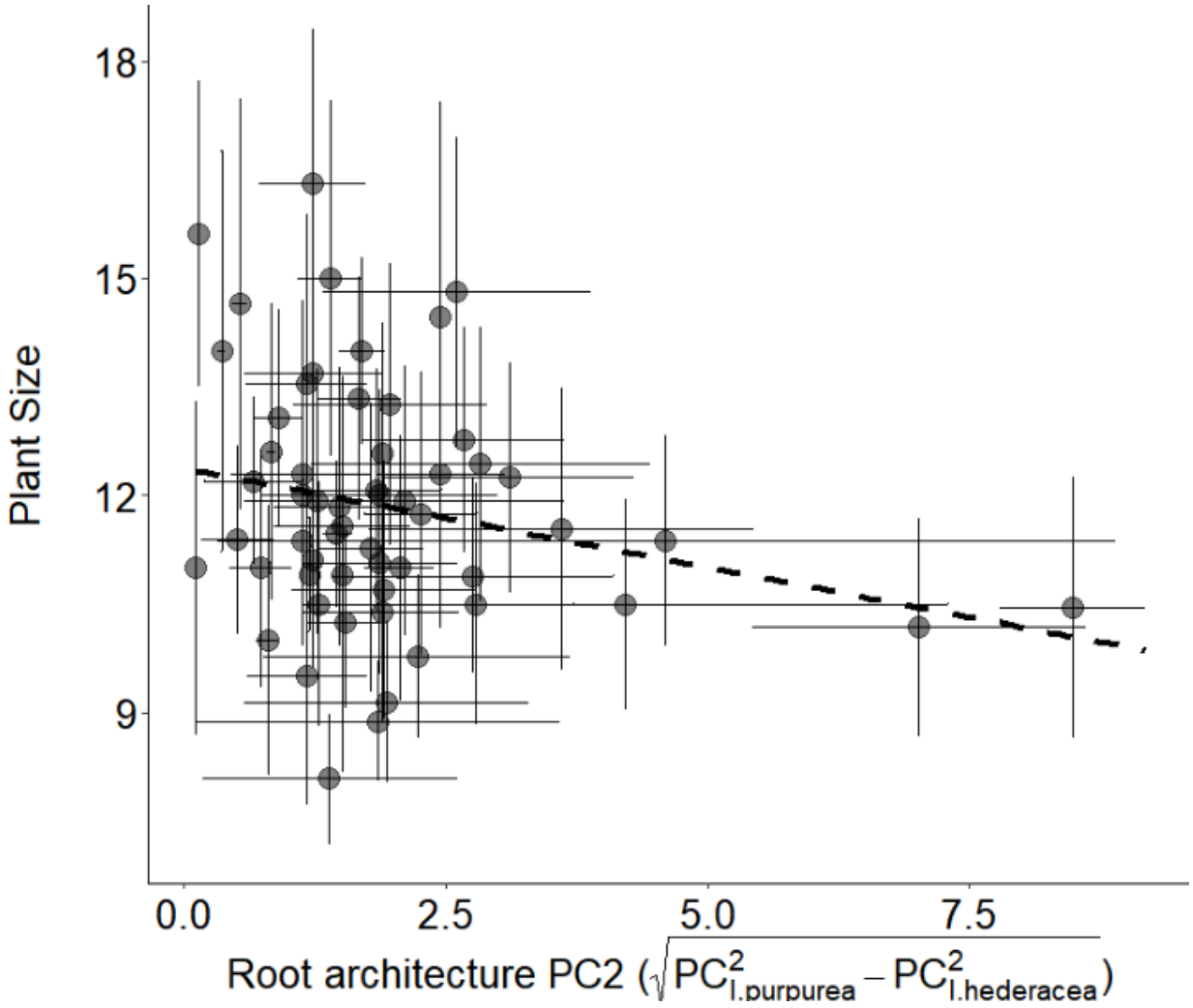


Fig. S4 Evidence of a marginally significant negative linear relationship (β = -0.27 ± 0.15, *p-value* = 0.07) between phenotypic distance of root architecture (PC2) and plant size (*i.e.,* leaf number averaged by combination pairing and maternal line) for *I. hederacea* when in competition with *I. purpurea*. The phenotypic distance of root architecture was calculated as the Euclidean distance in PC2 between competing pairs of *I. purpurea* and *I. hederacea* after the removal of Block effects, and then averaged by maternal line and species by maternal line combination type. Each point represents two to eight biological replicates. For each point, error bars were drawn based on observed values of relative fitness (Y-axis) and root architecture (X-axis) for a given maternal line within competition treatment, respectively, for *I. hederacea*.