

How to calculate root phenotypic plasticity as a trait for crop breeding programs

Problem

Agricultural production and its crop breeding programs are mainly oriented towards above-ground biomass. Nevertheless, phenotypic plasticity of the root system can improve resilience to environmental stress and ensure crop production under detrimental conditions.

Solution

The ability to alter phenotypic root traits in response to the environment can be integrated in breeding programs when the plasticity of individual root traits can be quantified. The relative distance plasticity index (RDPI), as described by Valladares et al. (2006), is a useful and easy to use index for the quantification of the plasticity of root traits. It can be applied in laboratory as well as in field conditions.

Benefits

By integrating root plasticity in breeding programs, the resilience of crops to drought, heat stress or limited nutrient availability can be improved.

Practical recommendations

R-script for calculating RDPI

1. Install R and RStudio.
2. Install standard R packages via the RStudio user interface: tidyverse (Wickham et al. 2019), agricolae (Mendiburu 2020) and psych (Revelle, 2024).
3. Download the specialised R packages directly from the respective developers and install in RStudio: Plasticity (Ameztegui, 2017) for calculating RDPI and ggradar (Bion, 2023) for creating spider plots.
4. Structure the root trait data as follows: a data frame including one column with data on trait name, one column for environmental factors, one column for species/genotype, and one column on trait value (numerical). Each row must be an independent observation.

Applicability box

Theme: plasticity, root traits, phenotypic, breeding, resilience, relative distance plasticity index (RDPI)

Equipment: R and RStudio

5. In Rstudio, using the `rdpi_matrix()` function from the Plasticity package (Ameztegui, 2017), calculate the relative distances for each observation. Consult the Plasticity package manual pages for guidance (https://rdr.io/github/ameztegui/Plasticity/man/rdpi_matrix.html).
6. For each root trait-treatment combination, calculate the RDPI as the mean of the relative distances as given in the `rdpi_matrix` and the standard error on the mean (SEM). The RDPI can be calculated as:

$$RDPI = \frac{\sum \left(\frac{|d_{ij} - i'j'|}{x_{ij} + x_{i'j'}} \right)}{n}$$

Where n is the total number of pairwise distances. Store these values in a separate data frame.

Interpretation and visualization of the results

- Using the RDPI values (mean of relative distances calculated in step 6), create a spider chart using the `ggradar` package (Bion, 2023) for visual comparison of plasticity index for different traits and genotypes. With a spider diagram, traits can be arranged to show the traits of most interest, for example, root traits versus shoot traits, and root traits for soil exploration versus traits for soil exploitation; see figure 1.
- Display calculated RDPI values with the associated SEM of the plasticity index using a dot chart for further comparison; see figure 2.

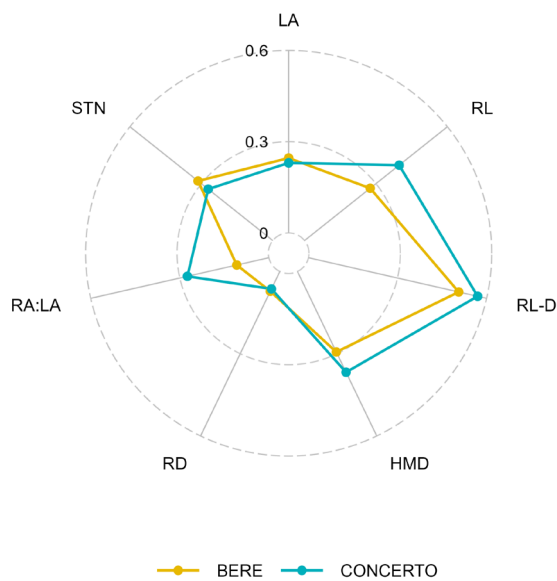


Figure 1: RDPIs for selected root and shoot traits for comparison between two barley genotypes; BERE (yellow) and CONCERTO (blue). This enables a quick overview and comparison of the RDPIs although it is limited by the number of traits that can be displayed simultaneously. LA: leaf area in cm^2 , RA: root surface area in cm^2 , RL: root length in cm, RL-D: root length density in cm/cm^3 , HMD: root half mean distance in cm, RD: root diameter in mm, Specific-RL: specific root length in cm/g , RA:LA: root:shoot surface area ratio and STN: shoot total nitrogen in mg. A value of 0 indicates low plasticity, a value of 1 indicates high plasticity. Data are from trials in controlled conditions in an experiment with increasing soil volumes available to the plants. Figure created by Doris Vetterlein, Jessica Clayton and Sebastian Blaser, 2023

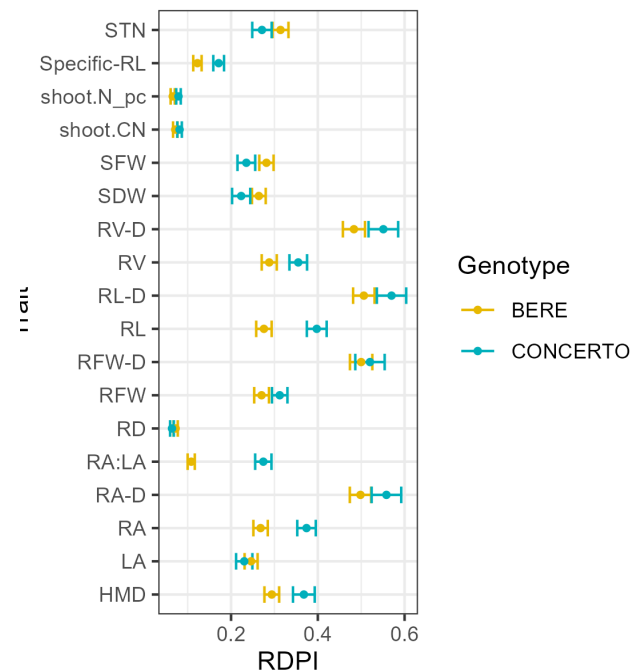


Figure 2: Dot chart showing the RDPIs of a higher number of selected traits, compared to the spider diagram in figure 1. The respective error (standard error of the mean) on the estimation of the index is also depicted. LA: leaf area in cm^2 , RA: root surface area in cm^2 , RL: root length in cm, RL-D: root length density in cm/cm^3 , HMD: root half mean distance in cm, RD: root diameter in mm, Specific-RL: specific root length in cm/g , RA:LA: root:shoot surface area ratio and STN: shoot total nitrogen in mg. A value of 0 indicates low plasticity, a value of 1 indicates high plasticity. created by Doris Vetterlein, Jessica Clayton and Sebastian Blaser 2023.

Further information

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About this practice abstract and Root2Resilience

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Root2Resilience: The project is running from September 2022 to August 2027. The overall goal of Root2Resilience – Root phenotyping and genetic improvement for rotational crops resilient to environmental change – is to develop root phenotyping, genetic and modelling tools and use them to define and test innovative genotype ideotypes able to enhance the tolerance to abiotic stress and carbon sequestration in soils

Project website: root2res.eu

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