Phenotypic spectrum: uncovering root architecture diversity in common bean (Phaseolus vulgaris)

Limeng Xie[1], James Burridge[2], Jonathan Lynch[2], and Alexander Bucksch[1]

[1]University of Georgia
[2]Pennsylvania State University

November 30, 2022

Abstract

Plant roots exhibit distinct architectural organization and overall shape. Current concepts to quantify architectural variation assume a homogeneous phenotype for a given genotype. However, this assumption neglects the observable variation in root architecture for two reasons: (i) sampling strategies are designed to capture architectural variation only for the most common phenotype, and (ii) traits are often measured locally within a root system and ignore the architectural organization. Here, we introduce a new concept: the phenotypic spectrum of crop roots to quantify architectural variation as the number of architecture types for one genotype in a specific environment. We use the shape descriptor DS-curve to characterize the whole root system architecture. Using DS curves as a core, we developed a computing pipeline that combines Kmeans++ clustering, outlier filtering and the Fréchet distance as a similarity metric to classify types of root architectures. Subsequently, we applied this pipeline to analyze a field dataset including three common bean (Phaseolus vulgaris) genotypes DOR364 (n=797), L88_57 (n=1772), and SEQ7 (n=768) under non-limiting and water-stressed conditions in 2015 and 2016. We found DOR364 showed five different root architecture types across environments, while L88_57 and SEQ7 showed four. The total variation within classified root architecture types of DOR364, L88_57, and SEQ reduced by 58.59%, 50.19% and 53.01%, compared to the variation of the complete data sets. DOR364 had stable fractions of root architecture types across environments. In contrast, L88_57 and SEQ7 showed more variation in their fractions. There was no significant biomass difference among root architecture types for all studied genotypes within each environment. As such, we hypothesize that the phenotypic spectrum might buffer the impact of environmental stresses as an acclimatization strategy by changing the composition of root architecture types at the population level.

Hosted file

`essoar.10508344.1.docx` available at https://authorea.com/users/546581/articles/608482-phenotypic-spectrum-uncovering-root-architecture-diversity-in-common-bean-phaseolus-vulgaris

Posted on 30 Nov 2022 — CC-BY-NC-ND 4 — https://doi.org/10.1002/essoar.10508344/v1 — This a preprint and has not been peer reviewed. Data may be preliminary.

Phenotypic spectrum: uncovering root architecture diversity in common bean (*Phaseolus vulgaris*)

Limeng Xie[1], James Burridge[2], Jonathan P. Lynch[2], Alexander Bucksch [1,3,4]

1. Department of Plant Biology, University of Georgia, Athens, GA 30602
2. Department of Plant Science, Penn State University, University Park, PA 16802
3. Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA 30602
4. Institute of Bioinformatics, University of Georgia, Athens, GA 30602

Plant roots exhibit distinct architectural organization and overall shape. Current concepts to quantify architectural variation assume a homogeneous phenotype for a given genotype. However, this assumption neglects the observable variation in root architecture for two reasons: (i) sampling strategies are designed to capture architectural variation only for the most common phenotype, and (ii) traits are often measured locally within a root system and ignore the architectural organization. Here, we introduce a new concept: the phenotypic spectrum of crop roots to quantify architectural variation as the number of architecture types for one genotype in a specific environment. We use the shape descriptor DS-curve to characterize the whole root system architecture. Using DS curves as a core, we developed a computing pipeline that combines Kmeans++ clustering, outlier filtering and the Fréchet distance as a similarity metric to classify types of root architectures. Subsequently, we applied this pipeline to analyze a field dataset including three common bean (*Phaseolus vulgaris*) genotypes DOR364 (n=797), L88_57 (n=1772), and SEQ7 (n=768) under non-limiting and water-stressed conditions in 2015 and 2016. We found DOR364 showed five different root architecture types across environments, while L88_57 and SEQ7 showed four. The total variation within classified root architecture types of DOR364, L88_57, and SEQ reduced by 58.59%, 50.19% and 53.01%, compared to the variation of the complete data sets. DOR364 had stable fractions of root architecture types across environments. In contrast, L88_57 and SEQ7 showed more variation in their fractions. There was no significant biomass difference among root architecture types for all studied genotypes within each environment. As such, we hypothesize that the phenotypic spectrum might buffer the impact of environmental stresses as an acclimatization strategy by changing the composition of root architecture types at the population level.

Key word: phenotypic spectrum, common bean, root system architecture