

phosphorus acquisition of maize. The objectives of the present study is to investigate the root morphological and rhizosphere differences among faba bean varieties and their effects on the growth and phosphorus uptake of associated maize, and to identify the mechanisms of efficient phosphorus acquisition in faba bean/maize intercropping.

A pot experiment was carried out to examine four faba bean cultivars, with difference in mobilizing soil sparingly soluble P and in root morphology, interacted with maize in three root interactive intensity (solid barrier, nylon mesh barrier and no barrier).

Results showed that acid phosphatase in rhizosphere soil of cultivar Lincan was 18.4% and 18.7% higher than that of cultivars Minqing and Zhangye. The citrate concentration in rhizosphere soil for cultivar Kangleniutabian was 2.1 times and 2.3 times as much as that of Minqin and Zhangye, and the malic acid concentration was 2.32 times and 2.31 times as much as those of Mingqin and Zhangye. The root length, root surface area and root volume of Lincan are all significantly higher than other cultivars. The rhizosphere processes of faba bean was positively correlated with not only P acquisition of faba bean itself, but also P acquisition of associated maize. The morphological parameters of faba bean roots was negatively correlated with P acquisition of associated maize.

The finding has shed a light on understanding the mechanism behind interspecific facilitation on P acquisition, but also have an importance in selecting a reasonable cultivar in intercropping.

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THE EFFECT OF COPPER TOXICITY ON SYNERGISMS AND ANTAGONISMS BETWEEN NUTRIENTS IN GRAPEVINE PLANTS

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Copper (Cu) accumulation in soils can induce toxicity and nutrient imbalances in several plant species. The aim of this work was thus to evaluate the effect of Cu toxicity on two grapevine rootstocks, Fercal and 196.17, and to elucidate if intercropping with oat can alleviate grapevine Cu toxicity using hydroponic trials and rhizobox experiments.

The hydroponic trial revealed that Cu-induced root exudation was correlated with genes expression (*VvPEZ*-like); furthermore the ionome analysis revealed that both mono- and intercropped 196.17 rootstocks display a synergistic effect on Zn and Mn in the root tissues at high Cu concentrations. An increase of Zn and Mn in roots was also reported for the intercropped Fercal rootstock at high Cu concentrations while an antagonistic relation was observed for root Zn in the monocropped Fercal rootstock. The rhizobox experiments further confirmed these results showing a different nutrient concentration depending on the rootstock and on the soil characteristics. Indeed, Cu availability is shaped by rhizosphere processes, which depend on soil properties and/or the co-cultivation of different plant species. The soil-based experiments revealed that nutrient availability and dissolved organic carbon including root exudates differ depending on soil properties and the rootstock rather than on the cultivation system. In particular, we did not observe any apparent competition

between the two plant species in the alkaline soil; on the other hand, in the acid soil, the intercropping revealed a beneficial effect reducing the available Cu in the rhizosphere.

Our results revealed that Fercal rootstock is able to take advantage from oat, while 196.17 seems disadvantaged by the intercropping system. Yet, even though the intercropping system seems to be a valuable tool to counteract grapevine Cu toxicity, the application of this agricultural practice has shown to be species and mostly soil type dependent and should be evaluated for each rootstock.

P.48 (will also be presented as poster pitch)

CHARACTERIZATION OF DIFFERENTIALLY ABUNDANT BACTERIA IN RHIZOSPHERE OF FIELD GROWN BRASSICA NAPUS GENOTYPES-IMPLICATIONS FOR BREEDING

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Successful integration of an ideal rhizosphere microbiome through targeted plant breeding is key to harnessing existing and new positive plant-microbial interrelationships in cropping agro-ecosystems. Here we examine the composition of bacterial communities in the rhizosphere of diverse *Brassica napus* (canola) genotypes to identify bacterial taxa that preferentially associate with particular genotypes. Rhizosphere soils of sixteen diverse *B. napus* genotypes sampled weekly over a ten-week period in three replicates were analyzed using a 16S rRNA gene amplicon sequencing approach. The *B. napus* rhizosphere microbiome is characterized by diverse bacterial communities with thirty-two named bacterial phyla, almost one third of the currently ~92 named phyla. The most abundant phyla were Proteobacteria, Actinobacteria and Acidobacteria. Compared with a reference *B. napus* genotype a total of 167 bacterial genera were significantly more abundant in at least one different *B. napus* genotype and 114 were significantly less abundant out of the total 982 genera. We observed the highest number of total and genotype specific differentially more abundant genera in the most diverse *B. napus* genotype. Proteobacteria and Actinobacteria were the major contributors of the differentially abundant bacterial genera, accounting for 64 to 70% of the differentially abundant taxa in each *B. napus* genotype. Other main contributors of the differentially abundant genera included Bacteroidetes and Firmicutes (12 to 17% of genera). The differential abundance analysis highlights potential beneficial *B. napus* -bacterial interrelationships that could be beneficial and potential targets for direct or indirect selection within breeding programs. Here we have identified potential beneficial roles including bacteria associated with disease suppressive soil, anti-fungal properties and plant growth promotion. This approach of identifying genotype specific differentially abundant taxa and major contributing bacterial groups could be a starting point that leads towards integrating plant microbiome considerations in canola breeding programs.