

## P232 Fine Root Dynamics and Its Possible Implications in Structuring the Rhizosphere Microbial Community in Sixteen *Brassica napus* (Canola) Lines

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In canola, root length was indicated as best indicator of seed yield. However, little is known about its root growth dynamics and possible implication in shaping rhizosphere microbial community. In this study, we examined weekly fine (FRL) (0.5 – 2mm), extra fine (< 0.5mm) and coarse root length (CRL) and root biomass in sixteen *Brassica napus* lines grown under field condition. We hypothesize that lines with distinct root dynamics would exhibit variability in their rhizosphere microbial community. Among the fifteen canola lines only Line 10 showed significant difference in all the measured root parameters with the reference Line. Line 10 followed by Line 9 exhibited the highest number of bacterial phyla, classes and orders that contributed to variability of canola lines with the reference line. This might indicate that their significant difference in root parameters with the reference line might have contributed to this difference. For all measured root parameters, mixed effect models indicated significant effect of sampling week. Hence, to further investigate the root growth dynamics along week we run generalized additive models. For FRL, reference line exhibited sharp increase up to the beginning of flowering followed by gradual decrease and stability till the end of flowering followed by increase and decline. Whereas Line 10 showed a gradual increase in FRL up to end of flowering followed by period of stability. Indicating differences in dynamics pattern. We will be further exploring the results to identify correlation between fine root responses and bacteria. This work contributes to the less explored area of linking root growth and development dynamics in crops with possible influence on rhizosphere microbial community.

## P233 Distribution and diversity of anammox bacteria in NW Portuguese coastal environments

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The discovery of anaerobic ammonium oxidation (anammox) revealed the existence of a shortcut in the classic nitrogen cycle where ammonium is converted directly to dinitrogen gas, and removed from the system. Anammox bacteria have been reported in a variety of habitats, from marine anoxic basins to freshwater lakes. Despite the widespread occurrence, low diversity of anammox bacteria has been reported with only five genera reported so far. In this study, we aimed to examine the diversity and distribution of anammox bacteria in natural habitats along the NW Portuguese coast. Sediment and soil samples were collected in different estuaries, coastal lagoons and saltmarshes. Total community DNA was extracted and anammox bacterial 16S rRNA gene and *hzsA* gene sequences were amplified. The amplicons were cloned and sequenced. Sequences were compared to reference sequences, aligned and submitted to phylogenetic analysis. Anammox-like sequences were recovered from samples from different locations including Cávado, Ave, and Douro estuaries, and agricultural soils. Phylogenetic analysis of the 16S rRNA genes has revealed the presence of *Candidatus Scalindua*, *Kuenenia*, and *Brocadia*. Obtained results will enable the selection of samples for further characterization using next generation sequencing to characterize community composition, and identify anammox lineages. The broad anammox bacterial distribution indicates that anammox might play an important role in removing fixed nitrogen from the sampled systems.