

HOW THE ROOT MICROBIOME AFFECTS YIELDS IN OIL SEED RAPE

Microbial colonisation, micro-organic activity in the root area (rhizosphere) and the root itself (root microbiome) have a considerable effect on the supply of nutrients, the vitality and growth not only of oil seed rape but all plant species. But what exactly does this mean and how can growers promote this?



While soil and climate conditions and the microbiome in the specific soil have a considerable influence on the microbial rhizosphere community, it is the genotype of the plant and hence the variety that is important for the endophytic root microbiome. This suggests that breeding can make a difference here (Fig.1).

Fungi and bacteria can increase yields

Shoots and roots are habitats of endophytic fungi and bacteria, many of which enhance the metabolic capabilities of their host plants. Unlike most species, oil seed rape doesn't develop mycorrhisation, i.e. it doesn't enter into a symbiosis with arbuscular mycorrhizal fungi. However, oil seed rape roots are also colonised by endophytic fungi and bacteria some of which have been shown to have growth-promoting and disease-inhibiting qualities.

The presence of endophytic fungi and bacteria can therefore increase yields or stabilise the yield potential of the crop and improve the yield quality. These effects result from the excretion of phytohormones which promote growth, improve the supply of nutrients and increase the plant's efficiency of absorbing the nutrients (especially N, P, Fe, Zn).

The root microbiome and its effects

The main effects of a growth-promoting root microbiome include an increased tolerance to stress (e.g. drought), an improved resistance to disease or significantly milder symptoms

FIGURE 2: ENDOPHYTIC COLONISATION OF GROWTH-PROMOTING FUNGI AND ITS EFFECT ON THE DEVELOPMENT OF CABBAGE HERNIA FOLLOWING AN INFECTION



Source: mod. according to Lahlali et al., 2014)
Lahlali R, McGregor L, Song T, Gossen BD, Narisawa K, Peng G (2014) Heteroconium chaetospora Induces Resistance to Clubroot via Upregulation of Host Genes Involved in Jasmonic Acid, Ethylene, and Auxin Biosynthesis PLoS ONE 9(4): e94144. <https://doi.org/10.1371/journal.pone.0094144>
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to compete with the pathogenic microorganisms in their immediate surroundings and by induced resistance of the plant (Fig. 2).

Which factors promote the root microbiome?

Soil management is the most effective and yet indirect measure to encourage the development of a growth-promoting root microbiome. Humus promoting cropping schemes such as spreading organic fertiliser and intercropping increase the density and activity of growth-promoting microorganisms and suppress the pathogens in the soil. Further effects on the quantity of growth-promoting microorganisms in the root zone of rapeseed are obtained by using a proper crop rotation in general and a proper preceding crop in particular.

Breeding offers the greatest potential

Breeding offers the greatest potential for using the root microbiome as a sustainable solution to increase yields and improve yield security and quality. Breeding can change the physiology and morphology of the root, for example.

Research currently focuses on the potential of making targeted use of growth-promoting endophytic microorganisms. These could already be used as seed microbiome in specific varieties. Yet it still takes further and comprehensive fundamental research before we can guarantee a reliable transfer across generations and unfailing effects in various conditions and climates. In principle, the root microbiome has the potential to significantly improve a plant's ability to absorb nutrients efficiently, to increase its resistance to soil-borne pests and its tolerance to abiotic stress such as drought. —

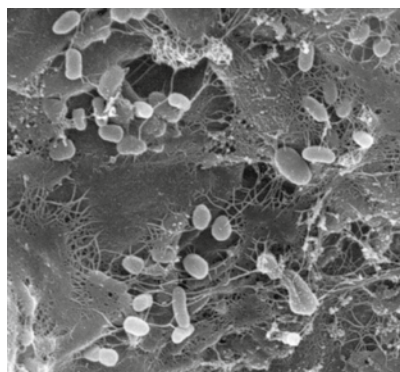
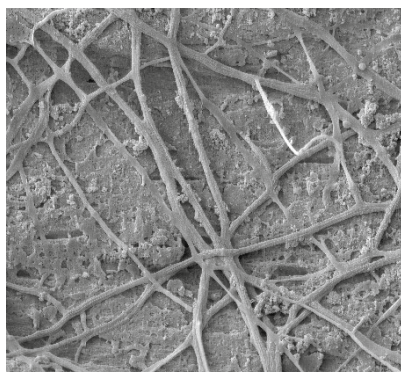
i The microbes

The root area of oil seed rape predominantly houses members of the Rhodoplanes and Sphingomonas genera whereas the root mostly hosts members of the Streptomyces, Rhizobium and Flavobacterium genera. The genus Streptomyces comprises many growth-promoting microbes that are able to improve plant health significantly by inducing resistance and increasing its tolerance to drought stress. Some members of this genus can fix nitrogen as symbionts of legumes but can also live non-symbiotically in the soil or in the roots of non-legumes. Also, a densely populated colony of rhizobia was found in the roots of oil seed rape that followed a crop of peas.

caused by this. In oil seed rape, this has been shown for infestation with cabbage hernia, sclerotinia and in particular with grey mould.

The pathogens are weakened by the presence of antibiotics and enzymes produced by the root microbiome and also by having

FIGURE 1: SEM RECORDINGS OF A SURFACE SETTLEMENT



A colony of fungi (left) and bacteria (right)
(REM images)

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