Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)
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Invisible helpers at the root:
How rapeseed gains more nitrogen with microbes

Press Release

Gatersleben, 11.02.2026 **The beneficial bacteria that colonise plant roots play a crucial role in nitrogen uptake and overall plant performance. An international research team, including scientists from the IPK Leibniz Institute, used rapeseed (*Brassica napus*) to demonstrate the interrelationship between genetic variation, transcriptional regulation, microbiome composition and resulting nutritional phenotypes. The study's results, which were recently published in the journal 'Nature Plants', are based on a large-scale field study employing modern data analysis techniques (multi-omics) and practical tests involving isolated bacteria.**

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Nitrogen is the most important nutrient for plants. Large quantities of nitrogen fertiliser are used worldwide, but this negatively impacts the environment and climate. Microbes promote the formation of lateral roots, helping plants to absorb nitrogen more effectively, especially when nutrients are scarce. If plants can make better use of the available nitrogen with the help of their natural root microbes, fertiliser use can be reduced and crop yields stabilised.

The research team analysed 175 different rapeseed lines at two locations in China. During flowering, the lateral roots and their rhizosphere were sampled in order to create rRNA profiles showing the bacterial composition.

The above-ground biomass was dried and a mineral profile comprising a total of twelve elements was created. A total of 1,341 linked datasets from genome, gene activity, microbiome and nutrient profiles were statistically analysed. The scientists then used various statistical methods to identify the plant genes and gene loci that control the frequency of certain bacteria.

“We have identified *Sphingopyxis* as a key bacterium. It promotes lateral root formation through the plant hormone auxin, increases biomass, and enhances nitrogen uptake, particularly at low nitrogen levels,” explains Dr. Guoliang Li, a scientist in the Quantitative Genetics research group at the IPK and one of the study's first authors. Explained visually: More lateral roots act like additional fingers, enabling the plant to ‘grasp’ nutrients from the soil more effectively. Sphingopyxis provides the signal that allows these ‘fingers’ to grow.

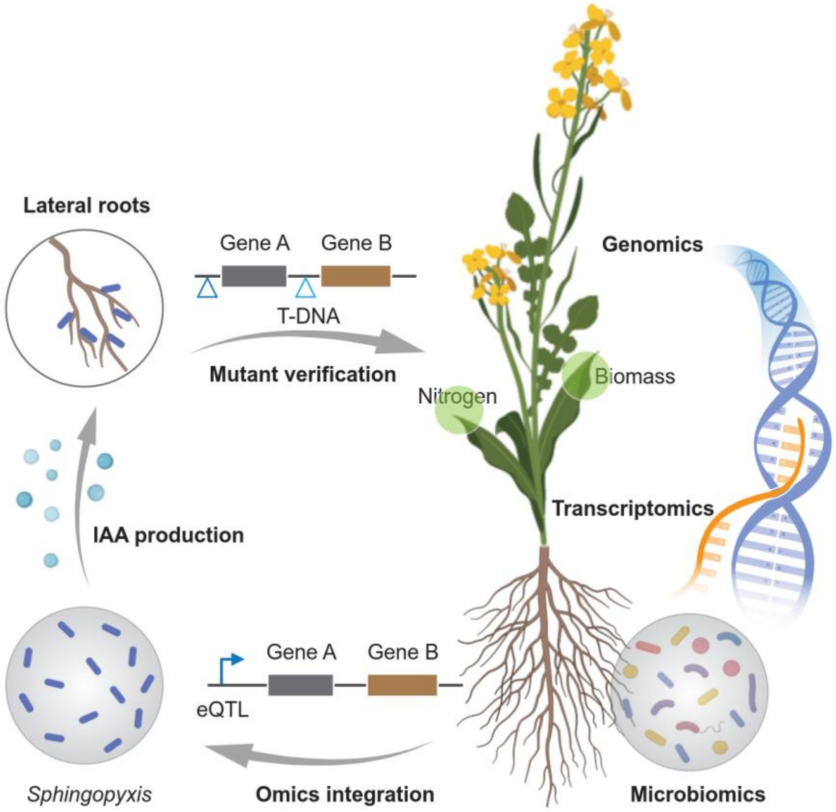
“We identified numerous genetic control points, or ‘eQTL hotspots’, which influence the abundance of specific bacteria in the root zone, particularly those associated with the plant's carbon and nitrogen metabolism,” explains Dr. Guoliang Li. The study shows that gene activity and microbiome properties can account for up to 45 per cent of the variation in nitrogen uptake. The composition of the microbiome is better described by genes and their activity than by the genome alone.

“Our current study provides a solid foundation for identifying the causal relationships between plant genetics, the microbiome, and nutrient uptake. The eQTL hotspots and candidate genes that we have identified are a good starting point for breeding and further functional studies," says Prof. Dr. Jochen Reif, head of the 'Breeding Research' department at the IPK. In the future, if varieties are bred specifically to attract and utilise beneficial microbes such as Sphingopyxis, they will be able to grow steadily with little fertiliser. This reduces costs, protects the soil, cuts emissions and ultimately helps to create more climate-friendly, sustainable production systems.

Original publication:

Li *et al.* (2025): Large-scale multi-omics unveils host-microbiome interactions driving root development and nitrogen acquisition. Nature Plants. DOI: 10.1038/s41477-025-02210-7

Graphic:



A schematic model depicting the potential of omics prediction on identification of causal plant-microbial interactions in *Brassica napus.*