

Soil provides new microbial sources for natural products

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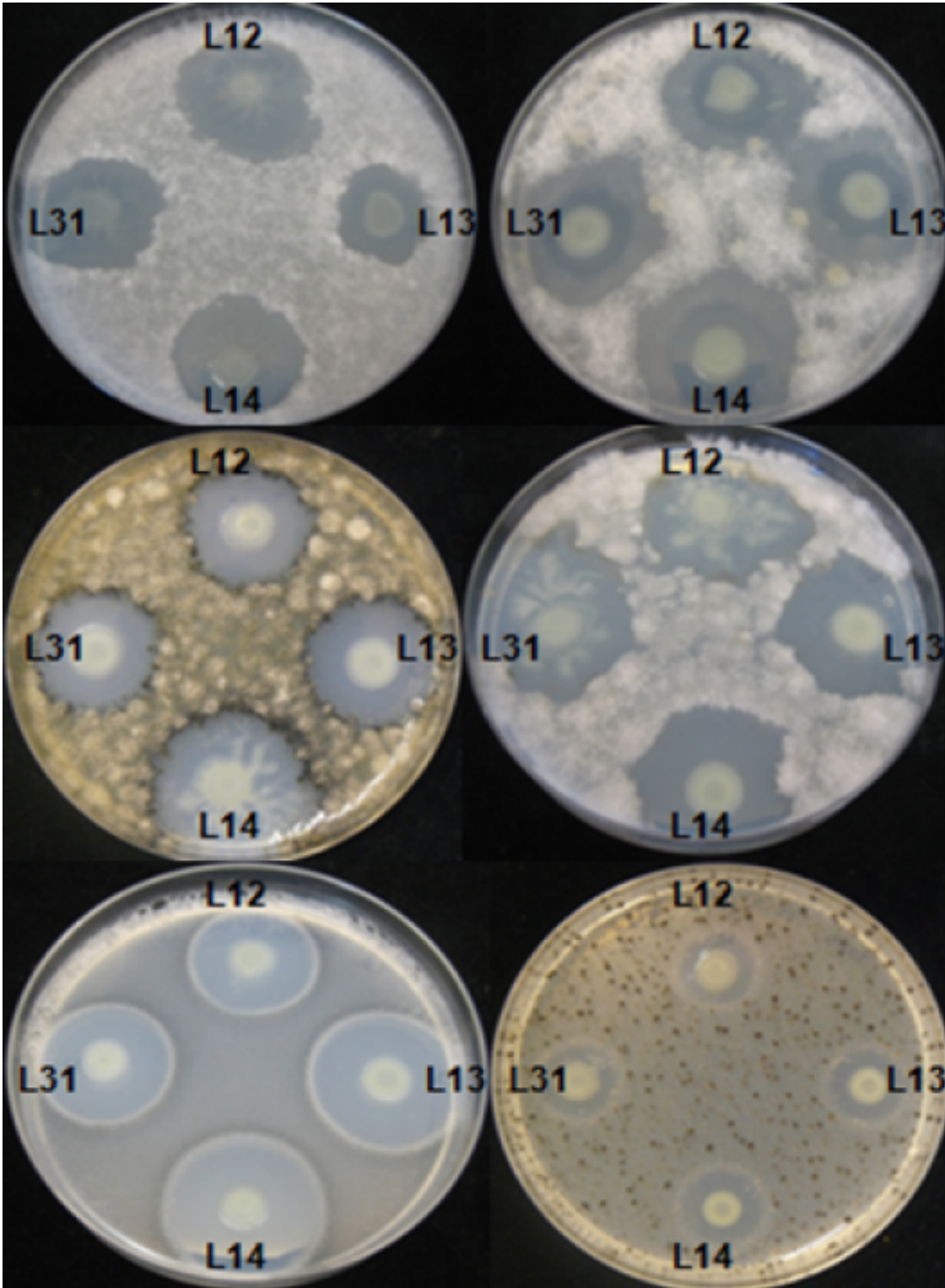
The role of the soil as a treasure trove of new, useful, natural products is again confirmed by the discovery of as yet unknown genes in *Lysobacter* bacteria. Research conducted by Wageningen UR and NIOO shows that these genes or gene clusters probably code for currently unknown antimicrobial substances.

Lysobacter [bacteria](#) are known for their disease-suppressing properties against the soil fungus Rhizoctonia. This fungus causes root rot in many crops, such as potatoes, sugar beets, vegetables and bulbs. Until now, however, little was known about how Lysobacter bacteria function. Researchers from Wageningen UR and the Netherlands Institute of Ecology (NIOO) therefore mapped out the properties and genes of various Lysobacter species. The results of this research not only confirmed the presence of genes for the production of previously known [antimicrobial agents](#) but also identified unknown genes or gene clusters that probably code for as yet unknown antimicrobials. This once again demonstrates the role of soil as an important [treasure trove](#) of new, useful, [natural products](#).

Disease-suppressing properties

The soil contains huge numbers of different types of micro-organisms with currently unknown properties. Prior research on soils with disease-suppressing properties has identified a large collection of bacteria of the genus Lysobacter that inhibits the growth of the Rhizoctonia fungus.

Four Lysobacter species



The Lysobacter isolates (L-numbers) inhibit various fungi; each dish contains a different fungus. Clockwise from top left: 2x Fusarium, Stemphylium, Aspergillus, Verticillium and Cercospora. Credit: Ruth Gómez Expósito, NIOO

For this study, eighteen *Lysobacter* isolates from four species were used to test their activity and differing ability to inhibit other micro-organisms. It turned out that most of the isolates could inhibit various plant-pathogenic fungi, bacteria and oomycetes. They also produce multiple enzymes, such as chitinases, glucanases and proteases. The degree of inhibition was affected by growing conditions, such as the type of medium, but also by the presence of the pathogenic fungus itself.

Genome mapped

The complete genome of four *Lysobacter* species was mapped. Comparison of these genome sequences with existing knowledge in data files shows the presence of genes for the production of known antimicrobial agents (such as Lysobactin, phenazine, WAP-8294A2 and dihydromaltophilin). In addition, the *Lysobacters* contain unknown genes or [gene clusters](#) which probably code for as yet unknown antimicrobials. Research into the metabolites profile of these *Lysobacters* supports the genetic information. Particularly interesting is the presence of a currently unknown metabolite which is only produced in the presence of *Rhizoctonia* by one of the *Lysobacter* species.

Variation per isolate

Lysobacter species have about 50% of their DNA sequences in common, while the other 50% are species or isolate specific. The ability to inhibit various micro-organisms also varies per isolate. This is supported by the genetic information for the production of various metabolites by [species](#).

More information: Ruth Gómez Expósito et al. Diversity and Activity of Lysobacter Species from Disease Suppressive Soils, *Frontiers in Microbiology* (2015). [DOI: 10.3389/fmicb.2015.01243](https://doi.org/10.3389/fmicb.2015.01243)

Irene de Bruijn et al. Comparative genomics and metabolic profiling of the genus Lysobacter, *BMC Genomics* (2015). [DOI: 10.1186/s12864-015-2191-z](https://doi.org/10.1186/s12864-015-2191-z)

Provided by Wageningen University

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