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Gammaproteobacteria in the guts of soil fauna may respond to soil pollutants

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Video Byte

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Abstract

Environment-derived gut microbes can contribute to host health. In soil invertebrates, the gut microbiome is gradually assembled from the specific soil microecological region that the host inhabits. However, the effects of environmental stress on soil invertebrate microbiomes remain unknown. To learn more, a new study sought to characterize the gut bacterial taxa of the soil invertebrate Folsomia candida in the presence or absence of environmental concentrations of soil pollutants. Sequencing revealed that exposure to the fungicide azoxystrobin (AO), the antibiotic oxytetracycline (OTC), or their mixture (AO) increased Gammaproteobacteria abundance. The Gammaproteobacteria response was closely associated with F. candida physiological and functional indicators, such as the locomotion (HAA) index and oxidative stress. Machine learning models based on metadata from other studies indicated that Gammaproteobacteria was the core bacterial taxon with the greatest gut colonization potential and the best indicator taxon of the response to environmental concentrations of soil pollutants. Gammaproteobacteria abundance was also linked to antibiotic resistance gene abundance. Although further functional analyses are needed, the results identify Gammaproteobacteria as an indicator taxon in soil invertebrate guts that can aid in assessment of soil ecological risk and evaluation of global soil ecological health.