Determining gene expression variation of *Folsomia candida* in natural Dutch soils

Soil pollution is a serious ecological problem that threatens the general publics’ health. It is estimated that 600,000 sites are polluted in the Netherlands alone, of which 60,000 need urgent evaluation. A certain prioritization is needed as to decide which sites need to be sanitised. Bioavailability, or to what extend organisms take up polluting chemicals, plays a major role in the actual toxicity of polluting chemicals. A standard ISO test bioassay, where survival and fecundity of the springtail *Folsomia candida* are measured, is used to determine bioavailability; however this test lacks specificity, sensitivity and speed. To solve these problems we are developing an alternative test where a microarray platform is used to measure gene expression patterns in *F. candida*.

To validate the new microarray platform, basal expression patterns obtained from *F. candida* cultured in natural soils, need to be established, to determine if it is possible to distinguish between healthy soils and polluted soils. We want to determine the variation of gene expression in *F. candida* on these healthy soils which we dubbed the Normal Operating Range (NOR) and to determine if abiotic conditions like soil pH and moisture content have an influence on gene expression.

This project is part of the "Assessing the living soil: an ecogenomics approach to sustainable life-support functions" project.

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**Participants**

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