Determination of the molecular stress response in *Folsomia candida*

Stress-related genes will be isolated from the parthenogenetic springtail *Folsomia candida* in a straightforward manner, using suppression subtractive hybridisation followed by PCR cloning. Candidates involve genes coding for DNA repair proteins, antioxidants, HSPs, MTs, kinases, and transcription factors (Korsloot et al. 2004). Once isolated these genes will be tested for differential expression under stressed conditions using Realtime Q-PCR. Eventually a molecular mechanism will be postulated for each of four stressors: (i) metals (e.g. cadmium), (ii) PAHs (e.g. phenanthrene), (iii) pesticides (e.g. diazinon), and (iv) mineral oil. The idea is that it will be possible to discriminate between genes involved in a general stress response and genes that are transcriptionally affected by each of the specific contaminants. The latter genes may represent specific endpoints of a toxic outcome due to exposure to a contaminant.


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

**Duration**

4 years (September 2004-August 2008)

**Participants**

Muriel de Boer, Dick Roelofs, Nico van Straalen