Summary

Pollution is a worldwide problem, and threatens proper functioning of soil. In order to assess soil quality, ecotoxicological methods are used such as bioassays. Springtails (Collembola) are abundant in soil and important for terrestrial ecosystems, and are therefore often used in soil bioassays. In particular the springtail *Folsomia candida* is used in bioassays, because it is easy to rear in laboratory, and it is often one of the most sensitive taxon to soil contaminants. Novel genomic tools, such as the microarray technique, have been proposed and shown to supplement ecotoxicology. This new science, called ecotoxicogenomics, is already applied to many aquatic non-model organisms. For ecologically relevant soil organisms, until now, only earthworms were used. The aim of this thesis was to explore the possibilities of genomics to enhance springtail ecotoxicology. The microarray technique can be used to gain more insight in toxic mechanisms or modes of action of contaminants, and genomic endpoints are faster and more sensitive than traditional ecotoxicological ones.

In *Chapter 2* a study is described wherein *F. candida* was exposed to soil containing the non-essential metal cadmium. A microarray was constructed to measure the expression of more than 5,000 genes of *F. candida* after 2, 4, and 7 days of exposure to the cadmium containing soil. The expression of 1,586 genes altered during one or more timepoints in response to cadmium, suggesting the induction of processes such as stress response, detoxification, and hypoxia. Also, the results imply the synthesis of antibiotics such as penicillin (or penicillin-like compounds) by *F. candida*, which have never been reported to be synthesized by animals before. Further research is needed to confirm antibiotic production by these animals.

*Chapter 3* reports a toxicogenomic study of *F. candida* exposed to the polycyclic aromatic hydrocarbon (PAH) phenanthrene. The springtail was exposed for two days to two different concentrations of phenanthrene, representing EC10 and EC50 on reproduction after 28 days. In total 405 (EC10) and 251 (EC50) transcripts were differentially expressed after phenanthrene exposure, of which only 50 were differential in response to either concentration. Induction of genes encoding cytochrome P450s, glutathione S-transferases, UDP-glucosyltransferases, and ABC-transporters suggested extensive biotransformation and xenobiotic detoxification processes. Also, an impaired immune response was observed, which is comparable with the transcriptional response to cadmium (*chapter 2*).
Heat is another type of stress which can be harmful to soil ecosystems. The heat induced transcriptome of *F. candida* was assessed in Chapter 4. Comparable with other organisms many heat shock proteins were upregulated in response to heat. Also, many genes were induced encoding enzymes involved in cellular respiration (e.g., oxidative phosphorylation), which suggested an increased need for energy. Overall the number of genes that responded to heat stress was low compared to transcriptomic studies in other organisms, which might suggest a mild response. This speculated mild response could be caused by genetic adaptation of *F. candida* to a stable (buffered) soil habitat, but more research is needed to confirm this.

In Chapter 5 microarrays were used for a more diagnostic method. Gene expression profiles were generated from *F. candida* exposed to soil that was spiked with either one of six different metals (Ba, Cd, Co, Cr, Pb, or Zn) at different concentrations, and to non-spiked soil. Using the USC method a gene set (classifier) was selected that was able to discriminate between the different metals. Validation on an independent set of samples showed an accurate prediction of 83% (error rate = 0.17). Additionally, prediction of contaminated field soil content was not possible, probably because more insight is needed in the transcriptional response of *F. candida* to different soil properties, and mixtures of toxicants.

This thesis describes the first toxicogenomic studies of *F. candida*. It shows that the microarray technology helps to elucidate toxic mechanisms and modes of action of contaminants in springtails. Furthermore, ecotoxicogenomics generates new fast, sensitive, and compounds specific endpoints. Nevertheless, more research is needed for proper integration of genomics into springtail ecotoxicology.