INTRODUCTION
Terrestrial Model Ecosystems (TME) can serve as an intermediate tool between laboratory and field tests in the Environmental Risk Assessment (ERA) of plant protection products. At the PERAS workshop in 2007 the question was posed, whether the stability of the soil coenosis is influenced by a sequential sampling strategy (Schäffer et al., 2010). Since for sampling of the fauna soil cores have to be removed from the system and thus sampling results in a continuous reduction of habitat space using sequential sampling, this side effect may influence the environmental conditions of the populations in the remaining soil layer in the TME. An alternative strategy is to use previously not sampled pristine TME, but these TME have to be discarded after use. One disadvantage is that for this sampling strategy with pristine TME much more TME have to be used to achieve the same statistical detection level. To test the possible influence of habitat loss on the soil biocenosis we carried out an experiment comparing both strategies over a sampling period of one year.

METHODS
Terrestrial Model Ecosystems (TME) were cored in an untreated meadow and placed in the gaiac TME facility at the RWTH Aachen University (Fig. 1). At six sampling dates soil cores for the extraction of mesofauna were taken. Two treatments were investigated: Pristine TME were sampled only once and thus were not underlying habitat loss before. Sequentially sampled TME were sampled at each sampling date. This resulted in a habitat loss of ~4% of the upper 5 cm soil layer per date (Fig. 2). Soil mesofauna - namely Collembola, Oribatida, Enchytraeidae and Nematoda - was extracted and determined to species and family level respectively (Fig. 1). Endpoints tested were:
- Population abundances on different taxonomic levels (order, family, species)
- Diversity measures (Shannon-Diversity, Evenness, Taxa richness)
- Community measures (Principle response curves - PRC)

RESULTS
More than 80000 individuals from 27 species of collembolans, 17 species of oribatid and 21 species of enchytraeids as well as 25 nematode families were extracted and determined over the whole study period (Fig. 3). Statistical analysis of abundances, diversity and community structure showed, that in MOST CASES NO SIGNIFICANT DIFFERENCES between results of the two sampling strategies were detected. 13 from 110 endpoints showed significant differences from which 7 occurred already at day 0. Thus, only for 5% of all endpoints significant differences were found between the two sampling strategies. Three endpoints may indicate an adverse effect of the sequential sampling strategy. However, a clear tendency of different abundances or a higher diversity in pristines vs. sequentially sampled TME have not been detected.

DISCUSSION
For 90% of the endpoints no significant differences between the tested TME series were observed. Most of the differences were already observed on day 0 when the sequential sampling had no influence yet. For the oribatid mites, the most significant differences in the starting community lead to significant differences at subsequent samplings in some population and community endpoints. However, these effects are not caused by the sampling strategy. Furthermore one enchytraeid species and two nematode families showed significantly different abundances between the treatments. However, these effects were observed only on a single sampling date. Thus, no continuous trend over several sampling dates occurred.

CONCLUSION
- The results of the present study demonstrate that the habitat loss due to sequential sampling did not markedly influence the soil mesofauna in the TME.
- No general tendency of decrease in species richness, diversity or population abundances due to sequential sampling was observed.
- The advantages of the sequential strategy are a reduced need of meadow space per study and/or the use of larger TME with less edge effects which are influencing the stability of the community.
- Therefore, the sequential sampling is recommended for testing the soil mesofauna in terrestrial model ecosystems.