Development of ecosystems to climate change and the interaction with pollution—Unpredictable changes in community structures

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ABSTRACT

Climate change has serious impacts on ecosystems, e.g. species diversity and abundance. It is well known that changes in temperature may have a pronounced influence on the reproductive output, growth and survival of various terrestrial species. However, much less is known on to how changes in temperature combined with exposure to pollution will influence biodiversity, the interaction between species, and the resulting change in species composition. In order to understand the effects of changes in temperature and copper pollution (individually and in combination) on soil communities and processes, a factorial multispecies experiment was performed. Six animal species (representing different functional groups) were exposed in control (30 mg Cu/kg) and copper-contaminated soil (1000 mg Cu/kg) to four temperatures (10, 14, 19, and 23 °C) representing the "summer" range (low to high) for Denmark, and three exposure periods (28, 61, and 84 days). The species composition, feeding activity and OM turnover were assessed throughout. Multivariate analysis displayed significant changes in the food-web both with different copper levels and temperatures, resulting in different species composition for each exposure scenario. The most important species were *Enchytraeus crypticus* (most sensitive to copper and temperature) and *Folsomia candida* (most abundant). Major changes in abundance due to temperature occurred in the first 28 days of exposure, where population growth was higher. A temperature dependent population growth rate could be modeled for an exposure period of 28 days, whereas after 61 and 84 days of exposure the data did not fit the model. Especially for treatments that also included Cu, modeling of the population growth was no longer possible. The results of our study indicate that when climate change occurs in polluted areas, the consequences on populations cannot be predicted based on data from non-polluted areas. The risk may be synergistic for certain species, as indicated in the present study, and the final balance may depend on the particular species composition of that ecosystem.

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1. Introduction

Climate change such as increase/decrease in temperature has caused severe impacts in the environment, e.g. on species abundance and distribution in soils (Angilletta et al., 2004; Messenger, 1959; Uvarov et al., 2011). As a consequence, such effects can be transferred into changes at the ecosystem services (Blankinship et al., 2010; Iglesias Briones et al., 2009; Nicolardot et al., 1994).

However, it is well known that temperatures influence the development of individual invertebrate species i.e. the thermal-time or degree day concept. Previous studies investigating interactions between temperature and contamination have primarily been using single-species test systems (Khan et al., 2007; Ma, 1984; Sandifer and Hopkin, 1997). Although, single-species-based ecotoxicological data are essential for a present time ecological risk assessment, they do not allow for the assessment of community-level effects caused by species interactions e.g. predation, mutualism, competition, etc. (Beare et al., 1995; Bogomolov et al., 1996). Such interaction combined with known species differences in optimum temperatures (Jansch et al., 2005), limits the ability of single species data to predict effects of climate change on communities.

Species interactions have been studied partly in field studies (Briones et al., 1997; Fountain and Hopkin, 2004; Holmstrup et al., 2007), partly in the laboratory (Alonso et al., 2006; Baker and Senft, 1995; Bogomolov et al., 1996; Forster et al., 2004; Kools et al., 2009; Kuperman et al., 1998; Parmelee et al., 1997; Pernin et al., 2006; Scott-Fordsmand et al., 2008). The multispecies systems presented by e.g. Pernin et al. (2006) or Scott-Fordsmand et al. (2008) attempt to combine the advantages of laboratory test systems (i.e. standardized conditions and monitoring) with ecologically important species interactions by making a fully standardized multispecies system. These systems can be used to estimate a community response to various environmental stressors.

Such multispecies studies investigated the influence of contaminants, but to our knowledge only very few studies reported on the interaction between chemicals and climate change related parameters, e.g. drought (Holmstrup et al., 2007; Kools et al., 2009) and precipitation (Kuperman et al., 2002). Many studies have been performed to determine the effects of increased copper (Cu) levels on ecosystem structure and function. Although essential, Cu is toxic when present at "high" concentration, leading to changes in community structures and altered the nutrient cycles (e.g. C and N) (Amorim et al., 2012; Howcroft et al., 2011; Strandberg et al., 2006; Vieira et al., 2009).

The aim of the present study was to assess the effects of changes in temperature in combination with Cu pollution on soil communities and processes/functions. A soil multispecies system (SMS) was designed consisting of six species representing different functional groups in a "food web design" community. This food web community was exposed to a range of temperatures (from mean annual values to extreme summer temperatures for Denmark) in a non-contaminated and a historically Cu-contaminated field soil (Pedersen et al., 1999). The measured parameters included species abundance, feeding activity and organic matter turnover.

2. Materials and methods

A laboratory food-web mesocosm experiment was conducted following the design of the soil multispecies test systems (SMS) described by (Scott-Fordsmand et al., 2008). In brief, the species composition of the SMS represents a Danish agro-ecosystem (Krogh et al., 1996). Six species were included: four Collembolan, one predatory mite and one enchytraeid. These belong to different functional groups with mutualism, competition, predation (and other less discriminated) interactions being represented. The soil was taken from a well-studied site with a history of Cu contamination and known Cu gradient. Soil, collected from clean and contaminated areas was first defaunated and then inoculated with a controlled microbial substrate. Soil community structure was followed over time, sampled at days 28, 61 and 84. Soil function parameters were also measured using bait lamina and litterbag tests to assess feeding activity and organic matter turnover, respectively. A total of 124 SMS units were prepared.

2.1. Experimental design and set up

The study was designed as a two-way factorial experiment: factor 1 – Cu exposure (control: 30 mg Cu/kg dw and contaminated soil: 1000 mg Cu/kg dw); factor 2 – temperature: 10–14–19–23 °C. Samples were taken after 28, 61 and 84 days. Five replicates per treatment were used.

The experimental SMS units consisted of polyethylene tubes (33 cm × 9.3 cm ø), having a surface area of 68 cm^2 and sample volume of 2241 cm^3. The tubes, closed on the bottom with a lid, were filled with 1000 g moist soil (800 g dry weight plus 200 ml aqueous microbial substrate). Experiments were performed in temperature controlled rooms (variation in temperature was ±1 °C). After the addition of animals, each unit was covered with a perforated lid, weighted and transferred to the controlled temperature test room with a 12 h:12 h light:dark cycle. The soil water content was maintained by replenishing water loss weekly.

2.2. Test soil

The soil was taken from a site in Hygum, Jutland, Denmark, where from 1911 till 1924 a timber impregnating factory labored, using mainly copper. From 1924 until 1991 the area has been used for agriculture purposes and thereafter it became fallow. This resulted in a Cu gradient, ranging from background levels up to approximately 3000 mg Cu/kg (dry weight), with a gradual increase toward the center of the field (Pedersen et al., 1999; Scott-Fordsmand et al., 2000; Strandberg et al., 2006).

The main physico-chemical characteristics of the soil are as follows: 20–32% coarse sand (>200 μm), 20–25% fine sand (63–200 μm), 11–20% coarse silt (20–63 μm), 12–20% silt (2–20 μm), 12–16% clay (<2 μm), 3.6–5.5% humus and pH (H$_2$O) of 6.3. The soil was sampled to a depth of 20 cm. To eliminate fauna, the soil was dried at 80 °C during 24 h in an oven (Memmert, Type UL40, Braunschweig, Germany), and then sieved through a 2 mm mesh to remove larger particles.

The soil was collected from two different locations, a control and a Cu-polluted with concentrations of ca. 30 and 1000 mg Cu/kg dried soil, respectively. The higher concentration was selected based on the known sensitivity of Enchytraeids to Cu at the reproduction level (EC$_{50}$ = 439 ± 130 mg/kg) and survival (no effect at 1000 mg/kg) (Maraldo et al., 2006). Further, species have been observed to be more sensitive when exposed individually than when in mesocosms with several species (Scott-Fordsmand et al., 2008).

2.3. Microbial substrate

The procedure to extract the microbial substrate and inoculate it into the experimental chambers was based on Scott-Fordsmand et al. (2008). Freshly collected soil from the control area of the field site (1 kg wet weight) was mixed with 2 l of deionized water and shaken for 3 h. After this, the soil–water solution was filtered through a 50 μm mesh and diluted 10 times for use in the experiment. The soil water content was adjusted to 20% of which 10% was added with the microbial inoculate.

2.4. Test organisms

All soil invertebrates used in the SMS were cultured in the laboratory and had been kept for several generations. The organisms were randomly selected among adult sized animals and added to the SMS at three different stages (see Table 1 for details).

Here we summarize the information on test species, respective group of organisms, known role in the food web/function and assumed/known interactions. Information on the life form of the organisms is based on Hopkin (1997) and Lokke and Van Gestel (1998). As can be seen from Table 1, the types of interactions that may occur between collembolans are numerous, e.g. competition, mutualism, neutralism or amensalism (Hopkin, 1997). Predation was included via the mites, which prey on collembolans and enchytraeids (Krogh, 1995). There are some functions less clear, e.g. we know that collembolans can be decomposers to a lesser extent (more important in acidic fields where few earthworms are present) or that some enchytraeid species may feed on fungal hyphae as a relevant substrate but it is not entirely understood if they feed on microorganisms (Lokke and Van Gestel, 1998).

2.5. Soil function analyses

2.5.1. Bait lamina test

The feeding activity of soil fauna was assessed using the bait lamina method (Kratz, 1998). In short, bait lamina are plastic lamina sticks, containing 16 holes which are filled with a cellulose-based substrate (70% cellulose, 25% nettle powder (organic grown), 5% activated charcoal). One bait lamina stick was used per SMS, added on days 7, 28 and 61, and removed one week after insertion date. The feeding activity was expressed as the percentage of empty (eaten) plus the partially eaten holes per day. Four extra SMS units were used, under the same test conditions and at 19 °C to determine the appropriate time period for bait-lamina sampling days.