DOES THE LONG-TIME WARMING AFFECT THE DIVERSITY OF MYXOMYCETES IN ARCTIC SOILS?

Leontyev D.V.[1,2]
[1]H.S. Skovoroda Kharkiv National Pedagogical University;
[2]Kharkiv State Zooveterinary Academy

В огляді наведено концепцію наукового проекту, який наразі реалізується сумісною нідерландсько-українсько-американською дослідною групою. Метою проекту є дослідження видового різноманіття міксоміцетів у ґрунтах Аляски в умовах штучно стимульованої зміни клімату. Дослідження ґрунтового метагеному у рамках проекту здійснюється за допомогою технології іонного напівпровідникового секвенування ДНК.

Ключові слова: біорізноманіття, міксоміцети, секвенування нового покоління, біологія ґрунтів.

The article describes the concept of the scientific project, which is currently realized by the join Netherlands-Ukrainian-American research group. The purpose of the project is the study of the species diversity of Myxomycetes in Arctic soil in conditions of simulated climatic changes. The study is based on the sequencing of the siol metagenome using the Ion-Torrent technique.

Key words: biodiversity, Mycetozoa, next generation sequencing, soil biology.

Myxomycetes (Myxogastrea, the plasmodial slime molds) are macroscopic terrestrial protozoans, which can be simplistically defined as giant fructifying amoebas. The life cycle of myxomycetes includes uninuclear amoeboid and flagellate cells, the giant multinuclear plasmodium and the fruiting body (sporophore), where millions of spores are formed.

Myxomycetes are found on a plant detritus in different terrestrial ecosystems. They newer feed with plant tissues, but consume bacteria, yeasts, microscopic algae etc. On the trophic stage of the life cycle, myxomycetes require a plenty of these food organisms, and the soil is the most suitable source of them. Myxomycete pseudopodia can reach bacterial prey in the tiniest soil pores, where they are inaccessible to other predators (Ekelund & Ronn, 1994). This explains their importance in the soil trophic chains, where myxomycetes occupy a unique position of ‘micro-predators’, regulating an abundance of soil bacteria, lower fungi and algae. The recent study of soil meta-transcriptome has shown that myxomycetes are the largest component of total protozoan bio-diversity of soil, comprising 25% of protozoan species (Urich et al., 2008).

With all that, our knowledge about soil myxomycetes is unexpectedly poor. The main problem is that these organisms cannot be identified at the amoeboid or plasmodial stage. The taxonomy of myxomycetes is based on the structure of their fruiting bodies, which are never formed in soil and may be never formed at all in some obligatory soil species (Fiore-Donno, 2010). The culture-based methods may help to stimulate a fructification, however, they still strongly underestimate an abun-

dance and diversity of the group, since (1) two cells of different mating types are normally required to form a plasmodium and (2) many of the plasmodia that appear in cultures fail to produce fruiting bodies, thus preventing their identification (Stephensosn et al., 2011).

An alternative approach for obtaining data on the species composition and distribution of myxomycetes is the analysis of soil metagenome using the next generation sequencing methods (NGS). This method allows to detect thousands of fungal operational taxonomic units in soil specimen (Buée et al., 2009, Geml et al., 2015, Morgado et al., 2015, Semenova et al., 2015). However, myxomycetes appear to be totally absent in most of environmental sampling studies (Stephenson et al., 2011). The reason is that myxomycetes belong to the very old group of organisms, and their ribosomal DNA sequences are extremely variable in size and structure (Fiore-Donno et al., 2008). So called 'eukaryotic universal primers' usually do not match even conserved regions of myxomycete genome. For instance, the primer EukB has four mismatches with most members of the Physarales, the major order of myxomycetes (Stephenson et al., 2011). In addition, myxomycetes SSU rDNA is longer than average and often contains numerous introns that can represent up to 70% of the entire sequence (Fiore-Donno et al., 2008).

As any general study of the soil metagenome using universal primers is not suitable for studying diversity of myxomycetes, the special study is needed, based on specific primers, that were developed for the group and have already shown their efficiency in phylogenetic studies of myxomycetes (Fiore-Donno et al., 2012, 2013, Leontyev et al., 2015). In the combination with NGS techniques, specific primers may show a hidden diversity of soil myxomycetes and help to understand their role in soil ecosystems.

Myxomycetes are rather abundant in polar and alpine ecosystems, being found even in Antarctica. A large and diverse ecological group, known as nivicolous myxomycetes, seems to specialize in fructifying on the edge of melting snow (Poulain et al., 2011). The global heating may strongly alter the abundance and species composition of these myxomycetes, which may have a consequent effect on soil bacteria, algae and microfungi, whose abundance is regulated by myxomycetes. However, the response of arctic myxomycetes to climate warming remains unknown. It is generally anticipated that richness of Myxomycetes will increase under the experimental warming as a con-sequence of increased litter accumulation across the warmed plots (Wahren et al, 2005), as leaf litter may provide a habitat to many myxomycete species. However, this needs to be proven.

Our project aims to study the species diversity of Arctic soil myxomycetes in conditions of simulated climatic changes. The soil samples, taken from both control and experimentally warmed plots, situated in arctic tundra of Alaska (Geml et al., 2015, Morgado et al., 2015, Semenova et al., 2015), will be DNA metabarcoded with Ion-Torrent NGS using specific primers. We expect to disclose (1) taxonomic variability of myxomycetes in arctic soil and (2) changes in richness and composition of taxonomical and ecological groups of myxomycetes in long-term climate simulations.

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