

3589 2008-1-276
synthases was then studied by performing multiple PCR experiments to obtain the subgene fragments and thus the sequences of *phaC1* and *phaC2* genes. The 16S ribosomal DNA sequences from these *Pseudomonas* strains were also determined for phylogenetic analysis. The BLAST analysis showed that the DNA sequences of the subgene fragments from our Antarctic *Pseudomonas* isolates have an average homology of 80% - 90% to those from non-polar *Pseudomonas* strains known to accumulate PHA, such as *P. fluorescens* PfO-1, *P. aureofaciens* and *Pseudomonas* sp. 61-3.

S3.3/P17 VIRUS-LIKE PARTICLES FROM ANTARCTIC DRY VALLEY SOIL

D.W. Hopkins, M. Swanson, L. Torrance, M. Taliany, T. Daniell
Scottish Crop Research Institute, Dundee, UK
david.hopkins@scri.ac.uk

Understanding of the microbial communities of soils on the polar desert soils of the Antarctic dry valleys is not very advanced. It is known that there are active bacteria and fungi in the soils, and that these organisms contribute to biogeochemical processes such as nutrient cycling. However, there is virtually no information about the factors that regulate microbial populations and the interactions between organisms. In this preliminary study, we have investigated and characterized viruses from dry valley soil. We have isolated virus-like particles from soils collected in the Garwood Valley, Ross Dependency, Antarctica. The soils contained a wide range of virus morphotypes including tailed, spherical, and filamentous particles observed by electron microscopy. Bacteria were also isolated from the soil and cultured from which virus-like particles were isolated in the culture medium by ultracentrifugation. Mitomycin C was then used to induce prophages from the same bacteria and VLPs were isolated.

S3.3/P18 EXPRESSED SEQUENCE TAGS ANALYSIS OF DESCHAMPSIA ANTARCTICA DESV. FROM KING GEORGE ISLAND, ANTARCTICA

I.C. Kim, H.Y. Lee, H.H. Cho, J.H. Yim, H.K. Lee, Y.K. Lee
Korea Polar Research Institute
yklee@kopri.re.kr

Deschampsia antarctica Desv. is the only monocot that thrives in the rough conditions of the Antarctic region and represents an invaluable resource for the identification of genes associated with tolerance to various environmental pressures. In order to identify genes that are differentially regulated between greenhouse-grown and Antarctic field-grown plants, we initiated a detailed gene expression analysis. Antarctic plants were collected in the Barton Peninsula on King George Island, Maritime Antarctic (62°14'29''S; 58°44'18''W) and greenhouse plants were used as controls. Two different cDNA libraries were constructed with these plants. A total of 2,112 cDNA clones was sequenced and grouped into 1,199 unigene clusters consisting of 243 consensus and 956 singleton sequences. Using similarity searches against several public databases, we constructed a functional classification of various categories of ESTs, such as genes related to response to stimulus as well as photosynthesis and metabolism. Real-time PCR analysis for several various stress responsive genes showed distinct regulation patterns by abiotic stresses like low temperature, high salt, and osmotic pressure, suggesting that these genes are involved in different responses for specific environmental factors. Although experiments have been carried out on a limited scale, this is the first report to employ ESTs to identify genes that appear to be related to environmental adaptation for flowering Antarctic plants.

S3.3/P19 SOIL MICROFUNGI FROM POLAR DESERT

I.Yu. Kirtsideli
Komarov Botanical Institute RAS, Saint Petersburg, Russia
irina_kir@rambler.ru

Saprotrophic filamentous microfungi were isolated by means of the soil dilution method from soil samples collected from different ecosystems of polar desert 1) archipelago Northern Land -Siberian sector of Arctic 2) Ellef Ringnes island - Canadian Arctic Archipelago 3) island North-Eastern Land (archipelago Spitsbergen)- European sector of Arctic. Different in some properties of microfungi communities were found between the soil samples from sectors (location) and ecosystems. A total 67 species from 17 genus were isolated. Most of isolates were species of *Geomyces*, *Phoma*, *Penicillium*, *Phialophora* and mycelium sterile. Almost 95% of them were psychrophiles and psychrotrophs. It was demonstrated the differently in indexes of population densities and abundance of species for microfungi complexes for three Arctic sectors. Adaptation to Arctic natural conditions appeared both at the level of system that is at level of microfungi complexes and at level of species and isolate. In soil the dynamics and mosaics in fungi distribution reflects diversity of microclimatic of their existence. The results of the present study suggest that the abundance of fungi in polar desert soil is mostly affected by the plant cover (and organic matter).