

10<sup>th</sup>  
BIOLOGY  
Symposium

Xth SCAR International  
Biology Symposium

# Xth SCAR International Biology Symposium



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Public Lecture

Antarctic Biology in the 21st Century  
-- Advances in and beyond IPY --

**Abstract**

**Date** July 26-31, 2009

**Venue** Conference Hall, Hokkaido University  
Sapporo, Hokkaido, Japan

## **P-1-1**

### **Distribution of soil microbial biomass and activity along a latitudinal gradient on the Antarctic peninsula**

**D.W. Hopkins**, P.G. Dennis, V.J. Ord, S.P. Rushton, K.K. Newsham, A.G. O'Donnell

*University of Stirling/Scottish Crop Research Institute*

We have determined the size and the heterotrophic activity (respiration and nitrogen cycling transformations) of the soil microbial communities from over 70 ice-free sites along the Antarctic peninsula between South Georgia and islands in the Ronne Entrance. The sites include both islands and ice-free promontories on the peninsula, high and low altitude sites, vegetated and non-vegetated sites, and sites which receive or have received inputs from sea birds. The data allow us to quantify the importance different biophysical factors in determining the distribution and activities of the organisms. There is no single relationship between the size or activities of the communities and latitude, but heterotrophic activity is strongly influence by autotrophic activity and the inputs from marine animals. We will also be able to explore the patterns of soil microbial diversity along the peninsula.

## **P-1-2**

### **Heterogeneity of ITS sequence in representatives of different populations of *Deschampsia antarctica* Desv. from different regions of Maritime Antarctic**

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The origin and expansion of *Deschampsia antarctica* Desv. and *Colobanthus quitensis* (Kunth) Bartl, the only Antarctic vascular plants, on the sixth continent still remains unresolved. In the present work we have analyzed for the first times 595 bp portion of 18-25S rDNA that include ITS1, 5,8S rRNA and ITS2 sequences obtained from 12 individual specimens of *D. antarctica* from 6 sites located at Argentine Islands, namely Galindez Island (1 localities), Biggest Yalour (2), Pitermann (1), Uruguay (1), cape Rasmussen (1), and more northerly located King George Island (Southern Shetland Islands) (6), as well as compare them to the known *D. antarctica* sequences of this genomic region from database.

The sequences studied show significant identity (96,3 %). The identity of ITS1 region was 93,5 %, ITS2 – 97,7 % and 5,8S rRNA gene – 98,2 %. The sequences are grouped in several clusters each included samples from different localities, thus supposing the genetic exchange among populations from different islands. Certain samples reveal significant identity (99,8 %) – with GenBank ITS1-5,8S rRNA gene-ITS2 sequence originated from Tierra del Fuego.