S11-1
Bioinformatics for eco-systems biology
Wataru Iwasaki
Atomosphere Ocean Res. Inst., Univ. Tokyo
生態系理解へのバイオインフォマティクス
岩崎 涉
東大・大海研
Key word : Bioinformatics, Genome, Metagenome
Microbial ecology faces with the ever-increasing amount of data. In particular, the recent development of DNA sequencing technologies has resulted in the abundant genomic, transcriptomic, and metagenomic data. To understand complex ecosystem-level processes based on this data deluge, bioinformatics should play a key role. In this presentation, we will present our approaches and discuss its future directions.

S11-2
Multi-omics study of the molecular mechanisms of extremo-tolerance in tardigrade
Ramazzottius varieornatus
Kazuharu Arakawa
マルチオミクス解析によって明らかになってきたクマムシ極限環境耐性の分子機構
荒川 和晴
慶大・先端生命研
Key word : tardigrade, anhydrobiosis, extremotolerance, metabolome, multi-omics
Limno-terrestrial tardigrades can withstand almost complete desiccation through a mechanism called anhydrobiosis, and several of these species have been shown to survive the most extreme environments through exposure to space vacuum. Molecular mechanism for this tolerance has so far been studied in many anhydrobiotic metazoans, leading to the identification of several key molecules such as the accumulation and vitrification of trehalose as well as the expression of LEA proteins to prevent protein aggregation. On the other hand, the understanding of comprehensive molecular mechanisms and regulation machinery of metabolic compounds during anhydrobiosis is yet to be explored. To this end, we have conducted a comprehensive multi-omics analysis using the tardigrade Ramazzottius varieornatus, which is a potential model species for anhydrobiosis. In order to analyze the dynamic changes in the active and dehydrated states, we measured the transcriptome by mRNA-Seq, proteome and metabolome by multiple mass spectrometry systems. While changes in gene expression profiles are limited in between active and tun states, dynamic changes were observed in the metabolism of this species in response to desiccation. Changes in the metabolic profiles suggested complex intracellular responses to oxidative and osmotic stress.