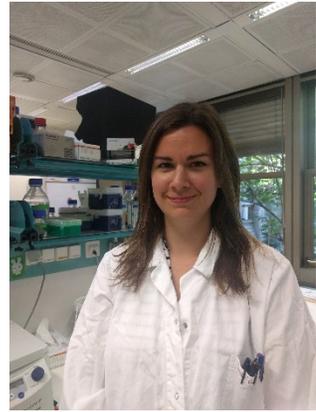


GERTRUD PLESKOT AWARD



Jessica Kozlowski, PhD
Department of Ecogenomics and Systems Biology

Could you just explain, what it is you work on and why it is important?

My current research is focused on cultivation and physiological analysis of microorganisms called the Lokiarchaeota. They represent a recently discovered candidate phylum within the domain Archaea with intriguing evolutionary implications. Specifically, genomes of Lokiarchaeota encode many eukaryotic signature proteins and phylogenetic analysis suggests that these prokaryotic single-celled organisms are closely related to eukaryotes.

The relative ease of sequencing environmental DNA and increased predictive power of genome-analysis programs have uncovered a vast diversity within the domain Archaea (see image from Hug *et. al.*, 2016). However, most newly discovered lineages remain uncultivated and all analyses of the Lokiarchaeota until now have been entirely *in-silico*. My current project is very important to pushing the Archaea field forward because our approach to studying the Lokiarchaeota will go beyond genomic predictions. It is focused on cultivation of these microorganisms in our lab to decipher how they make a living in the environment, which biogeochemical cycles they play a role in, and to visualize any unique cellular features they may have. I feel that cultivation and physiological analysis are still the best tools for understanding new and diverse microorganisms on our planet.

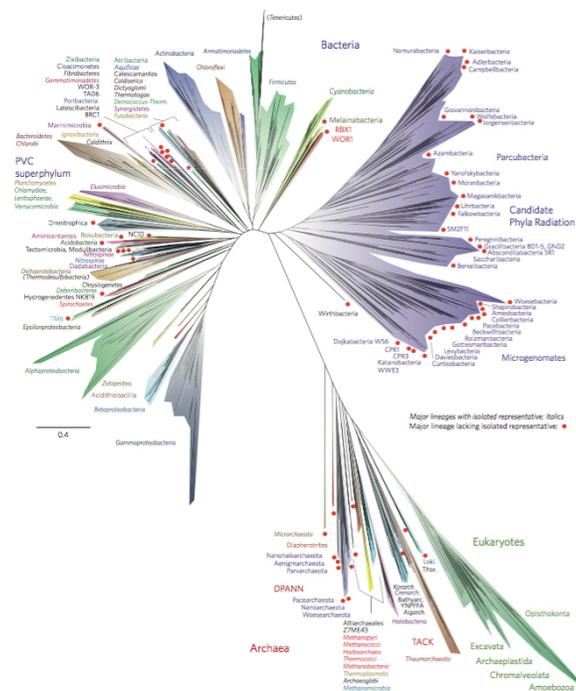


Figure 1 | A current view of the tree of life, encompassing the total diversity represented by sequenced genomes. The tree includes 92 named bacterial phyla, 26 archaeal phyla and all five of the Eukaryotic supergroups. Major lineages are assigned arbitrary colours and named with well-characterized lineage names, in *italics*. Lineages lacking an isolated representative are highlighted with non-*italized* names and red dots. For details on taxon sampling and tree inference, see Methods. The names Tenericutes and Thermodesulfobacteria are bracketed to indicate that these lineages branch within the Firmicutes and the Deltaproteobacteria, respectively. Eukaryotic supergroups are noted, but not otherwise delineated due to the low resolution of these lineages. The CPR phyla are assigned a single colour as they are composed entirely of organisms without isolated representatives, and are still in the process of definition at lower taxonomic levels. The complete ribosomal protein tree is available in rectangular format with full bootstrap values as Supplementary Fig. 1 and in Newick format in Supplementary Dataset 2.

Figure Caption: A current view of the tree of life, encompassing the total diversity represented by sequenced genomes, Hug *et al.*, 2016

What do you think is your project or paper that you were most proud of? Or most challenging maybe?

I am extremely proud of the work I did together with Professor Schleper and her lab group which led to our 2016 ISME Journal paper. This was a key piece of my PhD work on pathways and intermediates of nitrous oxide (N₂O) production from ammonia-oxidizing bacteria and archaea. When we began this work the field of Nitrogen cycling was aware of ammonia-oxidizing microorganisms from two domains of life, the Archaea and Bacteria, but their contributions to the global N₂O budget were not yet fully elucidated. To answer this question, we took a multidisciplinary approach employing our combined knowledge of the ecology of these microorganisms, the evolution of enzymes involved in their central metabolic pathways, geochemical parameters of their environments, and comparative physiology to reveal the differences in how each group contributes to N₂O emissions.

Where do you see yourself in the future?

I see myself continuing on with a research career and I would enjoy staying within a university setting. The combination of hypothesis driven research science together with teaching and outreach are priorities for me.