**WHAT CAN WE LEARN FROM LAB LICHENS?**

Klara Scharnagl1\*; Nick Talbot1

1 The Sainsbury Laboratory, Norwich Research Park, Norwich, Norfolk NR6 7UH UK;
\*E-mail: klara.scharnagl@gmail.com

What conditions the ability of two or more, anatomically simple micro-organisms to form a highly complex lichen thallus? This is a fundamental biological question in that has eluded generations of scientists. In order to gain a better understanding of the lichen symbiosis, biologists have attempted to re-form lichens away from the complex and hypervariable natural environment into controlled laboratory environments, breaking them down into their simplest component parts. We have learned a great deal from axenic cultures of lichen mycobionts and photobionts, and from their co-culture. Genomics tools, however, open up a whole new realm of understanding for how lichens develop. Here we present results from a laboratory growth study of lichen mycobionts, photobionts, co-cultures and whole thalli of *Xanthoria parietina* (L.) Beltr. and *Cladonia portentosa* (Dufour) Coem. We have tested multiple growth conditions including light, temperature, solid versus liquid media, and media/substrate type. We find that even among these two lichens, optimal growth conditions differ, and that in axenic culture, the two primary symbionts (mycobiont versus photobiont) respond differently to growth conditions. We also present results from the analysis of the genomes of these lichen symbionts, and discuss the potential role of unique or expanded gene families in lichenization, including genes involved in self/non-self recognition, G-protein signalling, and secondary metabolite production.