INSIGHTS FROM THE GENOME DATA OF *Protoparmeliopsis muralis*

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*Protoparmeliopsis muralis* is a common lichen that occur on different substrata and is distributed worldwide. It is always fertile and develops numerous apothecia. Several different *Trebouxia* species associate with this lichen-forming fungus and such flexibility allows successful colonization of new habitats and survival of the lichen. To better understand the biology of *P. muralis* the sequencing of genomic DNA was performed. Genomic DNA was isolated from mycelium of *P. muralis* and sequencing was performed using a whole-genome shotgun strategy with Illumina HiSeq 2000 to about 79-fold coverage using Macrogen (Korea) sequencing service ([www.macrogen.com](http://www.macrogen.com)). All sequences were assembled into 757 scaffolds containing 2575 contigs, with a genome size of 44.7 Mb and 43% GC content. Subsequent gene prediction analysis was performed using AUGUSTUS software. This presentation will focus on several genes that might be important for life strategy of *P. muralis.*

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