Comparing Lichen Phenotypic Expression with Genomic Verification

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Lichen species cover nearly 8% of the earth’s surface and are overlooked in genetic studies. Because lichen are composed of bacteria, fungi, and algae, separating and sequencing a three-part genetic organism proves to be challenging. The original goal for this project was to use general fungal forward primer 5'TCCGTAGGTGAACCTGCGG 3'and the reverse primer 5’TCCTCCGCTTATTGATATGC 3' to target and replicate certain fungal genomic regions with intentions to upload a novel lichen DNA sequences into the Barcode of Life Data System (BOLD) in the Student Data Portal (SDP). Although the original primer did yield results, the genetic bands were strongly expressed on a gel electrophoresis using a gel imager, but he bioinformatic report was not reliable due to sequence interruptions. Lichen Usnea strigosa, commonly known as “Old Mans Beard” is the focus since it yielded the best sequence with the highest query reading sequence. Therefore, it was concluded that is was the best sample for DNA extraction. The focus with U. strigosa is yielding the bacterial growth on an agar plate to purify the sample before applying PCR techniques with the designed oligo bacteria primer in preparation for related specie identification. The bacteria is separated from the lichen through DNA extraction, precipitation, and proper purification. A universal bacteria DNA oligo primer, 5’ CCTACGGGRSGCAGCAG ‘3, was created to target different genomic regions of the DNA sample. The lichen sample will be sent off for sequencing and will receive the exact genetic code of “Old Mans Beard.”

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