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The microbiome of the dominant algae in glacier-fed streams

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Hydrurus foetidus is a major primary producer at the base of the food web in glacier-fed streams across the globe. Although it has been reported since 200 years, little is known about this unicellular alga which is able to form long filaments (up to 30 cm) and bloom under oligotrophic conditions. In this study, we hypothesise *H. foetidus* harbours a distinct microbiome with which it may have symbiotic-like interactions, enabling it to thrive under the hard conditions of glacier-fed streams. Various streams of the Swiss Alps were screened and sampled for *H. foetidus* specimens and streamwater samples across three seasons. After DNA extraction, full-length 16S rRNA genes were sequenced using Nanopore technology to evaluate the microbiome composition within *H. foetidus* and streamwater. Preliminary results suggest *H. foetidus* indeed harbours its own microbiome which differs from the streamwater one with an enrichment in *Rhodoferax, Polaromonas, Flavobacterium* genera, as well as a genus from the Oxalobacteraceae family (CM1G08), a family associated with nitrogen-fixation processes. Further analyses will be performed to determine the community assembly processes driving both microbiomes as well as how the distance from the glacier affects *H. foetidus* microbiome composition. Due to climate change and glacier disappearance, glacier-fed streams are now changing towards conditions to which *H. foetidus* may not be adapted. Therefore, it is crucial to intensify research about this alga to better understand its relevance for the ecosystem and the effects climate change will have on its prevalence in glacier-fed streams.