

# When snows bloom: snow algae associated microbial communities are underpinned by trophic partitioning

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## Abstract

Snow microbial communities (algae, bacteria, and fungi) play major roles in snow ecosystem processes and are linked to snowmelt dynamics, but patterns and mechanisms underpinning their spatial distributions, community assembly, and maintenance dynamics are poorly understood. Here we examine nival microbial communities and physicochemical measures across a semi-continental scale and across categorical snow algae bloom zones to elucidate interrelation between communities and their environment. Evidence suggests that trophic partitioning may be a major driver of snow community sub-networks. Samples from snows from the Cascade Mountains (USA) and the Rocky Mountains (USA) were collected from active red snow algae blooms from the center of the bloom (medial), from the edge of the bloom (peripheral), and in adjacent ‘white’ snow. Medial sections of snow algae blooms show increased levels of anemophilous bisaccate pollen, lower oxidation-reduction potential, decreased algal and increased bacterial richness, and increased levels of potassium. Fungal communities between the Cascade and Rocky Mountains are distinct but bacterial and algal communities show little intracontinental differentiation. Ecological modules were identified using a weighted gene co-expression analysis (WGCNA), which shows that dominant microbial consortia correlate differentially to environmental parameters, suggesting complex subcommunities drive observed ecological patterns. Individual OTU networks (fungi and bacteria) show high levels of network connectivity compared to networks based on the snow algae *Sanguina nivaloides*, which underscores associative differences between algal dominated networks and other OTU networks, indicative of trophic partitioning.

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