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Microbial community structure and soil properties in the rhizosphere of understory dwarf bamboo in *Betula ermanii* forest, northern Japan

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To understand the relationships between understory bamboos and soil properties, we compared microbial communities structure of rhizosphere soil of *Sasa kurilensis* with *Sasa-removed* soil in a *Betula ermanii* boreal forest by a high-throughput DNA sequencing method. Understory *Sasa* strongly affected soil properties, such as total carbon, total nitrogen, nitrate and C:N ratio. Among fungal communities, the relative abundance of phylum *Ascomycota* in libraries was 13.9% in the *Sasa*-intact plot, while it was only 0.54% in the *Sasa*-removed plot. Most abundance value of phylum *Ascomycota* was attributed to family *Pezizaceae*. As for bacterial communities, phyla *Acidobacteria*, *Proteobacteria* and *Planctomycetes* were significant differences between the *Sasa*-intact and *Sasa*-removed plots. We found that the *Pezizaceae*, known as mycorrhizal fungi, was related to the amount of total carbon in the *Sasa*-intact plot. The lower abundance of genus *Cryptococcus* in the *Sasa*-intact plot than that in the *Sasa*-removed plot confirmed that the rhizosphere of *Sasa* had a drier soil environment. Furthermore, the species richness results suggested that bacterial phyla may have symbiotic species with ectomycorrhizas under the presence of *Sasa*. These results indicated that microbial communities in rhizosphere of *Sasa* under drier soil environments have function to change soil properties in *B. ermanii* boreal forest.