[P2] Farming System

Thu. Sep 9, 2021 12:15 PM - 2:00 PM Room 2 (Poster) (Farming System)

1:15 PM - 2:00 PM

[P2-10]DNA Barcoding of Weed Species in Hokkaido and Application to *ex-situ* Evaluate of Their Abundance

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In order to manage weeds efficiently, it is necessary to understand their occurrence and distribution patterns. Field investigation of weed population was usually based on morphological traits and spectral data such as Normalized Difference Vegetation Index (NDVI). However, the field observation for weed species identification was difficult in emerging populations in spring and often not suitable for analysis over a vast region. In this study, we constructed a DNA database for Hokkaido weed species and attempted to establish a new method for evaluating weed communities using next-generation sequencer (NGS). The *trnL* (UAA) intron region, which is a hypervariable region of the chloroplast genome, was determined for 40 weed species collected from Hokkaido University Biological Production Research Farm and 48 species from Obihiro Livestock University Farm. For the NGS-based evaluation, we used barnyardgrass (Japanese name 'Inubie' , *Echinochloa crus-galli*) and 'Ezonogishi-gishi' (*Rumex obtusifolius*). Total DNA was extracted from 0.3, 0.5, 1, 1.5 and 3 g of leaf by the CTAB method, and the *trnL* region was amplified by PCR. PCR amplicons were sequenced using Miseq. To compare DNA extraction efficiency and PCR amplification efficiency, an equal amount of rice DNA was added to each sample during or after weed DNA extraction. Rice DNA read count was used as reference to count read data of each weed species. Based on the results, we plan to further investigate biomass estimation methods using NGS.