The liverwort *Marchantia polymorpha* L. is one of the common weeds that grows in nursery crop production (Altland et al. 2007) and distributed widely around the world from tropical to arctic climates (Shimamura 2016). *Marchantia polymorpha* is one of the model organisms representing a basal group of land plants, so whole genome of *Marchantia polymorpha* subsp. *ruderalis* was sequenced including chloroplast genome (Bowman et al. 2017). Unlike the other two subspecies of *Marchantia*, *M. polymorpha* subsp. *ruderalis* is a weedy species usually found in human habitats (Bischler-Causee and Boisselier-Dubayle 1991). It is important to understand the effects of human activities on genetic diversity based on the geographical distribution because human activities have affected ecological environments in various ways (Lenzen et al. 2012).

We collected *M. polymorpha* subsp. *ruderalis* isolated in Mt. Cheonma, Korea (InfoBoss Cyber Herbarium (IN); Kwon W., IB-50002). Total DNA was extracted from fresh thalli of *M. polymorpha* subsp. *ruderalis* using a DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Genome sequencing was performed using HiSeq4000 at Macrogen Inc., Korea, and de novo assembly was done by Velvet 1.2.10 (Zerbino and Birney 2008). All bases were confirmed by alignment generated by BWA 0.7.17 (Li 2013) and SAMtools 1.9 (Li et al. 2009). Genes were identified by KEGG (Kanehisa and Goto 2000), Ensembl (Flicek et al. 2010), and PolyPhen-2 (Adzhubei et al. 2010) and were filtered based on the NCBI annotation. The length of chloroplast genome of *M. polymorpha* subsp. *ruderalis*, named as KBDI00084 (Genbank accession is MK202952), is 120,304 bp, which is similar to the reference genome. It consists of four subregions: 80,706 bp of large single copy (LSC) and 19,788 bp of small single copy (SSC) regions are separated by 9,905 bp of inverted repeats (IRs). It contains 134 genes (90 protein-coding genes, 8 rRNAs, and 36 tRNAs) and overall GC ratio is 29.0% and those in LSC, SSC, and IR regions are 26.6%, 25.1%, and 42.5%, respectively. Only four single nucleotide polymorphisms (SNPs) are identified in KBDI00084, while that of Poland isolate presents 69 SNPs and 660 insertions and deletions (INDELs). Phylogenetic trees show that four chloroplast genomes of *M. polymorpha* subsp. *ruderalis* are clustered into one clade. Taken together, the reason of low genetic diversity between Korea and Japan may be affected by human activities on *M. polymorpha* subsp. *ruderalis*.

The liverwort *Marchantia polymorpha* L. is one of the common weeds as well as a model organism of a basal group of land plants. To understand the genetic diversity of *M. polymorpha* subsp. *ruderalis* based on geographical distribution, we completed chloroplast genome of KBDI00084 isolated from Mt. Cheonma in Korea. Its length is 120,304 bp, consisting four subregions: 80,706 bp of large single copy (LSC) and 19,788 bp of small single copy (SSC) regions are separated by 9,905 bp of inverted repeats (IRs). 134 genes (90 protein-coding genes, eight rRNAs, and 36 tRNAs) were annotated successfully. The overall GC content of the chloroplast genome is 29.0% and those in the LSC, SSC, and IR regions are 26.6%, 25.1%, and 42.5%, respectively. Only four single nucleotide polymorphisms (SNPs) are identified in KBDI00084, while that of Poland isolate presents 69 SNPs and 660 insertions and deletions (INDELs). Phylogenetic trees show that four chloroplast genomes of *M. polymorpha* subsp. *ruderalis* are clustered into one clade. Taken together, the reason of low genetic diversity between Korea and Japan may be affected by human activities on *M. polymorpha* subsp. *ruderalis*. The length of chloroplast genome of *M. polymorpha* subsp. *ruderalis*, named as KBDI00084 (Genbank accession is MK202952), is 120,304 bp, which is similar to the reference genome. It consists of four subregions: 80,706 bp of large single copy (LSC) and 19,788 bp of small single copy (SSC) regions are separated by 9,905 bp of inverted repeats (IRs). It contains 134 genes (90 protein-coding genes, 8 rRNAs, and 36 tRNAs) and overall GC ratio is 29.0% and those in LSC, SSC, and IR regions are 26.6%, 25.1%, and 42.5%, respectively. We identified four single nucleotide polymorphisms (SNPs) and no insertions and deletions (INDELs) on KBDI00084 against the reference genome. In addition, chloroplast genome of another isolate, Takaragaike-1 (Takenaka et al. 2000), used for sequencing its Y chromosome (Yamato et al. 2007), was assembled from raw reads (SRR896230) presenting no variation against the reference chloroplast genome. It is a striking result because Korea and Japan are geographically isolated enough to be diverged from *M. polymorpha* subsp. *ruderalis*. In addition, Polish isolate (MG762001) chloroplast genome contains 69 SNPs and 660 INDELs against the reference genome, supporting that *M. polymorpha* subsp. *ruderalis* chloroplast has enough variations among different isolates from different regions.

Six *Marchantia* (Shimda and Sugiuero 1991; Bowman et al. 2017) and one *Dumortiera* (Kwon et al. 2019) complete chloroplast genomes were analyzed for constructing maximum likelihood and neighbor joining phylogenetic trees
utilizing MAFFT 7.388 (Katoh and Standley 2013) and MEGA X (Kumar et al. 2018). The trees present that *M. polymorpha* subsp. *ruderalis* from three countries are clustered in one clade (Figure 1). Taken together, the reason of low genetic diversity between Korea and Japan may be affected by human activities on *M. polymorpha* subsp. *ruderalis*, which is for next research.

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