

The complete chloroplast genome of Korean *Pyrus ussuriensis* Maxim. (*Rosaceae*): providing genetic background of two types of *P. ussuriensis*

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ABSTRACT

Pyrus ussuriensis Maxim. is one of the most important pear species cultivated in Asia, grown in northern China, far-east Russia, Korea, and Japan. Here we completed the chloroplast genome of wild *P. ussuriensis* collected in Bonghwa-gun, Korea, which was 159,986 bp in length consisting of four subregions: 87,947 bp of large single copy (LSC) and 19,255 bp of small single copy (SSC) regions are separated by 26,392 bp of inverted repeat (IR) regions. The genome contained a total of 130 genes including 85 protein-coding genes, eight rRNAs, and 37 tRNAs. The overall GC content was 36.5% and those in the LSC, SSC, and IR regions were 34.2%, 30.4%, and 42.6%, respectively. Phylogenetic analysis of 14 *Pyrus* chloroplast genomes provided the diverse genetic background for wild *P. ussuriensis* populations in Korea by confirming that wild *P. ussuriensis* sequenced in this study contained *Pyrus pyrifolia* type plastome. It revealed substantial sequence variations up to 121 single nucleotide polymorphisms and 781 insertions and deletions against another wild accession of *P. ussuriensis* (*P. ussuriensis* type) collected in Mt. Hambaek, Korea.

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Pear (*Pyrus*; *Rosaceae*), an important economic crop as the third most significant temperate fruit species after grapes and apples (Moazedi et al. 2014), has been cultivated in more than 50 countries since as early as 2,000 years ago in China (Bell 1990). The genus *Pyrus* contains 22 widely recognized primary species including at least six naturally occurring and three artificial interspecific hybrids (Bell et al. 1996). The species diversity is concentrated in two regions of Western Europe and Eastern Asia, forming two distinct groups of occidental and oriental pears (Rubtsov 1944).




Despite of high conservatism in *Pyrus* chloroplast genome (Katayama and Uematsu 2003), two large deletions in *accD-psal* and *rps16-trnQ* defined three types of *Pyrus* cpDNA: Type A (*P. ussuriensis* type) has no deletion, type B (*P. pyrifolia* type) has 228-bp deletion in *accD-psal* and type C (*P. communis* type) contains 141-bp deletion in *rps16-trnQ*.

Pyrus ussuriensis Maxim. is one of the important species of several Asian pear species cultivated. Wild *P. ussuriensis* cultivars are endemic to the northern part of China, far-east Russia, Korea, and Japan producing small and globose fruit with persistent calyxes (Bell et al. 1996; Wuyun et al. 2013). To investigate its genetic diversity, we characterized *P. ussuriensis* chloroplast genome isolated in Bonghwa-gun, Korea (Voucher, InfoBoss Cyber Herbarium (IN); IB-00593; GPI-187; Seoul, Republic of Korea), different from previous chloroplast genome (MK172841; Gil et al. under review).

Total genomic DNA of *P. ussuriensis* GPI-187 was extracted from fresh leaves using a DNeasy Plant Mini Kit (QIAGEN, Hilden, Germany). Genome sequencing was performed using HiSeq X (Macrogen Inc., Korea) and *de novo* assembly and sequence confirmation were done by Velvet version 1.2.10 (Zerbino and Birney 2008), SOAP GapCloser version 1.12 (Zhao et al. 2011), BWA version 0.7.17 (Li 2013), and SAMtools version 1.9 (Li et al. 2009). Geneious version R11 11.0.5 (Biomatters Ltd., Auckland, New Zealand) was used for chloroplast genome annotation based on *P. ussuriensis* chloroplast genome (MK172841).

The chloroplast genome of *P. ussuriensis* GPI-187 (Genbank accession is MK507863) was 159,986 bp long (GC ratio is 36.5%) long and had four subregions: 87,947 bp of large single copy (LSC; 34.3%) and 19,255 bp of small single copy (SSC; 30.4%) regions were separated by 26,392 bp of inverted repeat (IR; 42.6%). It contained 130 genes (85 protein-coding genes, eight rRNAs, and 37 tRNAs) and 20 genes (nine protein-coding gene, four rRNAs, and seven tRNAs) were duplicated in IR regions.

The neighbour-joining phylogenetic tree, which showed the same topology as maximum likelihood tree, was constructed by MEGA X (Kumar et al. 2018) after aligning fifteen whole chloroplast genomes using MAFFT version 7.388 (Kato and Standley 2013). *Pyrus ussuriensis* GPI-187 was nested within Type B clade sharing a 228-bp deletion with

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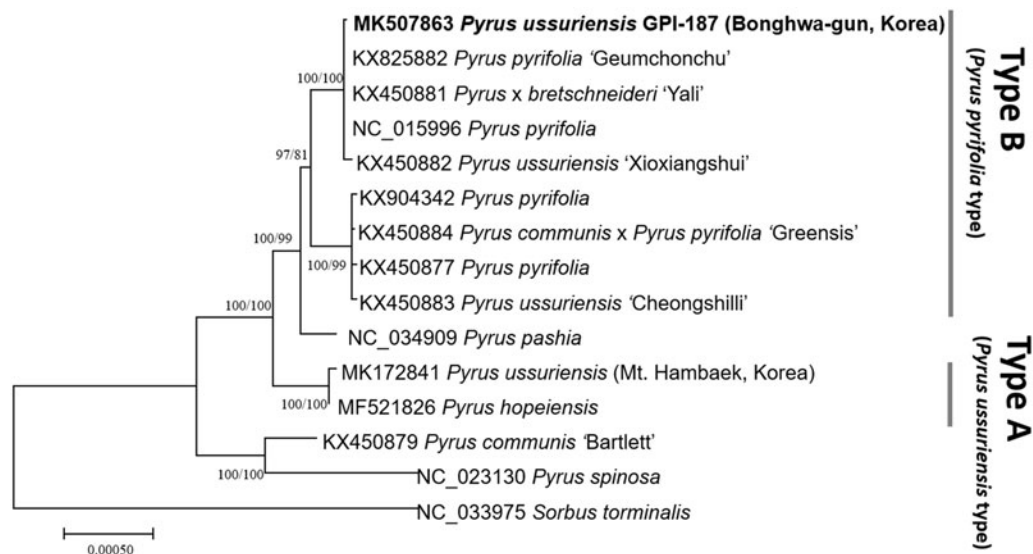


Figure 1. Neighbour-joining tree with bootstrap test (10,000 replicates) of fourteen *Pyrus* and one *Sorbus* chloroplast genomes: four *Pyrus ussuriensis* (MK507863 sequenced in this study, MK172841, KX450883, and KX450882), four *Pyrus pyrifolia* (NC 015996, KX825882, KX904342, and KX450877), *Pyrus x bretschneideri* (KX450881), *Pyrus pashia* (NC_034909), *Pyrus communis x Pyrus pyrifolia* (KX450884), *Pyrus hopeiensis* (MF521826), *Pyrus communis* (KX450879), *Pyrus spinosa* (NC 023130), and *Sorbus torminalis* (NC 033975). The numbers above branches indicate bootstrap support values of neighbour-joining and maximum likelihood phylogenetic trees, respectively.

two accessions of *P. ussuriensis* cultivars, displaying 121 single nucleotide polymorphisms, and 781 insertions and deletions identified against *P. ussuriensis* (MK172841) nested in Type A clade (Figure 1). It indicates that wild *P. ussuriensis* populations in Korea possess high genetic diversity harbouring both type A and B, probably resulted from introgression or chloroplast capture through procedure of species dispersal and/or interspecific crosses in cultivation.

Disclosure statement

No potential conflict of interest was reported by the authors.

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