

Allotetraploid origin and putative ancient introgression in *Plantago hakusanensis* (Plantaginaceae)

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Abstract

Plantago hakusanensis ($2n = 4x = 24$) is an endangered endemic species that occurs in subalpine zones in Japan. To clarify the unresolved taxonomic status of *P. hakusanensis* within the subgenus *Plantago*, we conducted a phylogenetic analysis based on the nuclear-encoded single-copy gene *sucrose-proton symporter 1* (*SUC1*) using 60 previously reported alleles from 24 taxa in the subgenus *Plantago*. We found that *P. hakusanensis* was closely related to *P. asiatica* var. *densiuscula*. The phylogenetic relationships between *P. hakusanensis* and *P. asiatica* var. *densiuscula* were examined by analyses of the *SUC1* nuclear regions and the internal transcribed spacer (ITS) of rDNA, genome-wide single-nucleotide polymorphism genotyping (via multiplexed inter-simple sequence repeat genotyping by sequencing), as well as additional analyses of three chloroplast (cp) regions (*trnL-F*, *ndhF-rpl32*, and *rpl32-trnL*) in 25 individuals of *P. hakusanensis* and 53 individuals of *P. asiatica* var. *densiuscula*. Monophyly of *P. hakusanensis* was suggested by the nuclear marker analyses, whereas the cp haplotypes of *P. hakusanensis* were shared with *P. asiatica* var. *densiuscula* and *P. asiatica* in China. The disparity between the nuclear and cp data may be explained by introgression of the cp genome (cp capture) during Quaternary climate changes. Our results provide (i) a molecular phylogenetic basis for the taxonomy and (ii) insight into the intraspecific diversification history of *P. hakusanensis*.

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Fig. 1 Ishikawa et al.



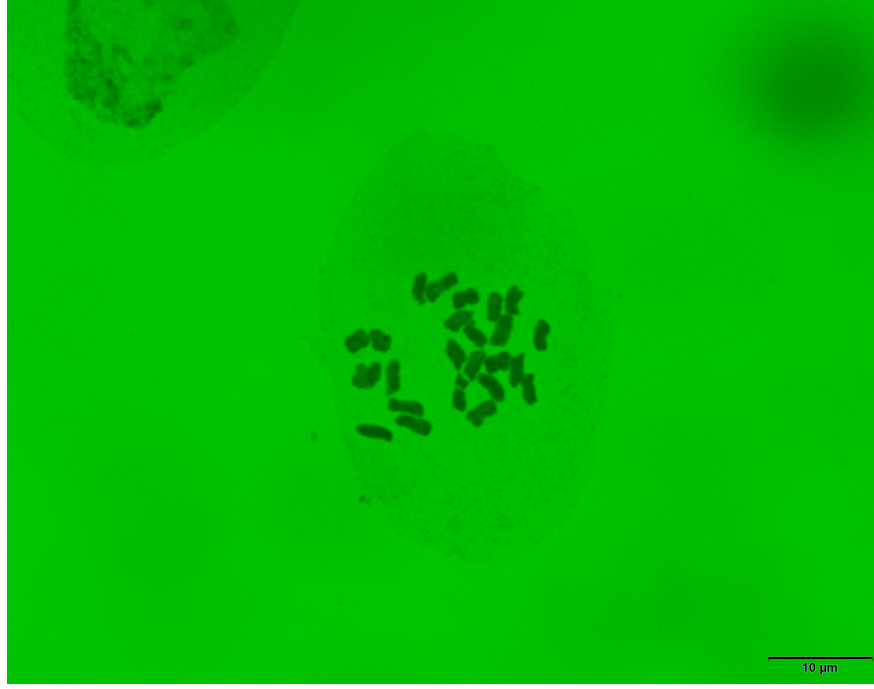


Fig. 3 Ishikawa et al.

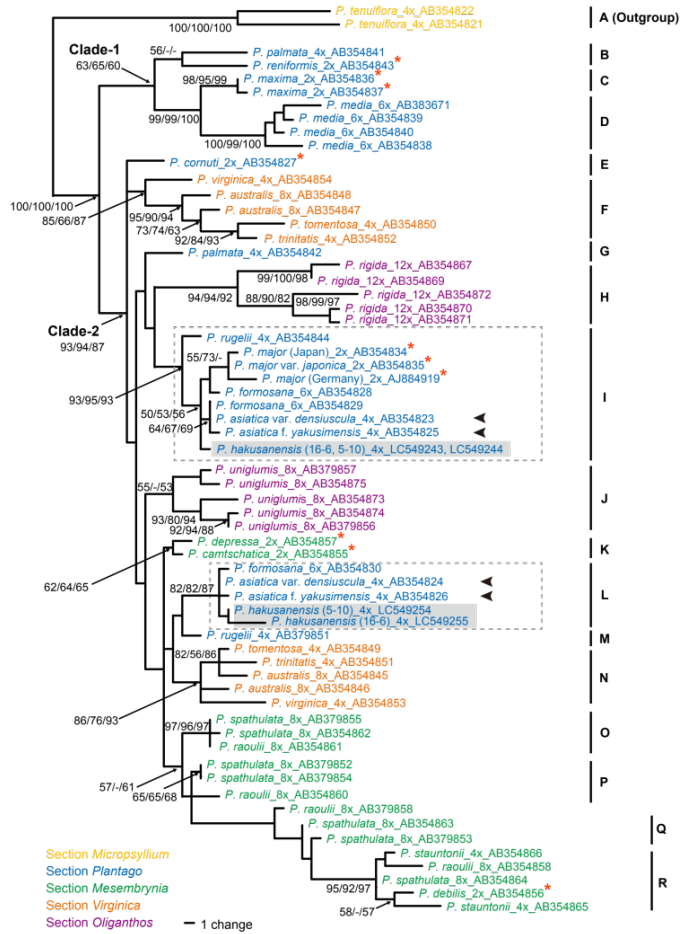


Fig. 4 Ishikawa et al.

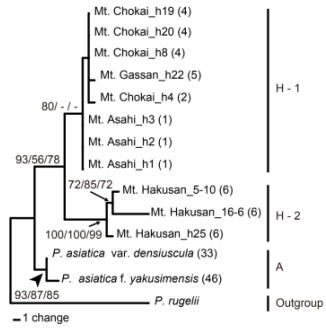


Fig. 5 Ishikawa et al.

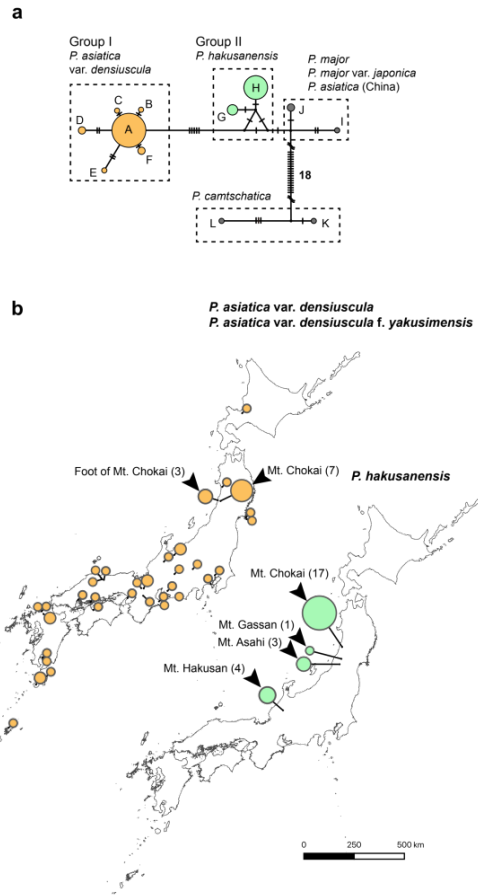


Fig. 6 Ishikawa et al.

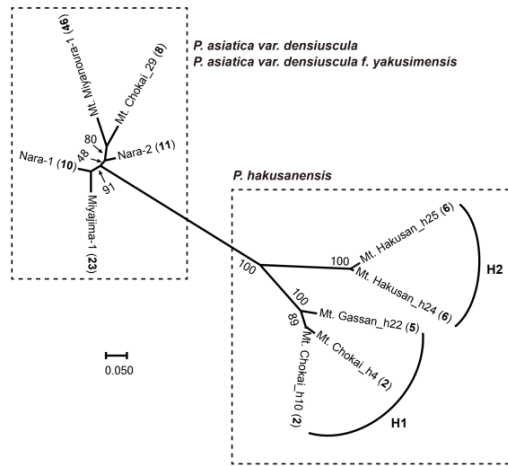
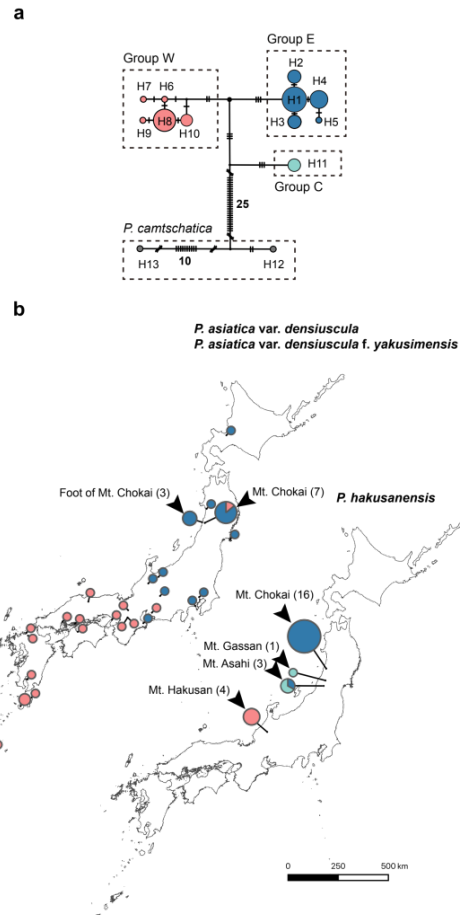


Fig. 7 Ishikawa et al.



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