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The complete chloroplast genome sequences of eight *Fagopyrum* species: insights into genome evolution and phylogenetic relationships

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Buckwheat (*Fagopyrum* genus, Polygonaceae), is an annual or perennial, herbaceous or semi-shrub dicotyledonous plant. There are mainly three cultivated buckwheat species, common buckwheat (*F. esculentum*) is widely cultivated in Asia, Europe, and America, while Tartary buckwheat (*F. tataricum*) and *F. cymosum* (also known as *F. dibotrys*) are mainly cultivated in China. The genus *Fagopyrum* is taxonomically confusing due to the complex phenotypes of different *Fagopyrum* species. In this study, the chloroplast (cp) genomes of three *Fagopyrum* species, *F. longistylum*, *F. leptopodium*, *F. urophyllum*, were sequenced, and five published cp genomes of *Fagopyrum* were retrieved for comparative analyses. We determined the sequence differentiation, repeated sequences of the cp genomes, and the phylogeny of *Fagopyrum* species. The eight cp genomes ranged, gene number, gene order, and GC content were presented. Most of variations of *Fagopyrum* species cp genomes existed in the LSC and SSC regions. Among eight *Fagopyrum* chloroplast genomes, six variable regions (*ndhF-rpl32*, *trnS-trnG*, *trnC*, *trnE-trnT*, *psbD* and *trnV*) were detected as promising DNA barcodes. In addition, a total of 66 different SSR (simple sequence repeats) types were found in the eight

Fagopyrum species, ranging from 8 to 16 bp. Interestingly, many SSRs showed significant differences especially in some photosystem genes, which provided valuable information for understanding the differences in light adaptation among different *Fagopyrum* species. Genus *Fagopyrum* has shown a typical branch that is distinguished from the *Rumex*, *Rheum*, and *Reynoutria*, which supports the unique taxonomic status in *Fagopyrum* among the Polygonaceae. In addition, phylogenetic analysis based on the cp genomes strongly supported the division of eight *Fagopyrum* species into two independent evolutionary directions, suggesting that the separation of *cymosum* group and *urophyllum* group may be earlier than the flower type differentiation in *Fagopyrum* plants.

Speaker Biography

Yu fan is studying the doctoral program of joint training in the Institute of crop science of Chinese Academy of Agricultural Sciences and Guizhou University. He has long been engaged in plant evolution, population genomics and the collection and protection of crop germplasm resources. At present, he has collected thousands of buckwheat germplasm resources and participated in the publication of a new species and a subspecies in *fagopyrum* plants.

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