

## Invited Review

# Classification and systematics of the *Fagopyrum* species

Takanori Ohsako\*<sup>1)</sup> and Chengyun Li<sup>2)</sup>

<sup>1)</sup> Laboratory of Plant Resource Science, Graduate School of Life and Environmental Sciences, Kyoto Prefectural University, 74 Kitainayazuma, Seika, Kyoto 619-0244, Japan

<sup>2)</sup> State Key Laboratory for Conservation and Utilization of Bio-Resources in Yunnan, Yunnan Agricultural University, Heilongtan, Kunming, Yunnan 650201, China

*Fagopyrum* (Polygonaceae) is a small genus including less than 30 species, mostly endemic to southern China. The genus includes two cultivated species, common buckwheat *F. esculentum* and Tartary buckwheat *F. tataricum*. *Fagopyrum* is clearly distinguished from other genus in Polygonaceae by the central position of embryo in achene. The genus is divided into two major groups, namely the cymosum group and the urophyllum group, based on morphological characters and molecular systematics. In the last three decades the number of species in the genus has doubled by the discovery of new species by Japanese and Chinese groups. Most of them are revealed to be included in the urophyllum group based on morphological and molecular genetic analyses. Molecular systematic surveys have also detected inappropriate treatment of some non-*Fagopyrum* species as new species or combination in the genus.

**Key Words:** classification, delineation of *Fagopyrum*, intraspecific variation, molecular systematics, new species.

### Overview of the genus *Fagopyrum*, a group of cultivated and wild buckwheat species

*Fagopyrum* (Polygonaceae) is a small genus comprised of less than 30 species (Jin *et al.* 2018). Most of the wild species show narrow distribution areas in Southern Asia, mainly on the southeastern edge of Qinghai-Tibetan Plateau (Ohnishi 1998a). Two species, common buckwheat *F. esculentum* and Tartary buckwheat *F. tataricum*, are cultivated, and a wild species *F. cymosum* is utilized as forage and a source of pharmaceutical drugs (Wang *et al.* 2005). For common buckwheat and Tartary buckwheat, cultivated and wild forms are distinguished and classified as subspecies (Ohnishi 1998b). Wild common buckwheat *F. esculentum* ssp. *ancestrale* was discovered at the first time in 1990 (Ohnishi 1990, 1998a) at Yongsheng, Yunnan, China. Now wild common buckwheat is found in northwestern Yunnan, western Sichuan, and eastern Tibet around the Three Parallel Rivers region where the Jinsha or upper Yangtze, Mekong, and Salween rivers flowing down north to south in parallel (Ohnishi and Konishi 2001). *F. esculentum* ssp. *ancestrale* is thought of as wild ancestor of cultivated buckwheat *F. esculentum* ssp. *esculentum* (Ohnishi 1998a, 1998b). AFLP analysis revealed that wild

common buckwheat populations distributed in eastern Tibet is the most closely related to cultivated forms (Konishi *et al.* 2005), indicating that cultivated common buckwheat was domesticated in the eastern Tibet to western Sichuan. Tsuji and Ohnishi (2000, 2001) performed phylogenetic analyses of cultivated (*F. tataricum* ssp. *tataricum*) and wild (*F. tataricum* ssp. *Potanini*) forms of Tartary buckwheat based on RAPD and AFLP data and showed that cultivated Tartary buckwheat was domesticated in eastern Tibet to northwestern Yunnan, the same area as the birthplace of common buckwheat.

The delineation of *Fagopyrum* differs among classification systems of Polygonaceae. Species recognized as the member of the genus *Fagopyrum* in the present day are listed in **Table 1**. Gross (1913) proposed many new combinations for the species in the section Polygoneae. In the study, two genera, *Tiniaria* and *Fagopyrum*, were reduced into a single genus *Fagopyrum* with respective sections *Tiniaria* and *Eufagopyrum* in the genus. Samuelsson (1929) listed 10 species in the section *Fagopyrum* of the genus *Polygonum*. Steward (1930) mostly followed the system of Samuelsson (1929) and included 10 species in the section *Fagopyrum* of the genus *Polygonum*. In the present day, most studies seem to follow the system of Hedberg (1946) that treats *Fagopyrum* as an independent genus.

*Fagopyrum* has been discriminated from other genera or sections by embryo morphology. Dammer (1894) stated a key to *Fagopyrum* as large folded cotyledons in achene. Gross (1913) characterized the section *Eufagopyrum* by

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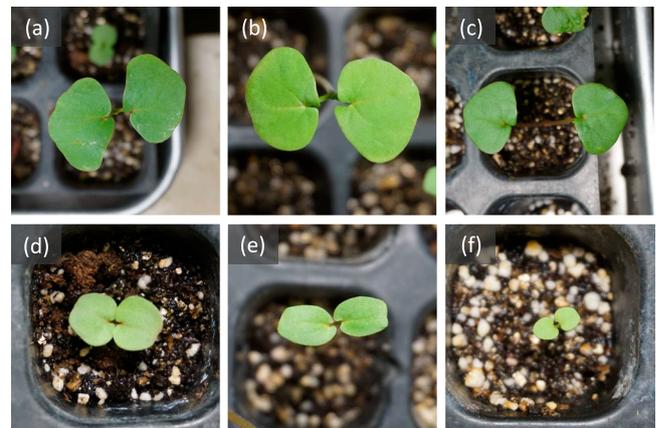
\*Corresponding author (e-mail: ohsako@kpu.ac.jp)

**Table 1.** *Fagopyrum* species

Group	Species	Distribution of natural populations	Chromosome number	Mating system	Reference
cymosum	<i>F. esculentum</i>	Sichuan, Yunnan, Tibet	16	SI	Moench (1794), Ohnishi (1998a)
	<i>F. homotropicum</i>	Sichuan, Yunnan, Tibet	16, 32	SC	Ohnishi (1998a)
	<i>F. tataricum</i>	Sichuan, Yunnan, Tibet, Nepal, Pakistan	16	SC	Gaertner (1791)
	<i>F. cymosum</i>	Southern China, Nepal, India, Bhutan, Myanmar, Vietnam, Thailand	16, 32	SI	Meisner (1857)
urophyllum	<i>F. urophyllum</i>	Sichuan, Yunnan	16	SI	Gross (1913)
	<i>F. lineare</i>	Yunnan	16	SI	Haraldson (1978)
	<i>F. leptopodum</i>	Sichuan, Yunnan	16	SI	Hedberg (1946)
	<i>F. statice</i>	Yunnan	16	SI	Gross (1913)
	<i>F. gracilipes</i>	Sichuan, Yunnan, Bhutan	32	SC	Diels (1901)
	<i>F. capillatum</i>	Yunnan	16	SI	Ohnishi (1998a)
	<i>F. rubifolium</i>	Sichuan	32	SC	Ohsako and Ohnishi (1998)
	<i>F. gracilipedoides</i>	Yunnan	16	SI	Ohsako <i>et al.</i> (2002)
	<i>F. gilesii</i>	Yunnan	16	SI	Hedberg (1946)
	<i>F. jinshaense</i>	Yunnan	16	SI	Ohsako <i>et al.</i> (2002)
	<i>F. pleioramosum</i>	Sichuan	16	SC	Ohnishi (1998a)
	<i>F. callianthum</i>	Sichuan	16	SC	Ohnishi (1998a)
	<i>F. macrocarpum</i>	Sichuan	16	SC	Ohsako and Ohnishi (1998)
	<i>F. tibeticum</i>	Tibet	48	unknown	Tian <i>et al.</i> (2011)
	<i>F. pugense</i>	Sichuan	16	SC	Tang <i>et al.</i> (2010)
	<i>F. qiangcai</i>	Sichuan	16	SC	Shao <i>et al.</i> (2011)
	<i>F. luojishanense</i>	Sichuan	16	SC	Hou <i>et al.</i> (2015)
	<i>F. crispatifolium</i>	Sichuan	32	SC	Liu <i>et al.</i> (2008a)
	<i>F. longzhoushanense</i>	Sichuan	16	SC	Wang <i>et al.</i> (2017)
<i>F. densovillosum</i>	Sichuan	16	SC	Liu <i>et al.</i> (2008b)	
Ambiguous	<i>F. wenchuanense</i>	Sichuan	16	SC	Shao <i>et al.</i> (2011)

conduplicate cotyledons or embryo in the central region in achene. Nakai (1926) also distinguished *Fagopyrum* by the centered position of embryo with conduplicate cotyledons. Two subgroups have often been recognized within *Fagopyrum*. Gross (1913) discriminated two subgroups in the section Eufagopyrum based on morphology of inflorescence and perianth on achene. The subgroups composed of *F. esculentum*, *F. tataricum*, *F. cymosum*, *F. suffruticosum* and *F. odontopterum* (*F. gracilipes* var. *odontopterum*) was characterized by cymose inflorescence with many branching and dense flowers and the other subgroups including *F. maireii* (*F. urophyllum*), *F. bonatii* (*F. gracilipes*), *F. Grossii* (*F. leptopodum* var. *Grossii*), *F. statice* and *F. tristachyum* (*F. cymosum*) by racemose inflorescence with sparse flowers. Roberty and Vautier (1964) amalgamated *Fagopyrum* species into two species based on the achene size. They united *F. esculentum*, *F. cymosum*, and *F. tataricum* into *F. esculentum sensu lato* and *F. gilesii*, *F. Grossii*, *F. gracilipes*, *F. statice* and *F. urophyllum* into *F. gilesii sensu lato*. These groupings are mostly concordant with the cymosum group and the urophyllum group of Yasui and Ohnishi (1998a). Differentiation between the cymosum and the urophyllum groups is strongly supported by both morphological characters and molecular data (described in detail below). Ohnishi and Matsuoka (1996)

defined two characters discriminating the two groups: laterally long cotyledons and achene partially covered with perianths as the key character of the cymosum group and round to longitudinally long cotyledons and achene completely covered with perianths as the key character of the urophyllum group (Fig. 1).



**Fig. 1.** Cotyledons of *Fagopyrum* species. (a) *F. esculentum* ssp. *esculentum*, (b) *F. tataricum* ssp. *tataricum*, (c) *F. cymosum*, (d) *F. urophyllum*, (e) *F. callianthum*, and (f) *F. leptopodum*.

### Diversity of mating system in the genus

About half of the *Fagopyrum* species exhibit heterostyly with short style-high anther flowers (thrum) and long style-low anther flowers (pin). Most species showing heterostyly also have self-incompatibility (SI), but some species such as *F. pleioramosum*, *F. callianthum*, and *F. macrocarpum* are self-compatible. Other species have homostylous self-compatibility (SC). Mating system of the two cultivated species is contrasting; common buckwheat exhibits heterostylous SI whereas Tartary buckwheat homostylous SC. In contrast to SI with homomorphic flowers in other families such as Brassicaceae and Solanaceae, the degree of SI of common buckwheat is extremely high such that self-fertilization rarely occurs. The possibility of selfing is slightly higher in thrum plants than in pin plants (Garber 1927).

### Chromosome number

Basic chromosome number of *Fagopyrum* species has been known to be  $x=8$ . Most species are diploid with  $2n=16$ . *F. gracilipes* and *F. rubifolium* are tetraploid with  $2n=32$ . *F. cymosum* and *F. homotropicum* have both diploid and tetraploid forms (Ohnishi and Asano 1999). *F. tibeticum* has a unique karyotype with a chromosome number  $2n=48$  (Tian *et al.* 2009).

### Recent discovery of the new species of *Fagopyrum* and their systematic position in the genus

Haraldson (1978) listed 12 species including a new combination *F. lineare*, which was originally described as a member of *Polygonum* section *Fagopyrum* by Samuelsson (1929). Samuelsson described two new species, *P. lineare* and *P. caudatum* in the section *Fagopyrum* of the genus *Polygonum*. In 1990s, Ohnishi and colleagues discovered a total of eight new species and one new subspecies (Ohnishi 1998a, Ohsako and Ohnishi 1998, Ohsako *et al.* 2002). Discovery of wild common buckwheat *F. esculentum* ssp. *ancestrale* (Ohnishi 1990) contributed largely to clarify the origin and domestication of common buckwheat. Intensive survey of wild common buckwheat revealed that the subspecies is distributed around the Three Parallel Rivers region from Tibet-Sichuan border to northwestern Yunnan (Ohnishi and Konishi 2001). The other important species is *F. homotropicum*. This species is morphologically very similar to wild common buckwheat but differs in that the species exhibits homostylous SC (Ohnishi 1998a). Distribution area of *F. homotropicum* is like that of wild common buckwheat but *F. homotropicum* shows wider distribution (Ohsako *et al.* 2017, Tomiyoshi *et al.* 2012). Other new species *F. capillatum*, *F. pleioramosum*, *F. callianthum*, *F. rubifolium*, *F. macrocarpum*, *F. jinshaense*, and *F. gracilipedoides* share key characters of the urophyllum

group (Ohnishi 1998a, Ohsako and Ohnishi 1998, Ohsako *et al.* 2002). *F. capillatum*, *F. rubifolium* and *F. gracilipedoides* are morphologically similar to *F. gracilipes*. These four species have heavily pubescent stipule and leaf blade (Ohsako and Ohnishi 1998, Ohsako *et al.* 2002). *F. capillatum* and *F. gracilipedoides* are diploid with chromosome number  $2n=16$  and possess heterostylous SI. *F. rubifolium* is a self-compatible tetraploid (Ohsako and Ohnishi 1998). *F. pleioramosum*, *F. callianthum*, and *F. macrocarpum* have relatively large flower and achene in the urophyllum group. Especially, flowers and achenes of *F. callianthum* and *F. macrocarpum* are the largest within the group (Ohsako and Ohnishi 1998). In addition, they share heterostylous SC. This characteristic is unique to these species in the genus (Ohsako and Ohnishi 1998). They are endemic to upper Min river valley in Sichuan (Ohnishi 1998a, Ohsako and Ohnishi 1998). *F. jinshaense* is endemic to Jinsha river valley of northwestern region of Yunnan. This species has similar morphological characters to *F. gilesii* but differs in morphology of inflorescence. *F. gilesii* has compact inflorescences with quietly short internodes whereas internodes on inflorescence of *F. jinshaense* elongate as seen in the other species in the urophyllum group (Ohsako *et al.* 2002).

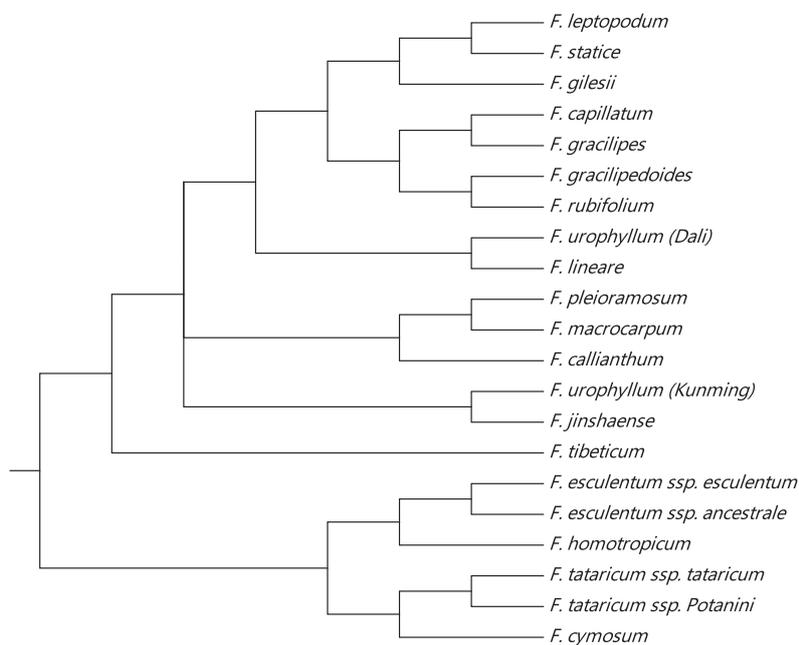
Phylogenetic studies of *Fagopyrum* had not been conducted until application of molecular genetic techniques to phylogenetic analysis become widespread in plant systematics. Ohnishi and Matsuoka (1996) applied isozyme markers and RFLP of chloroplast DNA (cpDNA) to phylogenetic inference of the genus *Fagopyrum*. Both data sets clarified that the genus is divided into two major groups, one including two cultivated species *F. esculentum* and *F. tataricum* and their wild relative *F. cymosum* and the other composed of other wild species with small achene. Yasui and Ohnishi (1998a) investigated the phylogeny of *Fagopyrum* including a new species *F. homotropicum* using nucleotide sequences of *rbcL-accD* region of cpDNA. They also showed the two major groups in the genus, and they named these as the cymosum group and urophyllum group, respectively. They further surveyed nucleotide sequences of internal transcribed spacer (ITS) of nuclear ribosomal RNA gene (Yasui and Ohnishi 1998b) to confirm the results obtained from cpDNA data. Phylogenies based on these four data sets showed good concordance with each other. These analyses clarified that (1) in the cymosum group, *F. tataricum* and *F. cymosum* are monophyletic and *F. homotropicum* is sister to *F. esculentum*, and (2) in the urophyllum group, new species *F. capillatum* is sister to *F. gracilipes* and *F. pleioramosum* and *F. callianthum* form a monophyletic group. Ohsako and Ohnishi (1998, 2000) and Ohsako *et al.* (2002) investigated phylogenetic relationships among species in the urophyllum group including new species *F. rubifolium*, *F. macrocarpum*, *F. gracilipedoides*, and *F. jinshaense* using allozymes and nucleotide sequences of ITS and cpDNA regions. These studies clarified that (1) *F. rubifolium* and

*F. gracilipedoides* form a monophyletic group with morphologically similar species *F. gracilipes* and *F. capillatum*, (2) *F. macrocarpum* is sister to *F. pleioramosum*, and (3) *F. jinshaense* is distantly related to *F. leptopodum* and *F. gilesii* despite their morphological similarity. Recent phylogenetic study revealed that a woody plant *Parapteropyrum tibeticum* is a member of *Fagopyrum* (Sanchez *et al.* 2009, Tian *et al.* 2011). This species was included into *Fagopyrum* under a new combination *F. tibeticum* (Sanchez *et al.* 2011). Phylogenetic relationships among *Fagopyrum* species, including new species and combination, are summarized in Fig. 2.

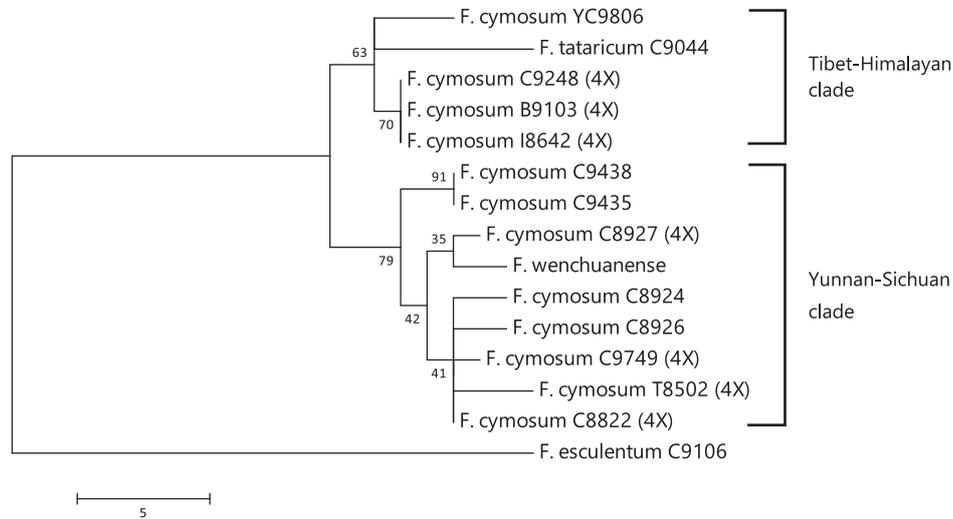
The members of *Fagopyrum* have dramatically increased during the last two decades by the discovery of new species. Chen (1999) described three species, *F. zuogongense*, *F. megaspartanium*, and *F. pilus*. *F. zuogongense* was found in Zuogong county of southeastern part of Tibet. The species is morphologically similar to *F. esculentum* but differs in that it is self-compatible and tetraploid. This plant is thought to be a type of tetraploid form of *F. homotropicum* based on its geographical distribution and characteristics in morphology, ecology, and chromosome number (Tsuji *et al.* 1999). *F. megaspartanium* and *F. pilus* are also indistinguishable from *F. cymosum* in morphology and should be treated as variation of *F. cymosum* (Tsuji *et al.* 1999).

Recently Zhou and colleagues reported several new species, most of which possibly belong to the urophyllum group. *F. pugense* (Tang *et al.* 2010) was first found in Luojishan, Puge county, Sichuan. This species is reported to show similar morphology to *F. gracilipes* whereas the chromosome number is  $2n = 16$ . Photograph in Zhou and

Ohnishi (2018) show shared characters between the species such as dense pubescence on stem and ochrea, small homostylous flower with slightly pink-colored perianths, and dentate wings on the edges of achene. The illustration presented in the original report indicates that the species bears heterostylous flowers as *F. capillatum*, a sister species of *F. gracilipes* (Yasui and Ohnishi 1998a, 1998b). However, *F. pugense* and *F. capillatum* should be treated as different species because *F. pugense* is partially self-fertilizing whereas *F. capillatum* is self-incompatible. Zhou and Ohnishi (2018) reported that *F. pugense* is also seen in Yanyuan, Huili, Huidong, Butuo, Zhaojue, Meigu, Mianning, Luding, and Kangding counties. Ohnishi explored some of these locations and did not find new species corresponding to *F. pugense* whereas he detected and collected *F. gracilipes* accessions in Yanyuan, Mianning, Kangding, and Luding. *F. densovillosum* (Liu *et al.* 2008b), *F. luojishanense* (Hou *et al.* 2015), and *F. longzhoushanense* (Wang *et al.* 2017) were also reported as diploid close relative of *F. gracilipes*. All these new species were discovered in Puge, Sichuan. They show similarity in karyotypes defined by chromosome number and arm ratios. They are discriminated merely by some quantitative traits such as stem thickness and morphology of wings on edges of achene. Molecular systematic survey considering intraspecific variation might contribute to reduce some of these species into a single species by treating them as different subspecies or varieties. Cross experiments might also be useful to confirm the validity of the classification because reproductive isolation could serve as a criterion for species delineation in the genus (Ohsako *et al.* 2002).



**Fig. 2.** Phylogenetic relationships among *Fagopyrum* species by building a consensus of the previous results of molecular systematic studies. Species without clear phylogenetic positions are not included.



**Fig. 3.** Phylogenetic relationships among diploid and tetraploid accessions of *F. cymosum*, *F. tataricum*, and *F. wenchuanense* inferred by parsimony method based on nucleotide sequences of *matK* region of cpDNA (GenBank accession AB093071–AB093087 and JF829982).

Liu *et al.* (2008a) described another new species *F. crispatifolium* as a close relative to *F. gracilipes*. This species is self-fertilizing tetraploid with a chromosome number  $2n=32$ . The unique characteristic of *F. crispatifolium* is rugged texture of leaf surface. Molecular systematic studies showed that the species is closely related to *F. gracilipes* and *F. pugense* (Jin *et al.* 2018, Zhou *et al.* 2012).

*F. qiangcai* was found at Kaku village, Wenchuan, where *F. pleioramosum* and *F. callianthum* distribute (Shao *et al.* 2011). *F. qiangcai* bears heterostylous flowers with pink perianths and sagittate leaves with red veins. These characteristics are very similar to those of *F. callianthum* (Ohnishi 1998a). These circumstances lead to the expectation that *F. qiangcai* is a very close relative or conspecific variation of *F. callianthum*, whereas comparative study has not yet been conducted. *F. wenchuanense* was reported as a new species from Wenchuan, Sichuan (Shao *et al.* 2011). This species has a chromosome number  $2n=16$ . The authors claim that the species is morphologically similar to *F. gracilipes*, but it seems to be closely related to *F. pleioramosum* based on chromosome number and morphological characters such as prostrate branch and hastate to cordate leaf slightly pubescent on both sides. These characteristics are well represented on the illustration in the paper and the photograph in a recently published book (Ohnishi and Zhou 2018). In addition, the illustration of *F. wenchuanense* in Shao *et al.* (2011) includes figures of short-styled and long-styled flowers, strongly suggesting that the species is heterostylous like *F. pleioramosum*. Surprisingly, *F. wenchuanense* was shown to be included in the cymosum group and closely related to *F. cymosum* by molecular systematic study (Zhou *et al.* 2014). The molecular data of *F. wenchuanense* can be analyzed in the context of the intraspecific diversity of *F. cymosum* because comparable sequences are available for multiple accessions of

*F. cymosum* (Yamane *et al.* 2003). Phylogenetic analysis of the cymosum group based on *matK* sequences indicated that the nucleotide sequence of *F. wenchuanense* is included in the Yunnan-Sichuan clade of *F. cymosum* (Fig. 3). If this phylogeny precisely reflects the evolutionary relationships among species, *F. wenchuanense* was derived from *F. cymosum* in Yunnan to Sichuan and acquired many morphological characteristics common to the species of urophyllum group by parallel evolution. These evolutionary events seem quite unlikely to occur. Molecular systematic studies using multiple accessions of the species and different markers on nuclear genome is needed to clarify evolutionary position of the species.

### Differentiation within species

Plant species usually exhibit considerable level of intra-specific variation both at phenotypic and molecular levels. When reconstructing phylogenetic relationships among closely related species, effects of intraspecific variation on the phylogenetic inference should be considered. Some studies on intraspecific differentiation within *Fagopyrum* species have shown that different lineages often exhibit nonmonophyly in relation to their sister species. A highly variable species *F. leptopodum* is sister to *F. statice* at species level, but lineages of these species intermingled with each other in the phylogeny based on nucleotide sequences of cpDNA regions (Ohsako and Ohnishi 2000, 2001). The phylogenetic relationships among accessions suggest that two groups of *F. statice* derived independently from different ancestral lineages of *F. leptopodum* or northern lineage of *F. statice* has hybrid origin between *F. leptopodum* and southern lineage of *F. statice*. Systematic studies have shown that a perennial species *F. urophyllum* is comprised of two subgroups highly differentiated from each other (Ohsako and Ohnishi 2000, Yasui and Ohnishi 1998a,

1998b). Kawasaki and Ohnishi (2006) investigated cpDNA variation within *F. urophyllum* using a total of 19 accessions covering the entire distribution range of the species. They confirmed that the accessions are separated into two phylogeographic groups, the Kunming and the Dali groups. These groups are distributed around central area of Yunnan and northwestern Yunnan-southern Sichuan region, respectively. They were positioned distantly to each other in the reconstructed phylogeny. The Kunming group became sister to *F. jinshaense* and the Dali group to *F. lineare*. This phylogenetic pattern suggests that these groups should be recognized as distinct species. Further investigation on morphological characters, ploidy level, reproductive isolation, and genomic variation is needed to refine taxonomic treatment of the species. Another perennial buckwheat species *F. cymosum* has also been known to be highly polymorphic both at morphological and molecular levels (Yasui and Ohnishi 1998a, 1998b). Molecular systematic analyses revealed that *F. cymosum* is more closely related to *F. tataricum* than to *F. esculentum* (Ohnishi and Matsuoka 1996, Yasui and Ohnishi 1998a, 1998b). Yamane *et al.* (2003) investigated intra- and interspecific relationships between *F. cymosum* and *F. tataricum* and revealed that (1) *F. cymosum* is divided into two groups that are geographically isolated by Hengduan Mountains, namely Yunnan-Sichuan clade and Tibet-Himalayan clade, (2) both groups were comprised of diploid and tetraploid forms, and (3) *F. tataricum* is included in Tibet-Himalayan clade.

### Delineation of the genus by molecular systematic study

Molecular data, especially nucleotide sequences of nuclear and organellar genome regions, have provide powerful means to delineate the genus *Fagopyrum* and validate the description of new species and combinations. *F. megacarpum* was originally described by Hara (1972). Afterward Hara (1982) placed the species in the genus *Eskemukerjea* under a new combination *E. megacarpum*. However, the species was placed again in *Fagopyrum* by Hong (1988) based on pollen morphology. *F. megacarpum* is endemic to Nepal, geographically apart from the species diversity center of *Fagopyrum*. Ohsako *et al.* (2001) surveyed phylogenetic position of *F. megacarpum* using nucleotide sequence of the *rbcL-accD* region of cpDNA. The *rbcL* phylogeny including two *Persicaria* and one *Rumex* species showed that *F. megacarpum* became sister to *R. acetosella* and excluded from monophyletic group comprised of all other species of *Fagopyrum*. Based on this result, *F. megacarpum* should not be treated as a member of *Fagopyrum*. Zhou *et al.* (2015) reported a new species *F. hailuogouense* from Luding, Sichuan. This plant is perennial forming rhizomes. Jin *et al.* (2018) surveyed illustration and photographs in the thesis by Zhang (2013) and Zheng (2012) and found that the *F. hailuogouense* is a synonym of *Bistorta pergracilis*. They also showed that the

plant occupied a position far from *Fagopyrum* and lied in the genus *Bistorta* in phylogenetic tree using a nucleotide sequences of a diverse array of species in Polygonoideae. Phylogenetic analysis by Jin *et al.* (2018) also confirmed that *Pterxygonum giraldii*, often treated as a member of *Fagopyrum*, is not a member of *Fagopyrum* but is a sister to *Pteroxygonum denticulatum*. Molecular phylogeny is a powerful tool to support classification of species and higher taxa, but comprehensive sampling is important to obtain precise conclusion on the systematic and taxonomic issues, as claimed by Jin *et al.* (2018).

### Author Contribution Statement

TO conducted phylogenetic analysis. TO and CL wrote the paper.

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### Literature Cited

- Chen, Q.F. (1999) A study of resources of *Fagopyrum* (Polygonaceae) native to China. Bot. J. Linn. Soc. 130: 53–64.
- Dammer, U. (1894) Polygonaceae. In: Engler, A. and K. Prantl (eds.) Die natürlichen Pflanzenfamilien, 3 (1a), 1st edn. Verlag von Wilhelm Engelmann, Leipzig, pp. 1–36.
- Diels, L. (1901) Die flora von Central China. Botanische Jahrbücher für Systematik, Pflanzengeschichte und Pflanzengeographie 29: 169–659.
- Gaertner, J. (1791) De Fructibus et Seminibus Plantarum, vol. 2. Academiae Carolinae, Stuttgart, p. 520.
- Garber, R.J. (1927) Self-fertilization in buckwheat. J. Agric. Res. 34: 185–190.
- Gross, M.H. (1913) Remarques sur les Polygonées de l'Asie Orientale. Bulletin de Géographie Botanique 23: 7–32.
- Hara, H. (1972) New or noteworthy flowering plants from Eastern Himalaya. J. Jap. Bot. 47: 137–143.
- Hara, H. (1982) Polygonaceae. In: Hara, H., A.O. Chater and L.B.J. Williams (eds.) An Enumeration of the Flowering Plants of Nepal, vol. 3, British Museum (Natural History), London, pp. 172–180.
- Haraldson, K. (1978) Anatomy and taxonomy in Polygonaceae subfam. Polygonoideae Meissn. emend. Jaretsky. Symbole Botanicae Upsalienses 22: 1–95.
- Hedberg, O. (1946) Pollen morphology in the genus Polygonum L. s. lat. and its taxonomical significance. Svensk Botanisk Tidskrift 40: 371–404.
- Hong, S.-P. (1988) A pollenmorphological re-evaluation of *Harpagocarpus* and *Eskemukerjea* (Polygonaceae). Grana 27: 291–295.
- Hou, L.L., M.L. Zhou, Q. Zhang, L.P. Qi, X.B. Yang, Y. Tang, X.M. Zhu and J.R. Shao (2015) *Fagopyrum luojishanense*, a new species of Polygonaceae from Sichuan, China. Novon 24: 22–26.
- Jin, J., D. Li, S. Chen and B. Li (2018) A common *Bistorta* was misidentified as a novel species in *Fagopyrum* (Polygonaceae): the confirmation of the taxonomic identify of *F. hailuogouense* by morphological and molecular evidences. Phytotaxa 348: 221–228.

- Kawasaki, M. and O. Ohnishi (2006) Two distinct groups of natural populations of *Fagopyrum urophyllum* (Bur. et Franch.) Gross revealed by the nucleotide sequence of a noncoding region in chloroplast DNA. *Genes Genet. Syst.* 81: 323–332.
- Konishi, T., Y. Yasui and O. Ohnishi (2005) Original birthplace of cultivated common buckwheat inferred from genetic relationships among cultivated populations and natural populations of wild common buckwheat revealed by AFLP analysis. *Genes Genet. Syst.* 80: 113–119.
- Liu, J.L., Y. Tang, M.Z. Xia, J.R. Shao, G.Z. Cai, Q. Luo and J.X. Sun (2008a) *Fagopyrum crispatifolium* J. L. Liu, a new species of Polygonaceae from Sichuan, China. *J. Syst. Evol.* 46: 929–932.
- Liu, J.L., Y. Tang, M.Z. Xia, J.R. Shao, G.Z. Cai, Q. Luo and J.X. Sun (2008b) *Fagopyrum densovillosum* J. L. Liu, a new species of Polygonaceae from Sichuan, China. *Bull. Bot. Res.* 28: 530–533.
- Meisner, C.F. (1857) Polygonaceae. In: de Candolle, A. (ed.) *Prodromus Systematis Naturalis Regni Vegetabilis*, vol. 14, Victoris Masson, Paris, pp. 1–186.
- Moench, C. (1794) *Methodus Plantas Horti Botanici et Agri Marburgensis: a staminum situ describendi*. Marburg, p. 790.
- Nakai, T. (1926) Taderui no shinbunruihou (A new classification of Linnaean Polygonum). *Rigakkai* 24: 289–301.
- Ohnishi, O. (1990) Discovery of the wild ancestor of common buckwheat. *Fagopyrum* 11: 5–10.
- Ohnishi, O. and Y. Matsuoka (1996) Search for the wild ancestor of buckwheat II. Taxonomy of *Fagopyrum* (Polygonaceae) species based on morphology, isozymes and cpDNA variability. *Genes Genet. Syst.* 71: 383–390.
- Ohnishi, O. (1998a) Search for the wild ancestor of buckwheat I. Description of new *Fagopyrum* (Polygonaceae) species and their distribution in China and the Himalayan hills. *Fagopyrum* 15: 18–28.
- Ohnishi, O. (1998b) Search for the wild ancestor of buckwheat III. The wild ancestor of cultivated common buckwheat, and of Tatar buckwheat. *Econ. Bot.* 52: 123–133.
- Ohnishi, O. and N. Asano (1999) Genetic diversity of *Fagopyrum homotropicum*, a wild species related to common buckwheat. *Genet. Resour. Crop Evol.* 46: 389–398.
- Ohnishi, O. and T. Konishi (2001) Cultivated and wild buckwheat species in eastern Tibet. *Fagopyrum* 18: 3–8.
- Ohnishi, O. and M.L. Zhou (2018) Annual self-incompatible species. In: Zhou, M., I. Kreft, G. Suvoroma, Y. Tang and S.H. Woo (eds.) *Buckwheat Germplasm in the World*, Academic Press, London, pp. 71–80.
- Ohsako, T. and O. Ohnishi (1998) New *Fagopyrum* species revealed by morphological and molecular analyses. *Genes Genet. Syst.* 73: 85–94.
- Ohsako, T. and O. Ohnishi (2000) Intra- and interspecific phylogeny of wild *Fagopyrum* (Polygonaceae) species based on nucleotide sequences of noncoding regions in chloroplast DNA. *Am. J. Bot.* 87: 573–582.
- Ohsako, T. and O. Ohnishi (2001) Nucleotide sequence variation of the chloroplast *trnK/matK* region in two wild *Fagopyrum* (Polygonaceae) species, *F. leptopodum* and *F. statice*. *Genes Genet. Syst.* 76: 39–46.
- Ohsako, T., S. Fukuoka, H.P. Bimb, B.K. Baniya, Y. Yasui and O. Ohnishi (2001) Phylogenetic analysis of the genus *Fagopyrum* (Polygonaceae), including the Nepali species *F. megacarpum*, based on nucleotide sequence of the *rbcL-accD* region in chloroplast DNA. *Fagopyrum* 18: 9–14.
- Ohsako, T., K. Yamane and O. Ohnishi (2002) Two new *Fagopyrum* (Polygonaceae) species, *F. gracilipedoides* and *F. jinshaense* from Yunnan, China. *Genes Genet. Syst.* 77: 399–408.
- Ohsako, T., C. Li and B. Tian (2017) Evolutionary relationship between a wild ancestor of common buckwheat *Fagopyrum esculentum* subsp. *ancestrale* and a self-compatible relative *F. homotropicum* based on microsatellite variability. *Genet. Resour. Crop Evol.* 64: 1595–1603.
- Roberty, G. and S. Vautier (1964) Les genres de Polygonacées. *Boissiera* 10: 7–128.
- Samuelsson, G. (1929) Polygonaceae. In: Handel-Mazzetti, H. (ed.) *Symbolae Sinicae* 7, Verlag von Julius Springer, Wien, pp. 166–188.
- Sanchez, A., T.M. Schuster and K.A. Kron (2009) A large-scale phylogeny of Polygonaceae based on molecular data. *Int. J. Plant Sci.* 170: 1044–1055.
- Sanchez, A., T.M. Schuster, J.M. Burke and K.A. Kron (2011) Taxonomy of Polygonoideae (Polygonaceae): A new tribal classification. *Taxon* 60: 151–160.
- Shao, J.R., M.L. Zhou, X.M. Zhu, D.Z. Wang and D.Q. Bai (2011) *Fagopyrum wenchuanense* and *Fagopyrum qiangcai*, two new species of Polygonaceae from Sichuan, China. *Novon* 21: 256–261.
- Steward, A.N. (1930) The Polygonaceae in Eastern Asia. *Contributions from Gray Herbarium of Harvard University* 88: 1–129.
- Tang, Y., M.-L. Zhou, D.-Q. Bai, J.-R. Shao, X.-M. Zhu, D.-Z. Wang and Y.-X. Tang (2010) *Fagopyrum pugense* (Polygonaceae), a new species from Sichuan, China. *Novon* 20: 239–242.
- Tian, X., R. Liu, B. Tian and J. Liu (2009) Karyological studies of *Parapteropyrum* and *Atraphaxis* (Polygonaceae). *Caryologia* 62: 261–266.
- Tian, X., J. Luo, A. Wang, K. Mao and J. Liu (2011) On the origin of the woody buckwheat *Fagopyrum tibeticum* (= *Parapteropyrum tibeticum*) in the Qinghai-Tibetan Plateau. *Mol. Phylogenet. Evol.* 61: 515–520.
- Tomiyoshi, M., Y. Yasui, T. Ohsako, C.-Y. Li and O. Ohnishi (2012) Phylogenetic analysis of AGAMOUS sequences reveals the origin of the diploid and tetraploid forms of self-pollinating wild buckwheat, *Fagopyrum homotropicum* Ohnishi. *Breed. Sci.* 62: 241–247.
- Tsuji, K., Y. Yasui and O. Ohnishi (1999) Search for *Fagopyrum* species in eastern China. *Fagopyrum* 16: 1–6.
- Tsuji, K. and O. Ohnishi (2000) Origin of cultivated Tatar buckwheat (*Fagopyrum tataricum* Gaertn.) revealed by RAPD analyses. *Genet. Resour. Crop Evol.* 47: 431–438.
- Tsuji, K. and O. Ohnishi (2001) Phylogenetic relationships among wild and cultivated Tatar buckwheat (*Fagopyrum tataricum* Gaertn.) populations revealed by AFLP analyses. *Genes Genet. Syst.* 78: 47–52.
- Wang, C.L., Z.Q. Li, M.Q. Ding, Y. Tang, X.M. Zhu, J.L. Liu, J.R. Shao and M.L. Zhou (2017) *Fagopyrum longzhoushanense*, a new species of Polygonaceae from Sichuan, China. *Phytotaxa* 291: 73–80.
- Wang, K.-J., Y.-J. Zhang and C.-R. Yang (2005) Antioxidant phenolic constituents from *Fagopyrum dibotrys*. *J. Ethnopharmacol.* 99: 259–264.
- Yamane, K., Y. Yasui and O. Ohnishi (2003) Intraspecific cpDNA variations of diploid and tetraploid perennial buckwheat, *Fagopyrum cymosum* (Polygonaceae). *Am. J. Bot.* 90: 339–346.
- Yasui, Y. and O. Ohnishi (1998a) Interspecific relationships in *Fagopyrum* (Polygonaceae) revealed by the nucleotide sequences of the *rbcL* and *accD* genes and their intergenic region. *Am. J.*

- Bot. 85: 1134–1142.
- Yasui, Y. and O. Ohnishi (1998b) Phylogenetic relationships among *Fagopyrum* species revealed by the nucleotide sequences of the ITS region of the nuclear rRNA gene. *Genes Genet. Syst.* 73: 201–210.
- Zhang, Q. (2013) Discovery of the new species—*Fagopyrum hailuogouense* J.R.Shao & Q.Zhang, and evidences for phylogenetic status. Sichuan Agricultural University, Ya'an, p. 50.
- Zheng, Y.D. (2012) Analysis of phylogenetic relationships of *Fagopyrum* Mill. based on ITS, matK and psbA-trnH sequences. Sichuan Agricultural University, Ya'an, p. 51.
- Zhou, M., D. Bai, Y. Tang, X. Zhu and J. Shao (2012) Genetic diversity of four new species related to southwestern Sichuan buckwheats as revealed by karyotype, ISSR and allozyme characterization. *Plant Syst. Evol.* 298: 751–759.
- Zhou, M., C. Wang, D. Wang, Y. Zheng, F. Li, X. Zhu, Y. Tang, J. Shao, Y. Tang and Y. Wu (2014) Phylogenetic relationship of four new species related to southwestern Sichuan *Fagopyrum* based on morphological and molecular characterization. *Biochem. Syst. Ecol.* 57: 403–409.
- Zhou, M.L., Q. Zhang, Y.D. Zheng, Y. Tang, F.L. Li, X.M. Zhu and J.R. Shao (2015) *Fagopyrum hailuogouense* (Polygonaceae), one new species from Sichuan, China. *Novon* 24: 222–224.
- Zhou, M.L. and O. Ohnishi (2018) Annual partially self-fertile species. *In*: Zhou, M., I. Kreft, G. Suvoroma, Y. Tang and S.h. Woo (eds.) *Buckwheat Germplasm in the World*, Academic Press, London, pp. 89–96.