臺中區農業改良場研究彙報 112:57-71 (2011)

蕎麥種源起源及傳播之探討[1]

廖宜倫、陳裕星、林訓仕[2]

摘要

蕎麥為蓼科蕎麥屬作物,栽培種可分為普通蕎麥(*Fagopyrum esculentum*)及韃靼蕎麥(*F. tartaricum*)，中國喜馬拉雅山域之13個蕎麥種源大部分均集中在雲南地區，且發現普通蕎麥祖先種(*F. esculentum* ssp. *ancestrale*)的形態與普通蕎麥相近，AFLP技術也顯示雲南地區的蕎麥祖先種與普通蕎麥遺傳距離較小，因此推測普通蕎麥的起源為位於中國雲南地區。另外由品種系分析結果顯示,雲南西北部及四川地區的韃靼蕎麥的種原歧異度較高，較有可能為韃靼蕎麥的起源地。日本的普通蕎麥栽培種與中國北部栽培種的遺傳距離大，但與中國南部的栽培種之遺傳距離則較近，推測蕎麥可能由中國南部直接傳播至日本等國家。

關鍵詞：普通蕎麥、韃韃蕎麥、起源、種源歧異度。

前言

蕎麥為蓼科(Polygonaceae)蕎麥屬(*Fagopyrum*)，有2個主要栽培種，分別為普通蕎麥(*F. esculentum* Moench)及韃靼蕎麥(*F. tataricum* Gaert.)(2)。蕎麥因種子的產量低且不穩定，只在部分的國家才具有經濟價值(1)；但因具有能生長於不良環境，可快速收穫，且病蟲害少的特性，因此蕎麥在世界各大洲上都有進行栽培(10)。普通蕎麥為異交作物，雌雄同花，但花器包含雌蕊較長型(pin)及雄蕊較長型(thrum),屬於花器異型態自交不親和,其遺傳質為異質性(10)，韃靼蕎麥則為自交作物。野生宿根種蕎麥(*F. cymosum*)亦具自交不親和性，屬異質性，其繁殖方法除種子繁殖外，亦可利用植體繁殖(2)；野生宿根種蕎麥與普通蕎麥及韃靼蕎麥在形態上不同處為其莖部、分枝及總狀花序，主要利用為畜禽類的飼料(1)，亦可當作藥用作物。另一個野生種蕎麥*F. homotopicum*具有自交能力，可與普通蕎麥進行雜交，具有改良普通蕎麥自交不親和的特性(9,10)。

作物由於馴化和育種作為導致遺傳岐異度的降低，喪失潛在優良基因，進而危及作物改良的延續力。窄化的遺傳基礎必須承擔因環境改變所帶來栽培種無法適應的壓力及風險，最嚴重可能會導致整個作物消失(7)。因此，了解蕎麥的起源並擴大遺傳歧異度，可藉此達到蕎麥遺傳育種增進的目的。

---

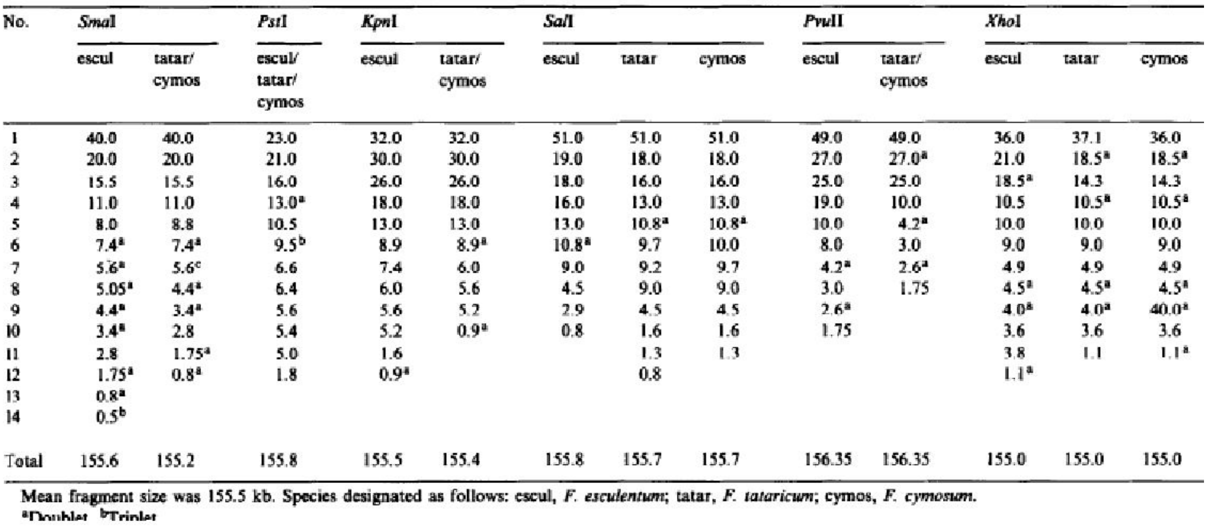
[1] 行政院農業委員會臺中區農業改良場研究報告第0769號。

[2] 行政院農業委員會臺中區農業改良場助理研究員、助理研究員、技佐。

普通蕎麥的起源

普通蕎麥廣泛的栽培於世界各地 ，早先認為起源於西伯利亞(Siberia)的阿默爾河(Amur River)，然而此說無法完全確定普通蕎麥祖先種的正確起源位置。早期報告認為普通蕎麥及韃靼蕎麥的祖先種為野生宿根種蕎麥*F. cymosum* (6)。Kishima等(1995)則利用*Sma*I、*Pst*I、*Kpn*I、*Sal*I、*Pvu*II及*Xho*I等六種限制酵素，針對普通蕎麥、韃靼蕎麥及野生宿根種蕎麥葉綠體DNA (ctDNA)進行偵測分析，發現普通蕎麥在六個酵素所偵測的ctDNA與另外兩種蕎麥的ctDNA大部分都不相同，韃靼蕎麥及野生宿根種蕎麥只有在*Sal*I及*Xho*I兩者酵素間有明顯不同(Table 1)；針對三個蕎麥種所建立系統關係(Fig. 1)，發現普通蕎麥與另外兩者的親緣關係較遠，所以排除宿根常年種為普通蕎麥的起源之假設。

Table 1. Summary for ctDNA fragments generated by six restriction enzymes in the three *Fagopyrum* species (kb)



No.	*Sma*I		*Pst*I	*Kpn*I		*Sal*I			*Pvu*II		*Xho*I		
	escul	tatar/ cymos	escul/ tatar/ cymos	escul	tatar/ cymos	escul	tatar	cymos	escul	tatar/ cymos	escul	tatar	cymos
1	40.0	40.0	23.0	32.0	32.0	51.0	51.0	51.0	49.0	49.0	36.0	37.1	36.0
2	20.0	20.0	21.0	30.0	30.0	19.0	18.0	18.0	27.0	27.0^{a}	21.0	18.5^{a}	18.5^{a}
3	15.5	15.5	16.0	26.0	26.0	18.0	16.0	16.0	25.0	25.0	18.5^{a}	14.3	14.3
4	11.0	11.0	13.0^{a}	18.0	18.0	16.0	13.0	13.0	19.0	10.0	10.5	10.5^{a}	10.5^{a}
5	8.0	8.8	10.5	13.0	13.0	13.0	10.8^{a}	10.8^{a}	10.0	4.2^{a}	10.0	10.0	10.0
6	7.4^{a}	7.4^{a}	9.5^{b}	8.9	8.9^{a}	10.8^{a}	9.7	10.0	8.0	3.0	9.0	9.0	9.0
7	5.6^{a}	5.6^{c}	6.6	7.4	6.0	9.0	9.2	9.7	4.2^{a}	2.6^{a}	4.9	4.9	4.9
8	5.05^{a}	4.4^{a}	6.4	6.0	5.6	4.5	9.0	9.0	3.0	1.75	4.5^{a}	4.5^{a}	4.5^{a}
9	4.4^{a}	3.4^{a}	5.6	5.6	5.2	2.9	4.5	4.5	2.6^{a}		4.0^{a}	4.0^{a}	40.0^{a}
10	3.4^{a}	2.8	5.4	5.2	0.9^{a}	0.8	1.6	1.6	1.75		3.6	3.6	3.6
11	2.8	1.75^{a}	5.0	1.6			1.3	1.3			3.8	1.1	1.1^{a}
12	1.75^{a}	0.8^{a}	1.8	0.9^{a}			0.8				1.1^{a}		
13	0.8^{a}												
14	0.5^{b}												
Total	155.6	155.2	155.8	155.5	155.4	155.8	155.7	155.7	156.35	156.35	155.0	155.0	155.0

Mean fragment size was 155.5 kb. Species designated as follows: escul, *F. esculentum*; tatar, *F. tataricum*; cymos, *F. cymosum*.
^{a}Doublet ^{b}Triplet

(Kishima *et al*., 1995)

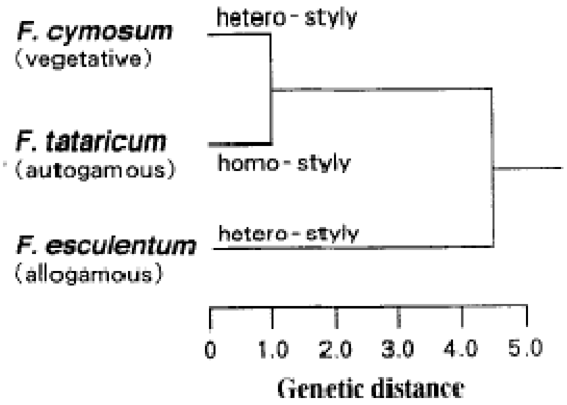
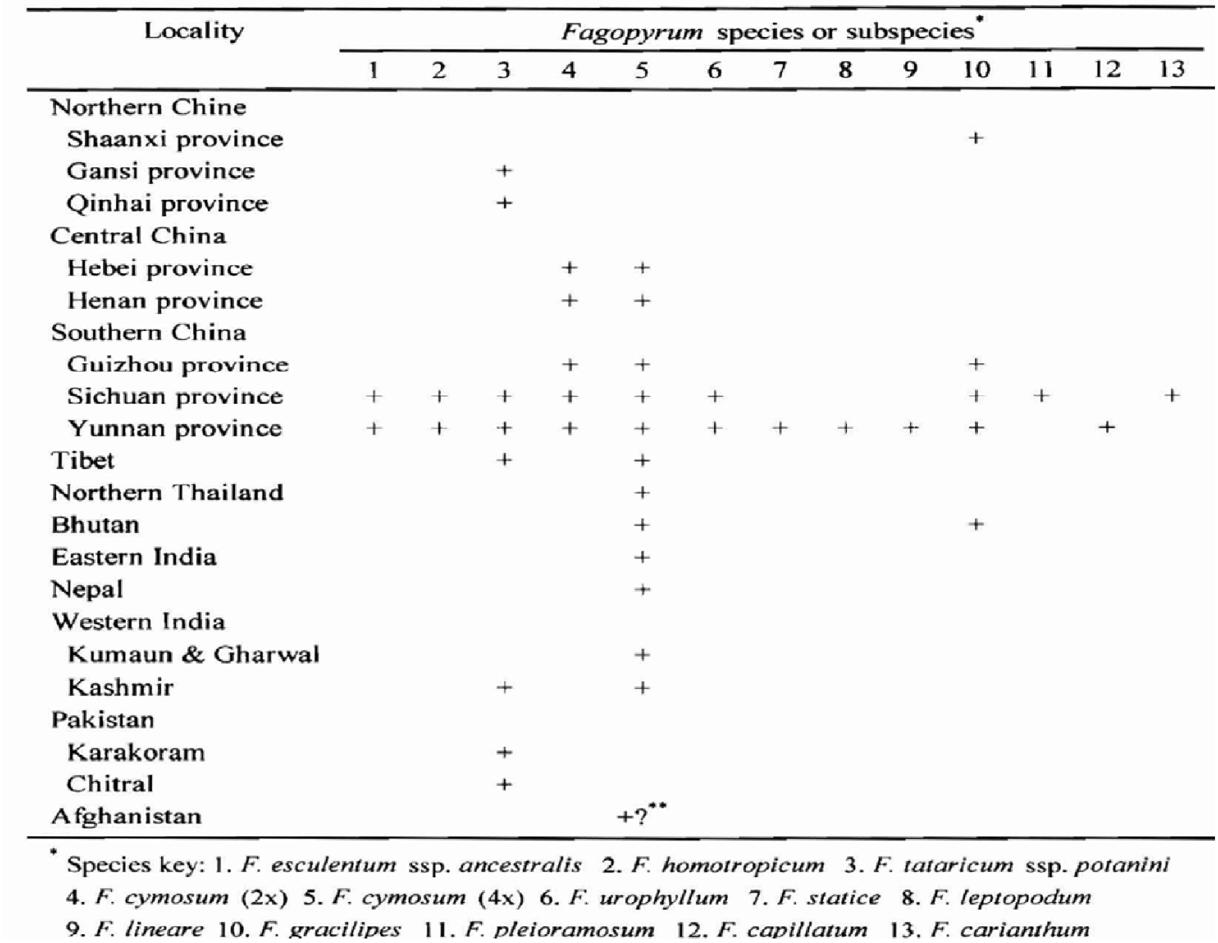


Fig. 1. The phylogenetic tree for three *Fagopyrum* species inferred from restriction site changes based on Wagner parsimony method. (Kishima *et al*., 1995)

普通蕎麥的起源地點一直無法確定，直到Ohnishi (1990)於中國雲南省發現一個普通蕎麥野生種，因為其形態與普通蕎麥栽培種非常相似，且可與普通蕎麥栽培種可相互雜交，此野生種與栽培種之差異為其種子與花比栽培種小，且種子具有易落粒性及休眠性強等野生種特性，生長期亦比栽培種長，所以Ohnishi推論其為普通蕎麥祖先種，將其命名為*F. esculentum* ssp. *ancestrale* Ohnishi [(5)]。另外，Ohnishi (1998)針對其在中國及喜馬拉雅山域等地區所發現並收集的普通蕎麥種原進行分布地區整理(Table 2)，發現除了*F. tataricum* ssp. *potanini*、*F. gracilipes*及*F. cymosum* (4X)外，其餘野生種分布的區域都集中於中國南部的雲南及四川等地區，顯示該區域蕎麥的種原非常豐富，因此Ohnishi (1998)推論普通蕎麥的起源為中國雲南省西北地區[(6)]。

Table 2. Distribution of wild *Fagopyrum* species in China and the Himalayan regions



Locality	*Fagopyrum* species or subspecies*												
	1	2	3	4	5	6	7	8	9	10	11	12	13
Northern Chine													
Shaanxi province										+			
Gansi province			+										
Qinhai province			+										
Central China													
Hebei province				+	+								
Henan province				+	+								
Southern China													
Guizhou province				+	+					+			
Sichuan province	+	+	+	+	+	+				+	+		+
Yunnan province	+	+	+	+	+	+	+	+	+	+		+	
Tibet			+		+								
Northern Thailand					+								
Bhutan					+					+			
Eastern India					+								
Nepal					+								
Western India													
Kumaun & Gharwal					+								
Kashmir			+		+								
Pakistan													
Karakoram			+										
Chitral			+										
Afghanistan					+?**								

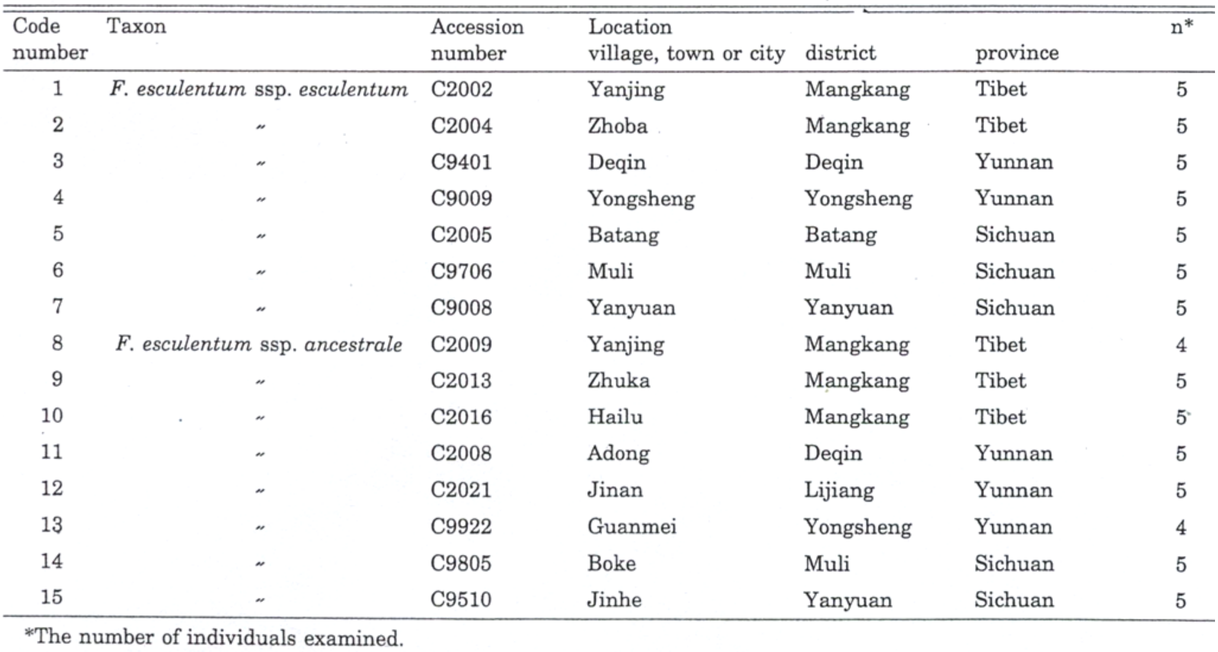
* Species key: 1. *F. esculentum* ssp. *ancestralis* 2. *F. homotropicum* 3. *F. tataricum* ssp. *potanini* 4. *F. cymosum* (2x) 5. *F. cymosum* (4x) 6. *F. urophyllum* 7. *F. statice* 8. *F. leptopodum* 9. *F. lineare* 10. *F. gracilipes* 11. *F. pleioramosum* 12. *F. capillatum* 13. *F. carianthum*

(Ohnishi, 1998)

Konishi等(2005)利用擴增片段長度多型性(amplified fragment length polymorphism, AFLP)分析從中國西藏、雲南及四川等不同地區所收集的普通蕎麥(*F. esculentum* spp. *esculentum*)及祖先種(*F. esculentum* spp. *accestrale*)族群(Table 3、Fig. 2)，藉著偵測所有的基因座探討兩者

之間的遺傳關係，並了解普通蕎麥的起源地；全部族群中以16個AFLP引子偵測396的基因座，其中有371個基因座具有多型性表現(比例為93.7%)；普通蕎麥栽培種偵測到382個基因座，其中有301個基因座為具有多型性(比例為78.8%)；普通蕎麥祖先種共偵測到394個基因座，其中363個基因座具有多型性，比例為92.1% (Table 4)；無論是栽培種或是祖先種的族群均有高度的歧異性存在，作者們推論普通蕎麥無論是栽培種或祖先種均具自交不親和性，屬於為異質性的族群(3)。

Table 3. Samples of cultivated and wild populations of common baucwheat used in this study



Code number	Taxon	Accession number	Location village, town or city	district	province	n*
1	*F. esculentum* ssp. *esculentum*	C2002	Yanjing	Mangkang	Tibet	5
2	〃	C2004	Zhoba	Mangkang	Tibet	5
3	〃	C9401	Deqin	Deqin	Yunnan	5
4	〃	C9009	Yongsheng	Yongsheng	Yunnan	5
5	〃	C2005	Batang	Batang	Sichuan	5
6	〃	C9706	Muli	Muli	Sichuan	5
7	〃	C9008	Yanyuan	Yanyuan	Sichuan	5
8	*F. esculentum* ssp. *ancestrale*	C2009	Yanjing	Mangkang	Tibet	4
9	〃	C2013	Zhuka	Mangkang	Tibet	5
10	〃	C2016	Hailu	Mangkang	Tibet	5
11	〃	C2008	Adong	Deqin	Yunnan	5
12	〃	C2021	Jinan	Lijiang	Yunnan	5
13	〃	C9922	Guanmei	Yongsheng	Yunnan	4
14	〃	C9805	Boke	Muli	Sichuan	5
15	〃	C9510	Jinhe	Yanyuan	Sichuan	5

*The number of individuals examined.

(Konishi *et al*., 2005)

Konsihi等也利用neighbor-joining (NJ)法估計每一對族群間的遺傳距離，並建構其發生系統樹(Fig. 3)，顯示所有的普通蕎麥栽培種全部在同一個群集上，而祖先種則被分成兩個族群，其中來自西藏及雲南的祖先種族群與栽培種具較小的遺傳距離。

韃靼蕎麥的起源

韃靼蕎麥在中國南部及喜馬拉雅山域等高山地區是很重要的作物，主要是因為他的耐冷特性，可在寒冷及貧脊地方進行栽培，為該地區人民的主要糧食。韃靼蕎麥的主要特徵是花器小，雙性花，花器不吸引昆蟲，開花前就已經完成閉花授粉(1)。韃靼蕎麥可分為栽培亞種(*Fagopyrum tataricum* ssp. *tataricum*)及野生亞種(*F. tataricum ssp. potanini*)，韃靼蕎麥野生亞種主要分布於中國南部山區、西藏及巴基斯坦等地方，Tsuji and Ohnishi (2000)為探討韃靼蕎麥的起源，利用於四川、雲南、西藏、及巴基斯坦等地方所收集的栽培亞種、野生亞種及雜草種族群進行隨機擴增多態DNA (random amplified polymorphic DNA, RAPD)分析(Table 5)，

共偵測到42個條帶，其中雲南西北部的韃靼蕎麥野生種有特殊的條帶(Fig. 4)；由系統圖顯示韃靼蕎麥有三個主要的群集，第一群為所有的栽培地方種以及來自西藏中部及巴基斯坦北部的野生亞種，第二群為雲南西北部的野生亞種，第三群為來自四川及雲南的野生亞種，其中代號32及33的雜草型種屬於第一群，代號為34的雜草型種屬則於第三群(Fig. 5)。在自然的族群中，來自四川及雲南西北部比西藏中部的族群及巴基斯坦北部的族群有更多的變異，且該地區的部分地方種及野生種有特殊的條帶(Table 5)，較有可能為韃靼蕎麥的起源地(8)。

一般判斷韃靼蕎麥栽培種與野生種的依據落粒性和休眠性，但韃靼蕎麥野生種並不具休眠性，可能是韃靼蕎麥栽培種傳播到西藏等地區後與該地區之野生種進行雜交，產生後裔分離的現象，所以西藏等地區的野生種有部份的基因是來自於韃靼栽培種，造成野生種與栽培種的親緣關係較為接近。

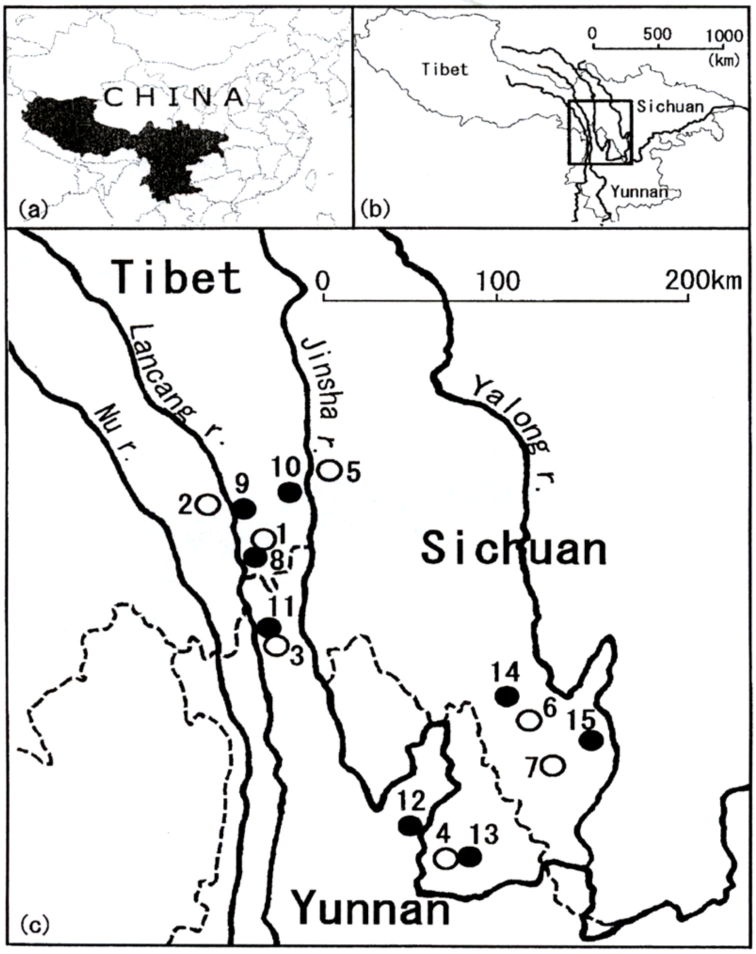
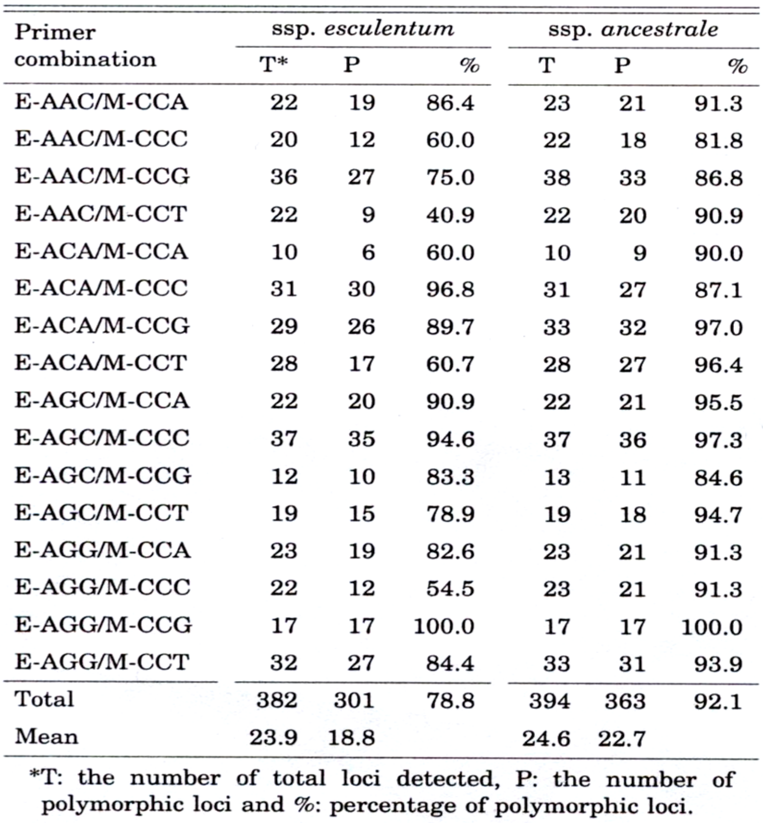


Fig. 2. a-c Location of the accessions used in the present study. The areas in gray color in (a) are yunnan, Sichuan and Tibet in (b). The area enclosed in (b) is magnified in (c). ○:*F.esculentum* ssp. *Esculentum*, ●:*F.esculentum* ssp. *Ancestrale*. Numbers indicated are code numbers of populations(see Table 2).

(Konishi *et al*., 2005)

Table 4. AFLP's result for the ssp. *esculentum* and ssp. *ancestral*



Primer combination	ssp. *esculentum*			ssp. *ancestrale*		
	T*	P	%	T	P	%
E-AAC/M-CCA	22	19	86.4	23	21	91.3
E-AAC/M-CCC	20	12	60.0	22	18	81.8
E-AAC/M-CCG	36	27	75.0	38	33	86.8
E-AAC/M-CCT	22	9	40.9	22	20	90.9
E-ACA/M-CCA	10	6	60.0	10	9	90.0
E-ACA/M-CCC	31	30	96.8	31	27	87.1
E-ACA/M-CCG	29	26	89.7	33	32	97.0
E-ACA/M-CCT	28	17	60.7	28	27	96.4
E-AGC/M-CCA	22	20	90.9	22	21	95.5
E-AGC/M-CCC	37	35	94.6	37	36	97.3
E-AGC/M-CCG	12	10	83.3	13	11	84.6
E-AGC/M-CCT	19	15	78.9	19	18	94.7
E-AGG/M-CCA	23	19	82.6	23	21	91.3
E-AGG/M-CCC	22	12	54.5	23	21	91.3
E-AGG/M-CCG	17	17	100.0	17	17	100.0
E-AGG/M-CCT	32	27	84.4	33	31	93.9
Total	382	301	78.8	394	363	92.1
Mean	23.9	18.8		24.6	22.7	

*T: the number of total loci detected, P: the number of polymorphic loci and %: percentage of polymorphic loci.

(Konishi *et al*., 2005)

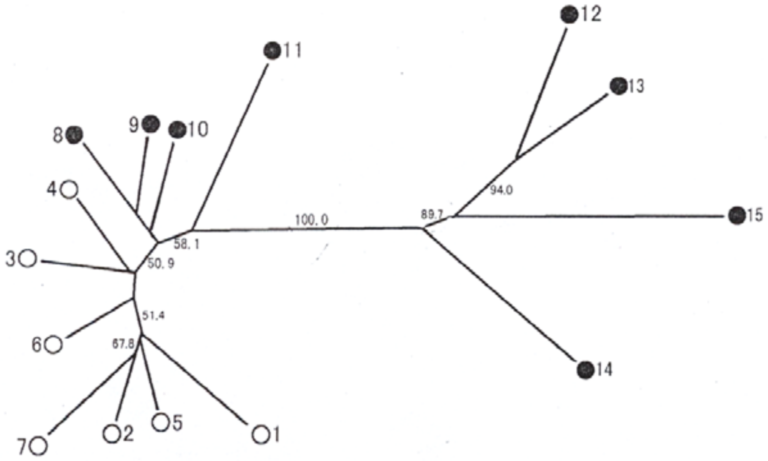


Fig. 3. A phylogenetic tree constructed by the neighbor-joining method based on the genetic distance estimated from gene frequency. ○:*F. esculentum* ssp. *Esculentum*, ●: *F.esculentum* ssp. *ancestrale*. Operational taxonomic units (OUT) are represent by the code number (see Table 2). The numbers on the branches indicate their bootstrap values of >50%(1000 replications).

(Konishi *et al*., 2005)

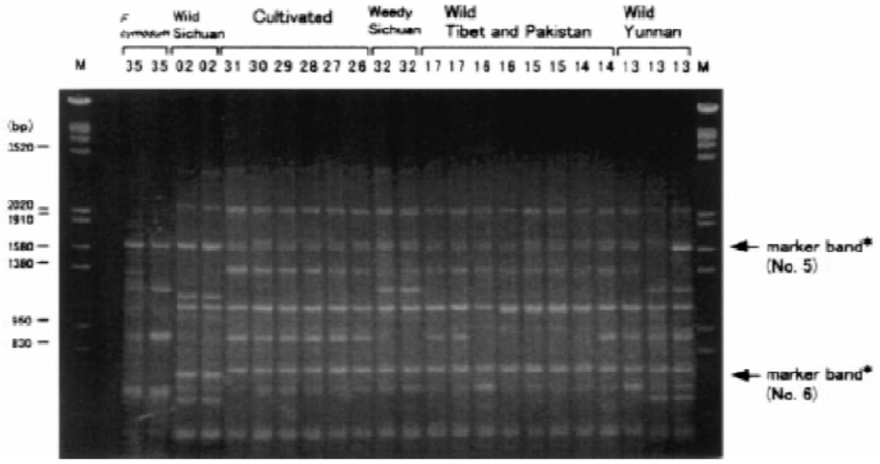


Fig. 4. A RAPD profile generated by the primer OPD-16.

(Tsuji *et al*., 2000)

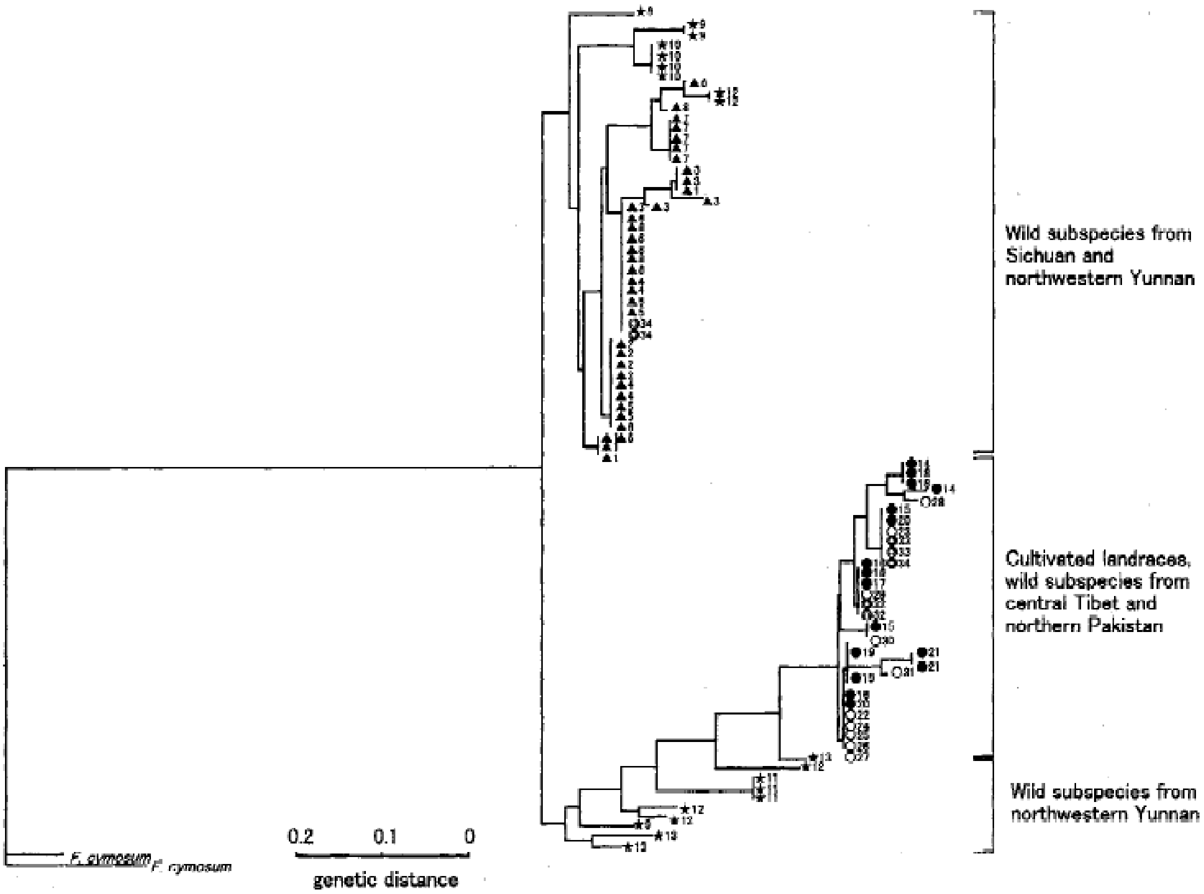


Fig. 5. Neighbor joining tree based on RAPD markers.○: Cultivated landraces; ●: wild subspecies from central Tibet and northern Pakistan; ▲:wild subspecies from Sichuan; ★: wild subspecies from northwestern; ◎: weedy type.

(Tsuji *et al*., 2000)

Table 5. Segregation of critical marker bands among the individuals examined

Type	Region	Code no. of population	Marker bands 1	2	3	4	5	5
Wild	Sichuan	1	0	1	0	1	0	1
Wild	Sichuan	1	0	1	0	1	0	1
Wild	Sichuan	1	0	1	0	1	0	1
Wild	Sichuan	1	0	1	0	1	0	1
Wild	Sichuan	2	0	1	0	1	0	0
Wild	Sichuan	2	0	1	0	1	0	0
Wild	Sichuan	2	0	1	0	1	0	0
Wild	Sichuan	2	0	1	0	1	0	0
Wild	Sichuan	3*	0	1	0	1	0	1
Wild	Sichuan	3*	0	1	0	1	0	1
Wild	Sichuan	3*	0	1	0	1	0	1
Wild	Sichuan	3*	0	1	0	1	0	0
Wild	Sichuan	3*	0	1	0	1	0	1
Wild	Sichuan	4	0	1	0	1	0	1
Wild	Sichuan	4	0	1	0	1	0	1
Wild	Sichuan	4	0	1	0	1	0	1
Wild	Sichuan	4	0	1	0	1	0	1
Wild	Sichuan	5	0	1	0	1	0	1
Wild	Sichuan	5	0	1	0	1	0	1
Wild	Sichuan	5	0	1	0	1	0	1
Wild	Sichuan	5	0	1	0	1	0	1
Wild	Sichuan	6	0	1	0	1	0	1
Wild	Sichuan	6	0	1	0	1	0	1
Wild	Sichuan	6	0	1	0	1	0	1
Wild	Sichuan	6	0	1	0	1	0	1
Wild	Sichuan	6	0	1	0	1	0	1
Wild	Sichuan	6	0	1	0	1	0	1
Wild	Sichuan	7	0	1	0	1	0	1
Wild	Sichuan	7	0	1	0	1	0	1
Wild	Sichuan	7	0	1	0	1	0	1
Wild	Sichuan	7	0	1	0	1	0	1
Wild	Sichuan	7	0	1	0	1	0	1
Wild	Sichuan	8	0	1	0	1	0	1
Wild	Sichuan	8	0	1	0	1	0	1
Wild	Sichuan	8	0	1	0	1	0	1
Wild	Sichuan	8	0	1	0	1	0	1
Wild	Yunnan	9*	0	1	0	0	0	1
Wild	Yunnan	9*	0	1	0	1	0	1
Wild	Yunnan	9*	0	1	0	1	0	1
Wild	Yunnan	9*	0	1	0	0	0	1
Wild	Yunnan	10	0	1	0	0	0	1
Wild	Yunnan	10	0	1	0	0	0	1
Wild	Yunnan	10	0	1	0	0	0	1
Wild	Yunnan	10	0	1	0	0	0	1
Wild	Yunnan	11	1	0	0	1	0	1
Wild	Yunnan	11	1	0	0	1	0	1
Wild	Yunnan	11	1	0	0	1	0	1
Wild	Yunnan	12*	1	0	0	0	1	0
Wild	Yunnan	12*	0	1	0	1	0	1
Wild	Yunnan	12*	0	0	0	0	0	1
Wild	Yunnan	12*	0	1	0	1	0	1
Wild	Yunnan	12*	0	0	0	1	0	1
Wild	Yunnan	13*	0	0	0	1	0	1
Wild	Yunnan	13*	0	0	0	1	0	1
Wild	Yunnan	13*	1	0	1	1	1	0
Wild	Tibet	14	1	0	1	0	1	0
Wild	Tibet	14	1	0	1	0	1	0
Wild	Tibet	15	1	0	1	0	1	0
Wild	Tibet	15	1	0	1	0	1	0
Wild	Tibet	16	1	0	1	0	1	0
Wild	Tibet	16	1	0	1	0	1	0
Wild	Tibet	17	1	0	1	0	1	0
Wild	Tibet	17	1	0	1	0	1	0
Wild	Pakistan	18	1	0	1	0	1	0
Wild	Pakistan	18	1	0	1	0	1	0
Wild	Pakistan	19	1	0	1		1	0
Wild	Pakistan	19	1	0	1	0	1	0
Wild	Pakistan	20	1	0	1	0	1	0
Wild	Pakistan	20	1	0	1	0	1	0
Wild	Pakistan	21	1	0	1	0	1	0
Wild	Pakistan	21	1	0	1	0	1	0
Cultivated	Sichuan	22	1	0	1	0	1	0
Cultivated	Sichuan	23	1	0	1	0	1	0
Cultivated	Sichuan	24	1	0	1	0	1	0
Cultivated	Sichuan	25	1	0	1	0	1	0
Cultivated	Yunnan	26	1	0	1	0	1	0
Cultivated	Yunnan	27	1	0	1	0	1	0
Cultivated	Yunnan	28	1	0	1	0	1	0
Cultivated	Yunnan	29	1	0	1	0	1	0
Cultivated	Tibet	30	1	0	1	0	1	0
Cultivated	Pakistan	31	1	0	1	0	1	0
Weedy	Sichuan	32	1	0	1	0	1	0
Weedy	Sichuan	32	1	0	1	0	1	0
Weedy	Pakistan	33	1	0	1	0	1	0
Weedy	Pakistan	33	1	0	1	0	1	0
Weedy	Pakistan	34*	0	1	0	1	0	1
Weedy	Pakistan	34*	0	1	0	1	0	1
Weedy	Pakistan	34*	1	0	1	0	1	0

1: Have the band, 0: do not have the band.
*: Polymorphic populations.

(Tsuji *et al*., 2000)

普通蕎麥族群的遺傳變異

除了在中國，亞洲其他國家如日本、韓國及尼泊爾等都有普通蕎麥的栽培，Ohnishi (1988)針對由中國、日本及韓國所收集的普通蕎麥(Fig. 6)進行調查，分析12個等位酵素的19個基因座之多型性，發現各族群的多型性基因座之對偶基因頻度並沒有很大的變化(Table 6)，例如所有族群中*pgm-2*的F對偶基因頻率幾乎是一致的；在日本及中國的族群中，*pgm-2*的S對偶基因也沒有很大的差異，在*Sdh-1*基因座上的U對偶基因、*Dia-2*基因座上的S對偶基因在所有的族群中也都幾乎有一致性的頻率。每一個族群的遺傳變異以平均異質性及多型性基因座百分率來進行估計(Table 7)，多型性基因座百分率介於31.6~42.1%，平均異質性為0.110~0.138，略高於普通的異交作物。利用族群間對偶基因的頻度來建構每對族群的遺傳距離(Table 8)，發現亞洲各國的蕎麥族群，多數有相似的遺傳結構$^{(4)}$。我們所熟知的普通蕎麥為異交作物，具有自交不親和性，利用昆蟲為媒介傳播花粉，因此其遷移率極大，在村莊或城市間進行花粉的傳播，或者隨著人類的引種或種子的交換行為而傳播到其他國家，可以導致亞洲地區的蕎麥遺傳族群極為相似的原因；惟日本的蕎麥族群與中國北方的蕎麥族群之遺傳距離仍較中國南方的遺傳距離稍為大一些，顯示普通蕎麥可能是由中國南部傳入韓國及日本。

Fig. 6. Location of the populations studied. ○:Only the name of province is know, ●:Exact location is know. (Ohnishi, 1988)

Table 6. Allelic frequencies at polymorphic loci

Population		Locus	Adh			Dia-2			Got-2			Mdh-1	
		Allele	S	F	N	S	F	N	U	S	N	F	N
1	Furen		0.0,	0.0,	100.0	3.0,	0.5,	96.5	23.9,	46.6,	29.5	17.0,	83.0
2	Noheji		0.0,	0.0,	100.0	7.1,	0.5,	92.9	10.7,	52.9,	36.4	15.9,	84.1
3	Kuzumaki		0.0,	0.5,	99.5	7.0,	0.0,	93.0	11.0,	61.3,	27.7	23.9,	76.1
4	Iwate-F		0.2,	0.0,	99.8	5.8,	0.3,	93.9	13.3,	55.5,	31.2	16.5,	83.5
5	〃 -S		0.0,	0.0,	100.0	8.3,	0.0,	91.7	9.8,	54.5,	35.7	20.5,	79.5
6	Miwa		0.0,	0.0,	100.0	5.8,	0.2,	94.0	14.7,	53.4,	31.9	15.9,	84.1
7	Kanasagoh		0.0,	0.0,	100.0	6.8,	0.5,	92.7	8.8,	55.8,	35.4	17.5,	82.5
8	Arakawa-F		0.0,	0.3,	99.7	2.5,	0.2,	97.3	10.7,	47.8,	41.5	21.8,	78.2
9	〃 -S		0.0,	0.0,	100.0	1.0,	0.3,	98.7	19.0,	53.8,	27.2	15.0,	85.0
10	Kannami		0.0,	0.2,	99.8	6.5,	0.5,	93.0	11.5,	53.0,	35.5	23.6,	76.4
11	Togakushi-F		0.0,	0.0,	100.0	1.5,	0.0,	98.5	8.8,	56.8,	34.4	25.5,	74.5
12	〃 -S		0.0,	0.0,	100.0	0.8,	0.0,	99.2	6.0,	67.8,	26.2	35.0,	65.0
13	Takane		0.0,	0.0,	100.0	3.2,	0.2,	96.6	14.0,	54.1,	31.9	21.6,	78.4
14	Niimi		0.0,	0.0,	100.0	6.7,	0.0,	93.3	11.6,	61.3,	27.1	24.3,	75.7
15	Geihoku		0.0,	0.0,	100.0	4.3,	0.0,	95.7	12.8,	53.8,	33.4	24.5,	75.5
16	Kanagi		0.0,	0.0,	100.0	6.9,	2.4,	90.7	11.9,	51.0,	37.1	16.5,	83.5
17	H-Iyayama		0.0,	0.0,	100.0	5.3,	0.3,	94.4	13.4,	52.6,	34.0	19.8,	80.2
18	N-Iyayama		0.0,	0.5,	99.5	3.8,	0.0,	96.2	9.8,	58.3	31.9	22.5,	77.5
19	Chiran		0.0,	0.8,	99.2	3.3,	0.3,	96.4	11.5,	54.0,	34.5	17.8,	82.2
20	Shiiba		0.0,	0.3,	99.7	3.4,	0.0,	96.6	14.7,	46.6,	38.7	20.8,	79.2
21	Takeda		0.0,	0.0,	100.0	6.0,	0.3,	93.7,	13.5,	53.8,	32.7	20.8,	79.2
22	Fukue		0.0,	0.0,	100.0	9.0,	1.3,	89.7	10.3,	58.0,	31.7	29.9,	70.1
23	Izuhara		0.0,	0.2,	99.8	5.5,	0.3,	94.2	16.5,	53.5,	30.0	23.8,	76.2
24	Kamiagata		0.0,	0.0,	100.0	5.0,	0.5,	94.5	18.0,	57.0,	25.0	21.8,	78.2
25	Che-ju		0.0,	0.0,	100.0	2.0,	0.0,	98.0	15.5,	51.3,	33.2	25.2,	74.8
26	Je-cheon		0.3,	0.0,	99.7	4.0,	0.3,	95.7	11.0,	53.5,	35.5	27.4,	72.6
27	Dun-nae		0.0,	0.0,	100.0	3.3,	0.0,	96.7	5.5,	59.3,	35.2	22.3,	77.7
28	Chilin #1		0.0,	0.3,	99.7	3.2,	0.0,	96.8	10.0,	50.3,	39.7	33.2,	66.8
29	〃 #2		0.3,	0.3,	99.4	2.2,	0.0,	97.8	12.0,	50.5,	37.5	37.3,	62.7
30	Inner Mong #1		0.0,	0.2,	99.8	2.3,	1.0,	96.7	11.5,	59.3,	29.2	43.9,	56.1
31	〃 #2		0.0,	0.2,	100.0	2.5,	0.0,	97.5	11.3,	55.8,	32.9	43.5,	56.5
32	Kuyang		1.0,	0.2,	98.8	5.5,	0.0,	94.5	11.8,	59.0,	29.2	42.9,	57.1
33	Hujuoxien		0.0,	0.0,	100.0	3.3,	0.0,	96.7	11.0,	60.3,	28.7	41.3,	58.7
34	Wuchuan		0.0,	0.0,	100.0	4.3,	0.5,	95.2	15.8,	55.8,	28.4	35.8,	64.2
35	Shensi #1		0.0,	2.0,	98.0	3.5,	0.3,	96.2	14.8,	55.0,	30.2	44.1,	55.9
36	〃 #2		0.0,	0.3,	99.7	4.3,	0.5,	95.2	11.3,	58.5,	30.2	37.8,	62.2
37	Yulin		0.0,	0.3,	99.7	8.0,	0.3,	91.7	8.0,	55.0,	37.0	46.5,	53.5
38	Hunan		0.0,	0.0,	100.0	3.2,	0.3,	96.5	10.8,	54.3,	34.9	35.5,	64.5
39	Szechuan		0.3,	0.3,	99.4	1.7,	0.0,	98.3	3.5,	50.5,	46.0	37.0,	63.0
40	Kweichow #1		0.0,	0.5,	99.5	3.5,	0.0,	96.5	8.5,	43.8,	47.7	29.7,	70.3
41	〃 #2		1.3,	2.3,	96.4	4.4,	0.3,	95.3	10.6,	53.6,	35.8	38.5,	61.5
42	Yunnan #1		0.5,	1.5,	98.0	2.4,	0.0,	97.6	14.0,	51.8,	34.2	31.2,	68.8
43	〃 #2		0.5,	3.5,	96.0	2.8,	0.3,	96.9	12.5,	50.0,	37.5	32.9,	67.1

F allele: fast allele; S allele: slow allele; U allele: slowest allele; N allele: neutral allele.

(Ohnishi, 1988)

Table 6. continued

Population		Locus	Mdh-3				6-Pgdh-1			Pgm-2			Sdh-1		
		Allele	S	F	U	N	S	F	N	S	F	N	S	F	U
1	Furen		13.5,	16.3,	0.0,	70.2	7.0,	0.6,	92.4	9.3,	3.7,	87.0	51.2,	48.8,	0.0
2	Noheji		9.5,	22.9,	0.0,	67.6	1.0,	0.0,	99.0	6.5,	2.4,	91.1	47.0,	53.0,	0.0
3	Kuzumaki		12.8,	22.3,	0.0,	64.9	8.8,	0.5,	90.7	4.3,	1.0,	94.7	50.4,	49.3,	0.3
4	Iwate-F		13.0,	25.0,	0.0,	62.0	5.7,	0.0,	94.3	12.8,	5.4,	81.8	52.0,	48.0,	0.0
5	〃 -S		13.8,	17.3,	0.0,	68.9	0.0,	0.0,	100.0	2.8,	9.0,	88.2	37.2,	62.8,	0.0
6	Miwa		12.3,	22.8,	0.0,	64.9	1.8,	0.3,	97.9	5.0,	3.8,	91.2	48.8,	50.7,	0.5
7	Kanasagoh		7.5,	25.8,	0.0,	66.7	1.5,	0.0,	98.5	5.7,	5.7,	88.6	53.0,	47.0,	0.0
8	Arakawa-F		12.9,	20.6,	0.7,	65.8	2.5,	0.0,	97.5	4.0,	4.8,	91.2	51.5,	48.0,	0.5
9	〃 -S		9.3,	29.0,	0.0,	61.7	1.5,	0.0,	98.5	9.7,	4.3,	86.0	32.2,	67.8,	0.0
10	Kannami		15.8,	25.5,	0.3,	58.4	4.5,	0.0,	95.5	3.7,	3.2,	93.1	52.0,	48.0,	0.0
11	Togakushi-F		16.8,	15.5,	0.0,	67.7	12.0,	0.3,	87.7	8.5,	2.5,	89.0	47.0,	53.0,	0.0
12	〃 -S		10.5,	21.0,	0.0,	68.5	16.3,	0.3,	83.4	8.0,	7.0,	85.0	44.7,	55.3,	0.0
13	Takane		8.7,	23.7,	0.0,	67.6	1.5,	0.0,	98.5	2.5,	2.2,	95.3	49.8,	50.0,	0.2
14	Niimi		15.4,	24.1,	0.0,	60.5	9.3,	0.0,	90.7	5.3,	3.3,	91.4	48.9,	51.1,	0.0
15	Geihoku		13.8,	19.9,	0.0,	66.3	4.3,	0.0,	96.7	6.0,	4.8,	89.2	48.7,	51.3,	0.0
16	Kanagi		12.9,	21.4,	0.0,	65.7	1.3,	0.0,	98.7	12.4,	3.2,	84.4	48.6,	51.4,	0.0
17	H-Iyayama		16.5,	17.5,	0.5,	65.5,	1.5,	0.3,	98.2	5.3,	3.5,	91.2	55.7,	42.3,	2.0
18	N-Iyayama		9.8,	33.8,	0.0,	56.4	0.8,	0.0,	99.2	6.0,	4.5,	89.5	53.5,	46.5,	0.0
19	Chiran		13.5,	25.8,	0.8,	59.9	0.3,	0.0,	99.7	6.5,	7.3,	86.2	53.0,	47.0,	0.0
20	Shiiba		14.5,	21.5,	0.0,	64.0	0.8,	0.3,	98.9	4.0,	4.5,	91.5	56.7,	42.8,	0.5
21	Takeda		12.0,	24.5,	0.0,	63.5	1.5,	0.0,	98.5	8.3,	4.5,	87.2,	52.0,	48.0,	0.0
22	Fukue		18.3,	27.8,	0.0,	53.9	1.7,	0.0,	98.3	5.9,	4.2,	89.9	44.0,	56.0,	0.0
23	Izuhara		18.3,	22.3,	0.0,	59.4	0.2,	1.0,	98.8	9.3,	4.4,	86.3	54.5,	44.5,	1.0
24	Kamiagata		14.3,	23.3,	0.5,	61.9	0.3,	0.5,	99.2	4.3,	6.0,	89.7	52.5,	47.5,	0.0
25	Che-ju		17.5,	21.5,	0.3,	60.7	0.2,	0.0,	99.8	4.5,	3.7,	91.8	55.5,	44.0,	0.5
26	Je-cheon		16.8,	17.5,	0.5,	65.2	0.7,	0.5,	98.8	7.3,	4.0,	88.7	51.5,	48.5,	0.0
27	Dun-rae		15.5,	22.0,	0.5,	62.0	1.8,	0.0,	98.2	6.8,	3.3,	89.9	43.0,	57.0,	0.0
28	Chilin #1		18.3,	17.5,	0.4,	63.8	2.4,	2.1,	95.5	11.8,	7.3,	80.9	45.1,	53.7,	1.2
29	〃 #2		18.3,	15.8,	1.1,	64.8	1.0,	3.3,	95.7	12.0,	10.0,	78.0	50.0,	49.6,	0.4
30	Inner Mong #1		16.0,	17.5,	0.2,	66.3	1.7,	1.9,	96.4	8.8,	4.3,	86.9	47.9,	51.3,	0.8
31	〃 #2		19.1,	12.7,	1.0,	67.2	4.8,	1.5,	93.7	13.3,	5.5,	81.2	54.1,	45.9,	0.0
32	Kuyang		19.3,	12.5,	0.8,	67.4	2.3,	0.5,	97.2	11.4,	5.0,	83.6	52.9,	46.8,	0.3
33	Hujucxien		20.5,	12.5,	0.3,	66.7	3.0,	1.5,	96.5	11.3,	5.3,	83.4	61.0,	38.0,	1.0
34	Wuchuan		19.3,	15.8,	0.5,	64.4	2.5,	1.5,	96.0	12.0,	5.5,	82.5	58.2,	41.5,	0.3
35	Shensi #1		19.0,	11.5,	1.0,	68.5	3.0,	0.8,	96.2	14.8,	4.8,	80.4	52.2,	47.1,	0.7
36	〃 #2		15.8,	18.0,	0.3,	65.9	2.0,	0.8,	97.2	14.5,	4.0,	81.5	52.5,	47.1,	0.4
37	Yulin		16.8,	13.0,	0.0,	70.2	2.0,	0.3,	97.7	14.3,	4.5,	81.2	59.0,	40.2,	0.8
38	Hunan		18.6,	11.3,	1.8,	68.3	1.8,	1.8,	96.4	14.5,	7.8,	77.7	45.3,	53.4,	1.3
39	Szechuan		29.4,	13.2,	2.8,	54.6	0.8,	3.8,	95.4	12.0,	6.0,	82.0	46.7,	52.4,	0.9
40	Kweichow #1		25.0,	21.3,	1.0,	52.7	1.2,	0.0,	98.8	14.8,	3.9,	81.3	45.2,	54.3,	0.5
41	〃 #2		18.8,	16.8,	0.5,	63.9	1.8,	0.5,	97.7	9.0,	7.5,	83.5	48.9,	49.8,	1.3
42	Yunnan #1		21.7,	17.7,	0.5,	60.1	3.3,	0.0,	96.7	9.8,	13.6,	76.6	43.0,	55.2,	1.8
43	〃 #2		15.3,	17.6,	0.5,	66.6	2.5,	0.2,	97.3	10.9,	7.9,	81.2	48.4,	50.0,	1.6

(Ohnishi, 1988)

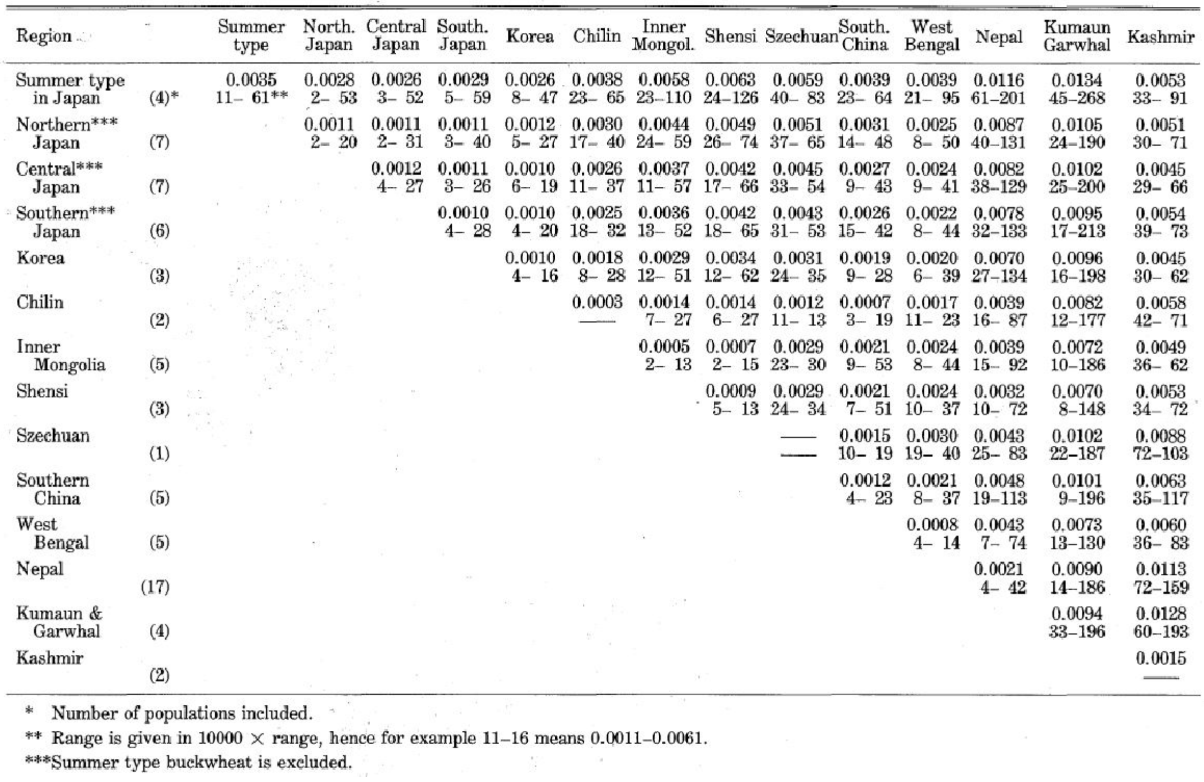
Table 7. Average heterozygosity (H), percentage of polymorphic loci (P), and average number of alleles per locus (A)*

No.	Population	H	P(%)	A
	Japan			
1	Furen	0.122	36.8	1.63
2	Noheji	0.113	36.8	1.52
3	Kuzumaki	0.122	36.8	1.63
4	Iwate-F	0.128	36.8	1.52
5	〃 -S	0.116	31.6	1.47
6	Miwa	0.116	36.8	1.57
7	Kanasagoh	0.116	36.8	1.57
8	Arakawa-F	0.117	36.8	1.63
9	〃 -S	0.112	36.8	1.52
10	Kannami	0.124	36.8	1.57
11	Togakushi-F	0.125	36.8	1.52
12	〃 -S	0.129	31.6	1.52
13	Takane	0.110	36.8	1.52
14	Niimi	0.127	36.8	1.52
15	Geihoku	0.122	36.8	1.52
16	Kanagi	0.121	36.8	1.57
17	Higashi-Iyayama	0.118	36.8	1.63
18	Nishi-Iyayama	0.118	31.6	1.57
19	Chiran	0.119	31.6	1.57
20	Shiiba	0.116	36.8	1.57
21	Takeda	0.122	36.8	1.52
22	Fukue	0.130	36.8	1.57
23	Izuhara	0.127	36.8	1.57
24	Kamiagata	0.120	31.6	1.63
	Average of Japan	0.120	35.7	1.56
	Korea			
25	Che-ju	0.117	31.6	1.52
26	Je-cheon	0.122	36.8	1.63
27	Dun-nae	0.115	36.8	1.57
	Average of Korea	0.118	35.1	1.57
	China			
28	Chilin #1	0.134	36.8	1.63
29	〃 #2	0.136	36.8	1.63
30	Inner Mongolia #1	0.128	36.8	1.68
31	〃 #2	0.134	36.8	1.63
32	Kuyang	0.132	42.1	1.68
33	Hujuoxien	0.129	36.8	1.63
34	Wuchuan	0.133	36.8	1.68
35	Shensi #1	0.136	42.1	1.73
36	〃 #2	0.129	36.8	1.63
37	Yulin	0.133	36.8	1.57
38	Hunan	0.133	36.8	1.68
39	Szechuan	0.134	36.8	1.68
40	Kweichow #1	0.133	36.8	1.68
41	〃 #2	0.136	42.1	1.79
42	Yunnan #1	0.138	42.1	1.73
43	〃 #2	0.135	42.1	1.73
	Average of China	0.133	38.5	1.67

*Including the alleles with a frequency of more than 0.5%.

(Ohnishi, 1988)

Table 8. Average and range of genetic distance between the populations



Region		Summer type	North. Japan	Central Japan	South. Japan	Korea	Chilin	Inner Mongol.	Shensi	Szechuan	South. China	West Bengal	Nepal	Kumaun Garwhal	Kashmir
Summer type in Japan	(4)*	0.0035 11– 61**	0.0028 2– 53	0.0026 3– 52	0.0029 5– 59	0.0026 8– 47	0.0038 23– 65	0.0058 23–110	0.0063 24–126	0.0059 40– 83	0.0039 23– 64	0.0039 21– 95	0.0116 61–201	0.0134 45–268	0.0053 33– 91
Northern*** Japan	(7)		0.0011 2– 20	0.0011 2– 31	0.0011 3– 40	0.0012 5– 27	0.0030 17– 40	0.0044 24– 59	0.0049 26– 74	0.0051 37– 65	0.0031 14– 48	0.0025 8– 50	0.0087 40–131	0.0105 24–190	0.0051 30– 71
Central*** Japan	(7)			0.0012 4– 27	0.0011 3– 26	0.0010 6– 19	0.0026 11– 37	0.0037 11– 57	0.0042 17– 66	0.0045 33– 54	0.0027 9– 43	0.0024 9– 41	0.0082 38–129	0.0102 25–200	0.0045 29– 66
Southern*** Japan	(6)				0.0010 4– 28	0.0010 4– 20	0.0025 18– 32	0.0036 13– 52	0.0042 18– 65	0.0043 31– 53	0.0026 15– 42	0.0022 8– 44	0.0078 32–133	0.0095 17–213	0.0054 39– 73
Korea	(3)					0.0010 4– 16	0.0018 8– 28	0.0029 12– 51	0.0034 12– 62	0.0031 24– 35	0.0019 9– 28	0.0020 6– 39	0.0070 27–134	0.0096 16–198	0.0045 30– 62
Chilin	(2)						0.0003 ——	0.0014 7– 27	0.0014 6– 27	0.0012 11– 13	0.0007 3– 19	0.0017 11– 23	0.0039 16– 87	0.0082 12–177	0.0058 42– 71
Inner Mongolia	(5)							0.0005 2– 13	0.0007 2– 15	0.0029 23– 30	0.0021 9– 53	0.0024 8– 44	0.0039 15– 92	0.0072 10–186	0.0049 36– 62
Shensi	(3)								0.0009 5– 13	0.0029 24– 34	0.0021 7– 51	0.0024 10– 37	0.0032 10– 72	0.0070 8–148	0.0053 34– 72
Szechuan	(1)									—— ——	0.0015 10– 19	0.0030 19– 40	0.0043 25– 83	0.0102 22–187	0.0088 72–103
Southern China	(5)										0.0012 4– 23	0.0021 8– 37	0.0048 19–113	0.0101 9–196	0.0063 35–117
West Bengal	(5)											0.0008 4– 14	0.0043 7– 74	0.0073 13–130	0.0060 36– 83
Nepal	(17)												0.0021 4– 42	0.0090 14–186	0.0113 72–159
Kumaun & Garwhal	(4)													0.0094 33–196	0.0128 60–193
Kashmir	(2)														0.0015 ——

* Number of populations included.

** Range is given in 10000 × range, hence for example 11–16 means 0.0011–0.0061.

***Summer type buckwheat is excluded.

(Ohnishi, 1988)

結　　語

中國西南部雲南省及四川省等地區發現了豐富的蕎麥種原，而且發現了普通蕎麥的祖先種，利用分子標誌技術建立各個種原之間的遺傳距離，了解蕎麥種原之間的歧異度及親緣關係，推估中國南部地區為普通蕎麥及韃韃蕎麥等蕎麥栽培種的起源中心；並從此處傳播到鄰近地區及其他亞洲國家，甚至於世界各地。起源中心富含種原資源，利用蕎麥遺傳歧異度的研究，可了解蕎麥的起源、分佈及傳播，並可掌握野生種的遺傳特性，這對改良蕎麥品種產量低及不穩定等特性有很大的幫助。

參考文獻

1. Campbell, C. 2003. Buckwheat crop improvement. Fagopyrum 20: 1-6.
2. Kishima, Y., K. Ogura, K. Mizukami, T. Mikami, and T. Adachi. 1995. Chloroplast DNA analysis in buckwheat species: phylogenetic relationships, orgin of the reproductive systems and extended inverted repeats. Plant Sci. 108: 173-179.

3. 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.
4. Ohnishi, O. 1988. Population genetics of cultivated common buckwheat, *Fagopyrum esculentum* Moench. VII. Allozyme variability in Japan, Korea, and China. Jpn. J. Genet. 63: 507-522.
5. Ohnishi, O. 1990. Discovery of the wild ancestor of common buckwheat. Fagopyrum 11: 5-10.
6. Ohnishi, O.1998. Search for the wild ancestor of buckwheat. I. Description of new *Fagopyrum* (Polygoaceae) species and their distribution in China and the Himalayan hills. Fagopyrum 15: 18-28.
7. Reif, J. C., P. Zhang, S. Dreisigacker, M. L. Warburton, M. van Ginkel, A. D. Hoisington, M. Bohn and A. E. Melchinger. 2005. Wheat genetic diversity trends during domestication and breeding. Theor. Appl. Genet. 110: 859-864.
8. Tsuji, K. and O. Ohnishi. 2000. Origin of cultivated Tatary buckwheat (*Fagopyrum tataricum* Gaertn.) revealed by RAPD analyses. Genet. Resour. Crop Evol. 47: 431-438.
9. Yamane, K., Y. Yasui, and O. Ohnishi. 2003. Intraspecific cpDNA variations of diploid and tetraploid perennial buckwheat, *Fagopyrum cymosum* (Polygonaceae). Am. J. Bot. 90(3): 339-346.
10. Yasui, Y., Y. Wang, O. Ohnishi, and C. Campbell. 2004. Amplified fragment length polymorphism linkage analysis of common buckwheat (*Fagopyrum esculentum*) and its wild self-pollinated relative *Fagopyrum homotropicum*. Genome 47: 345-351.

Study on the Origin and Dissemination of Buckwheat[1]

Yi-Lun Liao, Yu-Hsin Chen and Hsun-Shih Lin[2]

ABSTRACT

Buckwheat is crop belongs to the Genus *Fagopyrum*, Polygonceae family. There are only two species that the common buckwheat(*Fagopyrum esculentum*) and tartary buckwheat(*Fagopyrum tartaricum*) are cultivated. On 13 species of buckwheat among Himalayan area, and most of those are in the Yunnan in China, found a wild variety *F.esculentum* ssp. a*ncestrale*'s and its phenotype was similar with common buckwheat. After analysis by AFLP, the genetic distance of wild common buckwheat with common buckwheat was closed, suggested that Yunnan province of China was proposed to be the origin of common buckwheat. Analysis of tatary buckwheat accessions indicated that there were higher diversity in Yunnan and Sichuan than other places, Yunnan and Sichuan was thought to be the origin of tatary buckwheat. The genetic distance of buckwheat between southern China and Japan was shorter than northern China and Japan. This may infer that dissemination of buckwheat was from southern China to Japan.

Key words: common buckwheat, tatary buckwheat, origin, genetic diversity.

---

[1] Contribution No. 0769 from Taichung DARES, COA.

[2] Assistant Research Fellow, Assistant Research Fellow, and Associate Technician, Taichung DARES, COA.