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Title	Nuclear and mitochondrial DNA polymorphisms suggest introgression contributed to garden beet (Beta vulgaris L.) domestication
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1	Research article
2	Nuclear and mitochondrial DNA polymorphisms
3	suggest introgression contributed to garden beet (Beta
4	vulgaris L.) domestication
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#### 11 Abstract

12 Garden beet is the ancestor of fodder beets and sugar beets, but the origin of garden beet's genetic potential 13 to evolve novel beet types is debatable. In this study, we analyzed nuclear and mitochondrial DNAs in 47 14 garden beet accessions using DNA markers. Multiple analytical methods revealed a unified population 15 structure with subpopulations evident in the European and Caucasian accessions. We diagnosed 16 mitochondrial genome types (mitotypes) based on mitochondrial minisatellite loci in 541 plants from the 17 47 accessions, revealing a major mitotype and 11 minor mitotypes in garden beets from Europe and the 18 Caucasus region that were also present in endemic leaf beets and wild beets. Our data indicate that European 19 and Caucasian garden beets include genetically differentiated subpopulations. Provided that the occurrence 20 of minor mitotypes is a vestige from crosses with leaf beets and wild beets, the notion that introgression 21 contributed to increasing the genetic diversity in the garden beet gene pool is substantiated at the molecular 22 level.

23

#### 24 Introduction

Garden beet, or table beet, is a root crop that constitutes one of the cultivar groups belonging to the cultivated beet complex (*Beta vulgaris* L. ssp. *vulgaris*) that has three other intercrossable groups: leaf beets, fodder beets, and sugar beets (Lange et al. 1999). The cultivated beet complex is morphologically diverse, e.g., swollen roots and hypocotyls are seen in garden beet, fodder beet, and sugar beet groups but not in the leaf beet group (Biancardi 2020).

30 The ancestor of cultivated beet is its wild relative sea beet (B. vulgaris L. ssp. maritima), from 31 which leaf beet was first domesticated in a region spanning the Middle East to the Mediterranean coast 32 (Biancardi and Lewellen 2020; Goldman and Navazio 2003). Garden beet was selected from leaf beet for 33 its swollen root (Goldman and Navazio 2003). Roman writers described uses of beet root without clearly 34 mentioning that the root was swollen (Ford-Lloyd and Williams 1975). Zossimovic (1940) proposed that 35 the origin of swollen-root type beets is a region that includes Iraq, Iran, and Turkey (Galewski and McGrath 36 2020). A taxonomic group of presumptive common progenitors of swollen- and nonswollen-root-type beets 37 was found in Turkey (Ford-Lloyd and Williams 1975). Swollen-root type beets were described in the 12th 38 century, in Arabic (de Bock 1986). Therefore, the notion that garden beet originated in the Middle East and 39 spread north-westward is a possible scenario (Galewski and McGrath 2020) but may be an 40 oversimplification. Crop domestication generally invokes a reduction in genetic diversity (Hancock 2003); 41 however, garden beet landraces exhibit a range of morphological variations in traits such as root shape and 42 root color (Baranski et al. 2001). The expansion of phenotypic diversity in the garden beet group is inferred 43 to have occurred during its dissemination within Europe when crosses with leaf beet could have occurred 44 (Goldman and Navazio 2008). This phenotypic expansion was associated with the appearance of fodder 45 beet, whose establishment was no later than the 18th century (Goldman and Navazio 2003). According to 46 historical records, sugar beet evolved from fodder beet by artificial selection in the 19th century (Goldman 47 and Navazio 2003). Therefore, the cross between garden beet and leaf beet groups in Europe was a critical 48 factor in the evolution of the two more recently established cultivated beets. In other words, the genetic 49 potential to evolve a novel crop was provided by crosses between two cultivar groups; however, the 50 molecular evidence for this notion has not been assembled.

51 A molecular understanding of genomic diversity in beet has been advanced in the sugar beet 52 group; nuclear DNA polymorphisms were analyzed by several population-genetic methods, such as those 53 based on genetic distance and allelic frequency difference, to provide results consistent with the history of 54 the breeding lines (e.g., Galewski and McGrath 2020; Schneider et al. 1999; Adetunji et al. 2014; Laurent 55 et al. 2007; Li et al. 2010; Mangin et al. 2015; Simko et al. 2012; Stevanato et al. 2014; Andrello et al. 56 2017). Mitochondrial genome types (mitotypes) in sugar beet have been analyzed to show selection based 57 on mitotype should be adopted for hybrid breeding (Cheng et al. 2009). A similar analysis was used to 58 investigate mitotypes in other cultivated beets. In summary, the greatest mitotype diversity was found in 59 European leaf beet, and the lowest mitotype diversity occurred in swollen-root type beets (Cheng et al. 60 2011; Nishizawa et al. 2007; Yoshida et al. 2012).

Genomes of garden beet cultivars were analyzed concomitantly with those of sugar beet, and a puzzlingly large genetic diversity was revealed (Galewski and McGrath 2020; Mangin et al. 2015; Andrello et al. 2017). The details behind this large diversity, however, were unclear. Although we had previously examined mitotypes in garden beet (Cheng et al. 2011), the number of garden beet accessions used was rather small, and a combined analysis of nuclear DNA polymorphism was missing. We proposed that the evolutionary history of garden beet could be drawn by a combined analysis of nuclear and mitochondrial genome diversity among garden beet genetic resources.

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In this study, we have extended our analysis of nuclear and mitochondrial genome diversity to

69 a larger number of garden beet accessions. Our analysis of nuclear DNA polymorphism revealed the genetic 70 structure of garden beet genetic resources: one subpopulation included landraces with a broad origin, 71 including Europe, the Caucasus region, the Middle East, and West Asia. The origins of the other 72 subpopulations were confined to Europe and the Caucasus region. Our mitotype analysis revealed several 73 additional mitochondrial genome types (mitotypes) in garden beet, but they occurred infrequently, and the 74 general trend of mitochondrial DNA polymorphism was unchanged. To our surprise, minor mitotypes were 75 more frequent in European and Caucasian garden beet accessions. These minor mitotypes were identical to 76 those in European leaf- and wild beet accessions (Cheng et al. 2011). In conclusion, garden beet genetic 77 resources appeared to have experienced something that resulted in genetically differentiated subpopulations 78 in Europe and the Caucasus region. We propose that crosses with leaf beet or wild beet may explain how 79 these distinct subpopulations formed. 80 81 82 **Materials and Methods** 83 Plant materials 84 Forty-seven garden beet accessions were used in this study (Table 1). Although the mitotypes of BETA 85 1037, BETA 1058, BETA 1165, BETA 1343, BETA 1388, BETA 1478, BETA 1618, BETA 1795, BETA

86 1901, BETA 2040, BETA 2071, BETA 2129, and BETA 965 were first reported in Cheng et al. (2011), these 87 13 accessions were reanalyzed in this study. All 47 accessions were obtained from The Leibniz Institute of 88 Plant Genetics and Crop Plant Research (IPK), Germany. Three sugar beet lines were also used in this 89 study: NK-291mmBR-CMS, NK-195mmBR-CMS, and NK-315mmBR-O were developed at the Hokkaido 90 Agricultural Research Center, National Agriculture and Food Research Organization, Japan. Two wild beet 91 (B. vulgaris L. ssp. maritima) accessions were also used in this study: BETA 368, collected in Portugal and 92 obtained from IPK, and NGB 14676, collected in Denmark and obtained from The Nordic Genetic Resource 93 Center, Sweden.

94

95 DNA markers and polymerase chain reaction

96 Primers for 51 cleaved amplified polymorphic sequence (CAPS) markers for nuclear DNA analysis are

97 summarized in Table S1. The multiallelic nuclear DNA marker s17 was detailed in Taguchi et al. (2014).

98 The other nuclear DNA markers target gene-coding sequences or untranslated regions; ten DNA markers 99 are selections from Taguchi et al. (2019). Details about the development of the remaining 40 markers will 100 be described elsewhere. Mitochondrial minisatellite analysis and orf129 detection were conducted as 101 described in previous studies (Cheng et al. 2011; Nishizawa et al. 2000). Total cellular DNA was isolated 102 from green leaves according to a standard procedure (Doyle and Doyle 1990). DNA fragments were 103 electrophoresed in 2% (w/v) agarose gels.

104

105 Data analyses

106 Accessions were clustered according to the neighbor-joining method (NJ) and the unweighted pair-group 107 method with arithmetic averages (UPGMA) using GENEPOP ver. 4.7 (Raymond and Rousset 1995) and 108 visualized using MEGA X (Kumar et al. 2018). STRUCTURE software (ver. 2.3.4) (Pritchard et al. 2000) 109 was run with an admixture model in which the Markov Chain Monte Carlo steps were set to 100000 110 following a burn-in period of 100000. Posterior probabilities for each K value were calculated using ten 111 replicates. Fisher's exact test was executed at website (http://aoki2.si.gunmaа 112 u.ac.jp/exact/fisher/getpar.html). Analysis of molecular variance (AMOVA) was conducted using GenAlEx 113 6.2 (Peakall and Smouse 2006, 2012) with the permutation number set at 999. Wright's fixation index  $(F_{st})$ , 114 a measure of population differentiation, was also calculated by GenAlEx.

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116

#### 117 **Results and Discussion**

118 Nuclear DNA polymorphism in garden beet

119 We investigated nuclear DNA polymorphism in garden beet genetic resources, most of which are landraces 120 or old cultivars. Each of the 47 garden beet accessions was represented by a single plant. We also analyzed 121 two wild beets collected in Portugal and Denmark, both of which are distant from the area where garden 122 beet was domesticated (i.e., the Middle East). In addition, three sugar beet lines were included in the 123 investigation. The CAPS markers used in this study were distributed among the nine beet chromosomes; 124 each chromosome was covered by 4 to 12 markers. In summary, 109 alleles were identified from the 51 125 markers, i.e., each marker yielded 2.14 alleles on average (Table S2). 126

A total of 52 accessions/lines were clustered according to their genetic distance based on the

polymorphisms detected by the CAPS markers. Figure 1 shows the result of the NJ. We divided accessions into three groups, Group I, Group II, and Wild Beet. Group I consisted of 36 garden beet accessions. All three sugar beet lines were clustered into Group II with 11 garden beet accessions. UPGMA resulted in a different dendrogram (Fig. S1), but the members in each group were identical to those of the NJ.

131 We took another approach to infer the number of subpopulations (K) by a model-based 132 clustering method. The posterior probability increased when K was one to five but declined as K increased 133 (Fig. S2). A bar plot of K = 5 is shown in Fig. 2; the two wild beet accessions formed a distinct group, 134 shown as Pop C. Sugar beet lines were grouped into Pop A except for NK-315mmBR-O that was 135 incorporated into a garden beet group. Garden beet accessions were divided into Pops B, D, and E. Pop B 136 was a group with seven garden beet accessions and the sugar beet line NK-315mmBR-O. Pop D, the largest 137 group, consisted of 35 garden beet accessions. Pop E contained five garden beet accessions. Note that, of 138 the 35 accessions in Pop D, 34 were shared with Group I (Table 1). Accordingly, Group II well represented 139 the sum of Pops B and E. The exceptional garden beet accessions were BETA 187, K 7136, and BETA 140 1681, whose ancestry was complex as shown in the bar plots of Fig. 2.

141 We inferred the genetic diversity of Groups and Pops by AMOVA (Table 2). In the case of 142 Groups, the amount of variance among the groups was 11%, and  $F_{st}$  was 0.107. A permutation test 143 implemented with GenAlEx software reported a probability (P) value of 0.005. Pairwise population  $F_{st}$ 144 values were 0.066 to 0.306 with P values of 0.001 to 0.002 (Table S3). In the case of Pops, the variance 145 among Pops was 14%, and  $F_{st}$  was 0.139 with a P value of 0.001 (Table 2). In the matrix of pairwise  $F_{st}$ 146 values shown in Table S3, the value for Pop A vs. Pop B was given as 0 because the calculated value was 147 negative, and P = 0.430. This result may be related to the composition of these Pops since both Pop A and 148 Pop B contain sugar beet lines (Fig. 2). All the other pairwise  $F_{st}$  values were 0.110 to 0.290 with P values 149 of 0.001 to 0.0028 (Table S3). Collectively, these results provided a population structure for our garden 150 beet accessions. The distribution of Pops B, D, and E in Europe to West Asia is shown in Fig. 3. Pop B and 151 Pop E accessions were collected in Europe and the Caucasus region. Pop D was distributed widely from 152 Europe and the Middle East to West Asia. The distribution of Group I accessions corresponded to that of 153 Pop D, except for BETA 187 (Group I/ Pop B, collected in Georgia), BETA 1681 (Group II/ Pop D, Greece) 154 and K 7136 (Group I/ Pop B, Georgia). Group II is the merger of Pop B and Pop E. Accessions from Canada, 155 China, Cuba, and the USA belonged to either group.

The link between garden beet genetic diversity and its geographic origin was missing from previous studies. In our study, we combined nuclear DNA polymorphism data with information about the origin of the genetic resources. The results favor the notion that garden beet genetically diverged in Europe and the Caucasus region, although a more in-depth analysis will be necessary to make a definitive conclusion. This notion is consistent with the expansion of morphological variation of European garden beet varieties (Baranski et al. 2001). How genetic diversity increased is an intriguing question, for which introgression may be one of the possibilities (Goldman and Navazio 2008; see below).

The sugar beet lines used in this study were grouped into a garden beet group termed Group II or Pop B. Considering the domestication history of sugar beet, i.e., sugar beet was selected from fodder beet whose ancestor is garden beet, this result is not surprising. Interestingly, Group II and Pop B are the groups that occur in Europe and the Caucasus region. This finding implies that the genetically diversified garden beet contributed to the development of a novel type of swollen-root beet. The genetic diversity of garden beets is the key to understanding the domestication of sugar beet.

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#### 170 Mitotypes in garden beet

171 We raised the question of whether the garden beet subpopulations were characterized by their mitotypes. 172 Mitotypes were determined according to haplotypes that were defined by the number of repeat units in four 173 minisatellite loci of the beet mitochondrial genome (Nishizawa et al. 2000, 2007) (Table S4). One of the 174 mitotypes, min06, was further investigated to determine whether the plants possessed mitochondrial gene 175 orf129 that encodes a protein associated with male sterility (Yamamoto et al. 2008). All the min06 plants 176 in this study were PCR positive for orf129 and were designated as min06/+orf129. A summary of the 177 mitotypes found in 541 plants from the 47 accessions is shown in Table 1. We found 12 mitotypes, of which 178 seven (min07, min10, min11, min15, min17, min33 and min37) were newly discovered as garden beet 179 mitotypes. Mitotype frequency is summarized in Table 3. We tested whether the distribution of mitotypes 180 was different between Groups or Pops. Our results showed that pairwise combinations of Groups or Pops 181 differed significantly in terms of mitotype frequency (Table S5).

182 The most predominant mitotype in garden beet was min18 that was found in 88% of the 183 examined plants, or it occurred in 37 of the 47 accessions (79%) (Table 1). Mitotypes min09, min15, and 184 min18 were present in fodder beets and sugar beets; min18 was especially common among accessions of 185 both beet types (Cheng et al. 2009; Yoshida et al. 2012). The predominance of min18 is likely a common 186 feature among swollen-root beets. These mitotype features were consistent with the historical record and 187 currently proposed domestication hypothesis that all swollen root-type beets have a common ancestor (see 188 Introduction). The remaining nine mitotypes include those found in leaf- and wild beets of Europe and the 189 Middle East, where the mitotypes of these beets are the most diverse (Cheng et al. 2011; Nishizawa et al. 190 2007) (Table 4). The minor mitotypes in European garden beets were min07, min09, min10, min11, min15, 191 min17, min19, min33 and min37, of which all but min15, min17, min33 and min37 were identified 192 previously in European leaf beets (Cheng et al. 2011) (Table 4). The four previously unidentified mitotypes 193 were found in European wild beets (Nishizawa et al. 2007 and our unpublished data). We focused on non-194 min18 mitotypes because they are the principal contributors to garden beet mitotype diversity. As shown in 195 Fig. 4, the occurrence of non-min18 in garden beets was seen mainly in Europe and the Caucasus region, 196 suggesting that diversification of garden beet mitotypes predominated in these areas. In fact, multiple non-197 min18 mitotypes were found in France, Slovakia, Romania, and Greece. Multiple non-min18 mitotypes 198 also occurred in accessions from Pakistan and China; min06/+orf129 and min08 found in accessions from 199 Pakistan and China were absent from our European accessions (Table 1).

The origins of the minor mitotypes in garden beets identical to those of European leaf- and wild beets are likely due to past introgression. Another possible origin may be contamination of the germplasm collection. We cannot exclude this possibility but note that at maturity all 47 garden beet accessions had a garden beet-like phenotype when grown in our field. Illegitimate pollination during germplasm multiplication could not have contributed to mitotype introduction since mitochondria are maternally inherited.

Goldman and Navazio (2008) proposed a hypothesis that hybridization with leaf beet is associated with the phenotypic diversity of garden beet cultivars. This proposal reminds us of BETA 2056, whose origin is recorded as the French garden beet cultivar 'Crapaudine.' BETA 2056 belongs to Group II/ Pop B, and the plants have either min19 or min33. Interestingly, 'Crapaudine' is known for its carrot-like root; the roots of BETA 2056 plants are thin and long, unlike typical garden beets that have a globular roothypocotyl (our unpublished observations), a characteristic reminiscent of leaf-beet roots. Further study taking morphology into account will be necessary.

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Another possibility is that the leaf beet-like mitotype occurred in garden beet de novo. TR1,

one of the minisatellite loci, is highly polymorphic in *B. vulgaris* genetic resources (Nishizawa et al. 2007).
Multiple independent occurrences of the same number of repeated sequence units at this locus are possible.
On the other hand, sugar beet mitotypes are stable enough to diagnose cytoplasm in the breeding program
(Cheng et al. 2009). Moreover, some minor mitotypes such as min10, min19 and min33 differ from min18
at two or three loci, making their independent occurrence unlikely. The stability of mitotypes and detailed
analyses of mitochondrial DNA and plastid DNA should be investigated in the future.

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221

# 222 Conclusions

223 In garden beet, significant genetic diversity at the molecular level had been recognized before our study 224 (Galewski and McGrath 2020; Mangin et al. 2015; Andrello et al. 2017), although how diversity was 225 generated or maintained was unknown. In this study, we found a population structure in garden beet that 226 was supported by multiple analytical methods. What these subpopulations reflect is unknown because no 227 pedigree data are available from landraces; however, the evidence shows that subpopulations occurred in 228 Europe and the Caucasus region, a result supporting the notion that garden beet diversified in these areas. 229 Our analysis of mitochondrial DNA polymorphism revealed major and minor mitotypes in garden beet. 230 The minor mitotypes in Europe were also the subset of mitotypes in leaf beets and wild beets in Europe, 231 leading us to propose that these minor mitotypes are the vestiges of past introgressions. In summary, our 232 molecular data from nuclear and mitochondrial DNA analyses support the notion that the European garden 233 beet was genetically diversified by crosses with endemic leaf beet or wild beet populations, although other 234 possibilities cannot be excluded. The occurrence of subpopulations, minor mitotypes, as well as some 235 botanical studies (e.g. Ford-Lloyd and Williams 1975), led to our hypothesis that such crosses occurred 236 north-westward from an area in the Caucasus region toward Asia Minor and Greece.

237

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246	
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248	The authors declare no competing interest.
249	
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251	All data generated or analyzed during this study are included in this published article and its supplementary
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253	
254	Code availability
255	Not applicable.
256	
257	Authors' contributions
258	Conceptualization: Yohei Kanomata and Tomohiko Kubo; Methodology: Yohei Kanomata, Kosuke Satoh
259	and Kazuyoshi Kitazaki; Formal analysis and investigation: Yohei Kanomata, Ryo Hayakawa, Jun
260	Kashikura, Kazuyoshi Kitazaki; Writing - original draft preparation: Yohei Kanomata; Writing - review and
261	editing: Tomohiko Kubo; Funding acquisition: Hiroaki Matsuhira, Kazuyoshi Kitazaki and Tomohiko
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271	Not applicable

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# 350 Tables

Accession	Group	Рор	Number of plants in the mitotype											Country of		
			min06/	min	Total	origin										
			+orf129	07	08	09	10	11	15	17	18	19	33	37		
BETA 1032	Ι	D									12				12	Turkey
BETA 1037	Ι	D									20				20	Georgia
BETA 1058	Ι	D									21				21	Germany
BETA 1065	Ι	D									11				11	Iran
BETA 1159	Ι	D									15				15	Greece
BETA 1165	Ι	D									12				12	Greece
BETA 1229	Ι	D									18				18	Turkey
BETA 1257	Ι	D									8				8	Uzbekistan
BETA 1285	Ι	D									15				15	Azerbaijan
BETA 1306	Ι	D		7				1							8	Greece
BETA 1343	Ι	D	19		4										23	Pakistan
BETA 1388	Ι	D									14				14	Soviet Union
BETA 1463	Ι	D									8				8	Greece

# 351 Table 1. Groups, Pops and mitotypes of garden beet accessions

BETA 1468	Ι	D							10				10	Greece
BETA 1478	Ι	D							19				19	Greece
BETA 155	II	Е							9				9	Russia
BETA 1594	Ι	D							11				11	Turkey
BETA 1618	Ι	D							23				23	Unknown
BETA 1681	II	D		5	5								10	Greece
BETA 1723	II	В				4							4	Italy
BETA 1744	Ι	D							7				7	Greece
BETA 1774	II	Е							1				1	Germany
BETA 1777	Ι	D							9			1	10	Germany
BETA 179	Ι	D	2			8							10	China
BETA 1795	Ι	D							5				5	The
		D												Netherlands
BETA 184	Ι	D							6	4			10	Slovakia
BETA 187	Ι	В							13				13	Georgia
BETA 1901	II	Е						3			20		23	France
BETA 2040	Ι	D							13				13	The
		D												Netherlands

BETA 2056	II	В							3	8	11	France
BETA 2071	Ι	D						21			21	Italy
BETA 2129	Ι	D						9			9	USA
BETA 222	Ι	D						8			8	Poland
BETA 223	II	В						16			16	Georgia
BETA 245	Ι	D						12			12	Iraq
BETA 248	II	В		4							4	Spain
BETA 273	Ι	D						12			12	Tajikistan
BETA 33	II	Е						7			7	Canada
BETA 334	Ι	D				2	4				6	Romania
BETA 336	II	В		4							4	Slovakia
BETA 340	Ι	D						11			11	Romania
BETA 355	II	Е						3			3	Georgia
BETA 3818	Ι	D						7			7	Cuba
BETA 3861	Ι	D						4			4	Georgia
BETA 3881	Ι	D						12			12	Georgia
BETA 965	Ι	D						15			15	Unknown
K 7136	Ι	В			11			5			16	Georgia

Total		21	12	4	13	12	12	2	7	422	7	28	1	541	
(# of		(2)	(2)	(1)	(3)	(2)	(2)	(1)	(2)	(37)	(2)	(2)	(1)		
accessions															
with the															
mitotype)															

# 353 Table 2. Summary of AMOVA statistics

		Groups			
	df	Mean squares	Variance	%	$F_{st}$
					( <i>P</i> )
Among Groups	2	46.954	1.376	11	
Within a Group	49	14.997	3.465	27	0.107
Between accessions	52	8.067	8.067	62	(0.005)
Total	103		12.908	100	
		Pops			
	df	Mean squares	Variance	%	$F_{st}$
					( <i>P</i> )
Among Pops	4	38.475	1.815	14	
Within a Pop	47	14.359	3.146	24	0.139
Between accessions	52	8.067	8.067	62	(0.001)
Total	103		13.028	100	

Group/ Pop		Mitotypes											Total
	min06	min07	min08	min09	min10	min11	min15	min17	min18	min19	min33	min37	
Group I	21	7	4	0	8	1	2	4	381	4	0	1	433
Group II <sup>1</sup>	0	5	0	13	4	11	0	3	41	3	28	0	108
Total	21	12	4	13	12	12	2	7	422	7	28	1	541
Pop B <sup>1</sup>	0	0	0	8	4	11	0	0	34	3	8	0	68
Pop D	21	12	4	5	8	1	2	4	368	4	0	1	430
Pop E	0	0	0	0	0	0	0	3	20	0	20	0	43
Total	21	12	4	13	12	12	2	7	422	7	28	1	541

# 357 Table 3. Summary of mitotype frequency in garden beet subpopulations

358 <sup>1</sup>Sugar beet lines were excluded.

## 363 Table 4. Comparison of mitotypes between garden beets and leaf beets<sup>1</sup>

## Garden beet

									Mitot	ypes an	d the nu	mber of	f plants						
		# of		min	min														
Origin		# 01	min	06/+	06/-	min	min	min	min	min	min	min	min	min	min	min	min	min	Total
		acc.	04	orf	orf	07	08	09	10	11	15	17	18	19	20	21	33	37	Total
				129	129														
Europe		26				12		13	4	1	2	7	202	7			28	1	277
Non-	Georgia and	7								11			75						96
Europe	Azerbaijan	/								11			15						80
	Turkey	3											41						41
	Iran and Iraq	2											23						23
	Pakistan,																		
	Uzbekistan,	2		10			4						20						42
	and	3		19			4						20						43
	Tajikistan																		
	Other								0				(1						71
	countries	6		2					8				61						/1

	Total	47	0	21	0	12	4	13	12	12	2	7	422	7	0	0	28	1	541
Leaf beet																			
Europe		13	2	3	1	20	2	51	2	1			28	4	10	7			131
Non-	Georgia	2			1	1		4					12						18
Europe	Turkey	2			3		1		5				10						19
	Iraq and	7		1	30			1	3	1			26						64
	Israel	/			52			1	5	1			20						04
	Total	24	2	4	37	21	3	56	10	2	0	0	76	4	10	7	0	0	232

364 <sup>1</sup>Leaf beet data were reported in Cheng et al. 2011

368	Figure legends
369	Fig. 1 Dendrogram of accessions based on the results of the NJ. Black bars on the right identify Groups
370	I and II and the Wild Beet group
371	
372	<b>Fig. 2</b> Accessions resulting from the analysis using STRUCTURE software ( $K$ =5). Red, green, blue,
373	yellow, and purple bars represent different ancestries. A scale bar on the top indicates the proportion of
374	ancestry for each accession
375	
376	Fig. 3 Countries of origin for garden beet accessions. Filled circles represent accessions: green, yellow,
377	and purple indicate Pop B, Pop D, and Pop E, respectively
378	
379	Fig. 4 Countries of origin for garden beet accessions. Blue filled circles and white open circles indicate
380	the presence or absence of non-min18 mitotypes in the accessions, respectively.
381	
382	
383	Supporting information
384	Figure S1 Dendrogram of accessions based on UPGMA results. Black bars on the right identify the three
385	groups resulting from this analysis.
386	Figure S2 Posterior probability (vertical axis) for each $K$ value (horizontal axis) calculated by
387	STRUCTURE software.
388	Table S1         Summary of DNA markers used in this study
389	Table S2         Alleles detected in the accessions used in this study
390	Table S3 Pairwise population $F_{st}$ values among Groups and Pops. <i>P</i> values are shown in parentheses.
391	Table S4Numbers of repeat units in the minisatellite loci of mitotypes
392	Table S5 Probabilities of mitotype differentiation for each pair of Groups and Pops calculated using
393	GENEPOP software
394	









Table S1 Summary of DNA markers used in this study								
Genomic location	Name of marker <sup>*1</sup>	Fw primer	Rv primer	Restriction endonuclease	Reference			
Chr 1	Chr11105371"BamH1	5'-TGCTTGTTGAACGGATGACC-3'	5'-TCTCTCCCAAGGCGTTGTTT-3'	Bam HI	This study			
Chr 1	Chr15062537"EcoR1	5'-TTGAAACCATGGCACTCCAC-3'	5'-CAACCCATTCCATGGCACTA-3'	Eco RI	This study			
Chr 1	Chr1_10739771"EcoR1	5'-TCCTGGCAGAGTTGCTTCAA-3'	5'-AGACCTCACCTGGCTTGCAT-3'	Eco RI	This study			
Chr 1	Chr1_15721785"BamH1	5'-GACGATAGACTCGACTCCGTATGA-3'	5'-TCGTCCCTTAAACGAGCGTA-3'	Bam HI	This study			
Chr 1	Chr1_20340637"EcoR1	5'-CGGCTATGACAGGGTGAAGA-3'	5'-GGGGAAGATGTTGGTGTGCT-3'	Eco RI	This study			
Chr 1	Chr1_24038662"EcoR1	5'-CTGACATTGACATGGCAGCA-3'	5'-CTTCAAGCAGCAGGAGCTGA-3'	Eco RI	This study			
Chr 1	Chr1_30462492"EcoR1	5'-GCATGACCCTTCATCACTGC-3'	5'-CCTGCTGGATCTGAACTTCTCA-3'	Eco RI	This study			
Chr 1	Chr1_35823465"EcoR1	5'-TAAAGTCGCATGGGTTGTGG-3'	5'-TGAAGCACTATCTCCCCCACT-3'	Eco RI	This study			
Chr 1	Chr1_40893642"EcoR1	5'-GCGTGGGAAAGTGAAAAGG-3'	5'-ACCGAGGGTCCTCAAGAACA-3'	Eco RI	This study			
Chr 1	Chr1_47187792"Hind3	5'-GGGATATGGATTTGGGGTGA-3'	5'-GGATCCTTGGCTTCTTTTCC-3'	Hin dIII	This study			
Chr 1	Chr1_51277414"BamH1	5'-GCGATAGATGCCACATTGGA-3'	5'-GCAAGCGGTGAACAAACAAG-3'	Bam HI	This study			
Chr 1	Chr1_56725886"Hind3	5'-TCAATTCAGGCAAGCTGCAC-3'	5'-ACAATTTGGCAGGGAGCAAG-3'	Hin dIII	This study			
Chr 2	MP0180	5'-AAAGGCTCCAACTAACCTCC-3'	5'-ACAGGTTCATCGTGCTACAC-3'	Hae III	Taguchi et al. 2019 <sup>*2</sup>			
Chr 2	Chr21408494"EcoR1	5'-GCCTCTCCAGTATTTTGGCTTC-3'	5'-CTCGATTTGCAAAGGGGATG-3'	Eco RI	This study			
Chr 2	Chr2_10970256"EcoR1	5'-TTTGCGTCTACCGCTACCAC-3'	5'-AGGGGATGGGTTGGTTTTTC-3'	Eco RI	This study			
Chr 2	Chr2_36165939"BamH1	5'-GGGAGGGGTTGTTCCTAGTTT-3'	5'-GATTTTGGTCCTTCTGGACACC-3'	Bam HI	This study			
Chr 2	Chr2_50304382"EcoR1	5'-GATGAAATGACGCTCGCTTG-3'	5'-GCCGGAAATCACACTTCACA-3'	Eco RI	This study			
Chr 3	s17	5'-CAATCTGTGGTGCTGACCAA-3'	5'-GATTAAAGAGGGCTGCTGAAGCCGAGA-3'	Hap II + Hin dIII	Taguchi et al. 2014 *3			
Chr 3	tk	5'-GGTTTTGGSTCTCCTAACAAG-3'	5'-GAGCATMAGAATGTTGGGCAT-3'	Hha I	Taguchi et al. 2019			
Chr 3	Chr3_10122025"Hind3	5'-CCATGATAATTGGCGGGTTG-3'	5'-TTCGGCAACTCTGGGAGAAT-3'	Hin dIII	This study			
Chr 3	Chr3_25572418"EcoR1	5'-AGACAACGCCGGAGAAGGTA-3'	5'-TGGATACCCTGCATTCACCA-3'	Eco RI	This study			
Chr 3	Chr3_39227764"Hind3	5'-TAAGGAAGGTGGAGGCTGGA-3'	5'-TCCCAACAGCGATTCACATC-3'	Hin dIII	This study			
Chr 3	Chr3_53929307"EcoR1	5'-CAACTAAAAGGCGCTGCAAG-3'	5'-TGGACTATGACCGACCCTCA-3'	Eco RI	This study			
Chr 4	nir	5'-GTTAGRCTCAAGTGGCTTGG-3'	5'-GGCATTCTCTCTCWACCTC-3'	Hae III	Taguchi et al. 2019			
Chr 4	Chr4_15005279"Hind3	5'-AGAACTCTCCCTCTGTGGCCTA-3'	5'-TCAACCGGTGTTCTGCATTC-3'	Hin dIII	This study			
Chr 4	Chr4_29996367"Hind3	5'-GCATCGAACCCGAAGAAGAA-3'	5'-AGGACTTCCCCAGGGATTTG-3'	Hin dIII	This study			
Chr 4	Chr4_46068100"Hind3	5'-TGCAATCCAATGCACTACGC-3'	5'-GTGGCGCTTCGAAATTCTCT-3'	Hin dIII	This study			
Chr 4	Chr4_60476329"EcoR1	5'-GCACGTTCTACTTCCTGCAATG-3'	5'-CAAGCCACCTAGCCAGAAAA-3'	Eco RI	This study			
Chr 5	invvac *6	5'-TTACCAGTACAACCCTGCAG-3'	5'-CAATGGCAGGCTTCTCAGGC-3'	Hae III	Taguchi et al. 2019			
Chr 5	Chr5_15697877"EcoR1	5'-TTGGCACTTGAGGAGAGTGG-3'	5'-TCCGTCTTCTGCTGTTGCTC-3'	Eco RI	This study			
Chr 5	Chr5_30062100"EcoR1	5'-AACTCTCCGTTCTTCTCCAAGG-3'	5'-TTTCCAGCCTCCAGGTTCTC-3'	Eco RI	This study			
Chr 5	Chr5_45072440"BamH1	5'-CAATGGCCAATCTGTCCTGA-3'	5'-GCGCACAGTTGGAGTTGTTC-3'	Bam HI	This study			
Chr 6	сто	5'-TTCTTGCTTGTGGAAGTGGC-3'	5'-AGGATCAAAAGCATGGGCCT-3'	Afa I	Taguchi et al. 2019			
Chr 6	Chr6_15454218"EcoR1	5'-CGATAGAGCATCGGCATCAA-3'	5'-AGCCAGCAGGGTCTCTTCAA-3'	Eco RI	This study			
Chr 6	Chr6_28786817"EcoR1	5'-GAGTGCGTGCCTGTGTGTTT-3'	5'-TTCGGGGGAAGGACAGATAG-3'	Eco RI	This study			
Chr 6	Chr6_60470324"Hind3	5'-CAAGTTCAGCTCCGCGTACA-3'	5'-ATTGGCAAGGGAGATGCTGT-3'	Hin dIII	This study			
Chr 7	7M20	5'-GCTGATCTTCCTAGGTTGG-3'	5'-GCATGAGTAATGCTCTCAGG-3'	Hae III	Taguchi et al. 2019			
Chr 7	2G14	5'-GGTTTGCACTTTTCTTAGATGG-3'	5'-GAGCCAATCAATCTTCAGCC-3'	Hha I	Taguchi et al. 2019			
Chr 7	SS	5'-CTCTGAACTGAATGTGGAGC-3'	5'-GGAGCCTGAAGGATATCTAG-3'	Xsp I	Taguchi et al. 2019			
Chr 7	Chr7 11043867"Hind3	5'-TGTAAACCGTCGTCCCTTCA-3'	5'-CATGGAAGCTCCTTCTGTGG-3'	Hin dIII	This study			

Chr 7	Chr7_26398346"Hind3	5'-GCGCGAGATTCGAAGGAAA-3'	5'-GGCTATCATCGCTAGTCCATTG-3'	Hin dIII	This study
Chr 7	Chr7_42026336"EcoR1	5'-GGCTGCCGGTGTCTGAATTA-3'	5'-ATGCAACCTGCTGATGCACT-3'	Eco RI	This study
Chr 7	Chr7_57077272"Hind3	5'-TTTGAGCCACCAACTCCAGA-3'	5'-CTGCGCATGAAGGTCAAAAG-3'	Hin dIII	This study
Chr 8	sps	5'-AGCTGTTATGGAAGGTTCATG-3'	5'-TCGGGTCAGGCCTAGCAA-3'	Hae III	Taguchi et al. 2019
Chr 8	Chr89906841"Hind3	5'-CATGGTCTCCAAGTCCCACA-3'	5'-CATGGGTGCTTGCAGGATTA-3'	Hin dIII	This study
Chr 8	Chr8_25436072"EcoR1	5'-TTGAGCAGTTGCACGATCAG-3'	5'-CCACTGTGCATCCATCACCT-3'	Eco RI	This study
Chr 8	Chr8_43259046"EcoR1	5'-AGCGTGTTTCCCAGTTCAGA-3'	5'-CAGTGGCTGCAAAAGTGGAC-3'	Eco RI	This study
Chr 9	mp0018	5'-AAGCAAACACAGCATTAGCC-3'	5'-GTATGCAAAGTCCAGACAGAAG-3'	Hae III	Taguchi et al. 2019
Chr 9	Chr98948514"Hind3	5'-CGCCCAAAATCAGATCACAG-3'	5'-GTCCTCCAATCACCCTTGCT-3'	Hin dIII	This study
Chr 9	Chr9_22312475"EcoR1	5'-ATGCAGTTCCCCTTTCCAGA-3'	5'-CTGCTGGACTTTGCTTCACC-3'	Eco RI	This study
Chr 9	Chr9_36154592"BamH1	5'-TCCTTCTCCATATCCCAACACC-3'	5'-GATCGTGGTGGAAGCTGATG-3'	Bam HI	This study
Mt	mt-TR1	5'-AGAACTTCGATAGGCGAGAGG-3'	5'-GCAATTTTCAGGGCATGAACC-3'	NA	Nishizawa et al. 2000 *4
Mt	mt-TR2	5'-TTAATTGCGAGACCGGAGGC-3'	5'-GAGCTTGCTCGCAGCTTATG-3'	NA	Nishizawa et al. 2000
Mt	mt-TR3	5'-AGATCCAAACAGAGGGACTG-3'	5'-CGGATCACCCTATTCATTTG-3'	NA	Nishizawa et al. 2000
Mt	mt-TR4	5'-AATGAGACCCGATTCTCTTC-3'	5'-GTTAAAAGCCCTTCTATGCC-3'	NA	Nishizawa et al. 2000
Mt	orf129	5'-ATCCATGGTGATGAATCCTTATATTCTGC-3'	5'-CTAGAGCTCTCACTGTGAGAGATAG-3'	NA	Cheng et al. 2011 *5

\*1 The number following the chromosome coordinates to the nucleotide sequence of sugar beet nuclear genome (Funk et al. Plant J 2018;95: 659-671.).

<sup>\*2</sup> Taguchi K, Kuroda Y, Okazaki K, Yamasaki M. Breed Sci 2019;69: 255-265.

<sup>\*3</sup> Taguchi K, Hiyama H, Yui-Kurino R, Muramatsu A, Mikami T, et al. Crop Sci 2014;54: 1407-1412.

<sup>\*4</sup> Nishizawa S, Kubo T, Mikami T. Curr Genet 2000;37: 34-38.

<sup>\*5</sup> Cheng D, Yoshida Y, Kitazaki K, Negoro S, Takahashi H, et al. Genet Resour Crop Evol 2011;58: 553-560.

<sup>\*6</sup> Invvac marker was assigned to chr 2 in Taguchi et al. (2019) <sup>\*2</sup> but it should be assigned to chr 5 according to the alignment of its primer sequences to the reference sequence of sugar beet <sup>\*1</sup>.

Table S2 Alleles detected in the accessions used in this	study																																						
s17 MP	0180 k	mp0	018 7M	0 2G	14 sps	ni	r so	inv	vac cmo	Chrl_	_110Chr1508Ci	hr1_107. Ch	hr1_157; Chr	1_2034 Chr1_24	403 Chr1_3044	Chr1_3582	Chr1_4085 Cl	ar1_4718C	r1_5127Chr	_5672Ch	hr2_140Chr2_1097Chr2_30	16Chr2_503	0Chr3_1012	Chr3_255 Chr3_	3921 C	hr3_539 Chr4_1500 Chr4_2999 Chr4	4_4606 Chr	4_6047 Chr5_15	Schr5_300eChr5_	450 Chr6_1545	Chr6_28780	hr6_6047Chr7_1	10-Chr7_263 Chr7_	420; Chr7_57	07 Chr8990	Chr8_254 Chr8	_432! Chr989	Chr9_22310	hr9_36154592"Baml
pop BETA1285, AZERBAIJAN 55	11	22	22	11	22	11	12	23	11	12	12 22	23	12	22	24 22	12	12	11	11	22	11 22	12 22	11	12	22	22 11 11	33	11 1	1 12	12 22	11	12	11 22 *	1	2 12	12	12 11	12	12
pop BETA1037, GEORGIA 55	11	11	22	11	22	11	12	22	22	12	12 22	23	12	22	24 12	12	12	11	11	12	22 12	11 22	2 11	11	22	22 11 11	22	12 2	2 22	12 22	11	22	11 22	11 1	2 12	12	12 11	11	11
pop BETA3881, GEORGIA 55	11	11	22	11	22	11	11	22	12	12	12 22	23	12	22	22 22	22	22	11	11	22	11 22	11 22	12	12	22	22 11 <sup>a</sup>	22	11 1	1 22	12 *	11	22	11 22	11 1	2 12	12	12 11	13	11
pop BETA3861, GEORGIA 55	11	11	22	11	22	22	11	33	22	12	12 22	23	12	22	22 12	12	22	11	11	22	11 22	11 22	11	11	22	22 11 11	22	12 1	1 22	12 22	11	22	11 23	11 2	2 12	12	12 11	11	11
pop BETA187, GEORGIA 35	11	11	22	12	12	11	11	22	12	12	11 22	23	12	22	22 22	12	22	11	11	11	22 11	11 22	2 12	12	11	22 12 11	22	11 1	1 12	12 22	11	22	11 22	11 1	2 12	11	12 11	11	12
pop K7136, GEORGIA 55	11	12	22	11	22	11	11	23	22	12	12 22	23	12	22	22 22	12	12	11	11	12	11 11	11 22	22	12	22	22 11 11	23	11 1	2 12	12 22	11	11	11 23	11 1	2 12	12	12 11	11	12
pop BETA223, GEORGIA 22	11	11	22	11	22	11	11	22	22	44	12 22	11	12	12	33 12	12	12	11	11	12	12 11	12 22	22	*	22	22 12 11	23	11 2	2 22	12 22	11	22	11 22	22 1	1 12	12	12 11	11	11
pop BETA1065, IRAN 55	11	12	22	11	22	11	11	23	22	12	12 22	23	12	22	33 12	- 11	22	11	12	12	11 11	11 22	2 12	*	22	22 13 *	23	11 1	1 12	12 11	11	22	11 23	11 1	2 12	11	22 11	12	12
pop BETA245, IRAQ 55	11	12	22	11	22	11	22	22	22	12	12 22	23	12	22	33 12	12	22	11	11 *		12 12	11 22	12	11	12	22 11 *	33	11 1	1 12	12 22	11	22	11 23	22 1	2 12	11	22 11	12	12
pop BETA1343, PAKISTAN 55	11	11	22	11	12	11	22	22	22	12	12 22	23	12	22	24 22	22	22	11	11	22	11 11	11 22	12	12	22	22 11 11	33	11	11	12 22	11	22	11 22	11 1	2 12	11	12 11	11	12
pop BETA273, TAJIKISTAN 55	11	12	22	11	12	11	11	23	12	12	12 22	23	12	22	24 22	11	22	11	11	12	11 22	11 22	2 22	11	22	22 22 *	23	11 2	2 12	12 22	11	22	11 23	11 1	2 12	12	12 11	12	12
pop BETA1594, TURKEY 55	11	11	22	11	22	22	11	22	22	12	12 22	23	12	22	24 11	12	22	11	11	12	11 22	11 22	11	11	22	22 11 11	23	11	11	12 22	11	22	11 23	11 1	2 12	12	22 11	22	12
pop BETA1032, TURKEY 55	11	12	22	11	22	11 *		22	22	12	12 22	23	12	22	24 12	12	22	11	11	22	22 12	11 22	12	11	22	22 11 *	22	12 1	1 12	12 22	11	22	11 23	11 1	2 12	11	22 11	11	11
pop BETA1229, TURKEY 45	11	12	22	11	22	11 *		22	22	12	12 22	23	12	22	44 11	11	12	11	11	22	11 22	11 22	22	12	22	22 11 *	23	11	1 22	12 22	11	22	11 22	11 1	2 12	11	12 11	12	12
pop BETA1257, UZBEKISTAN 55	11	12	22	11	22	22	11	22	22	12	11 *	23	12	22	24 12	*	22	11	12	22	11 12	11 22	13	12	12	22 11 11	22	- 11 - 1	11	12 22	11	22	11 22	11 1	2 12	12	12 11	12	11
pop BETA2056, FRANCE 55	11	11	22	11	11	11	12	22	22	12	12 12	12	12	11	34 22	22	12	11	11	22	11 11	11 22	2 23	12	22	12 11 11	33	11 1	11	12 22	11	22	11 23	11 1	2 12	12	12 11	- 11	12
pop BETA1058, GERMANY 55	- 11	11	22	11	12	11	12	22	22	12	12 22	23	12	22	44 11	11	12	11	11	22	12 11	12 22	11	12	12	22 11 11	33	11 1	1 12	12 22	11	22	11 23 *	1	2 12	12	22 11	12	11
pop BETA1777, GERMANY 55	11	11	22	11	11	11	22	22	11	12	12 22	23	12	22	33 22	11	22	11	11	22	12 22	11 22	11	*	22	22 11 *	23	11 1	2 12	12 22	11	22	11 22	11 1	2 12	11	22 11	12	12
pop BETA1478, GREECE 55	- 11	11	12	11	11	22	22	22	22	12	12 22	23	12	12	22 22	12	22	11	11	22	11 22	11 22	2 11	11	12	22 11 11	33	- 11 - 1	1 12	12 22	11	22	11 23	11 1	2 12	11	12 11	12	12
pop BETA1165, GREECE 55	11	11	22	11	22	11	22	22	22	12	12 12	23	12	22	24 12	12	12	11	11	22	11 12	12 22	2 12	11	22	22 11 11	33	11 1	1 11	12 22	11	22	11 23	11 1	1 12	12	12 11	12	12
pop BETA1159, GREECE 35	- 11	11	22	11	11	22	22 *		22	12	12 22	12	12	22	44 11	11	12	11	11	22	22 12	11 22	2 12	11	11	22 11 11	33	- 11 - 1	1 12	12 22	11	22	11 23	11 1	2 12	11	22 11	12	12
pop BETA1306, GREECE 55	11	11	22	11	12	11	22	22	22	12	12 22	23	12	- 11	22 22	11	22	11	11	11	22 12	11 22	11	11	11 *	11 11	23	11 1	1 11	12 22	11	22	11 22	11 1	2 12	12	12 11	12	12
pop BETA1463, GREECE 55	11	12	22	11	12	22	22	22	22	12	12 22	23	12	22	24 12	11	12	11	11	22	22 12	11 22	2 12	11	22	22 11 *	22	12 1	1 12	12 22	11	22	11 22 *	1	2 12	11	12 11	12	11
pop BETA1744, GREECE 55	11	11	22	11	22	22	22	22	22	12	12 22	23	12	22	24 12	11	22	11	11	22	11 22	11 22	2 12	11	22	22 11 11	23	11 1	1 12	12 22	11	22	11 23 *	1	2 12	11	22 11	11	12
pop BETA1468, GREECE 55	11	12	22	11	12	22 *		22	22	12	12 22	23	12	22	24 12	12	22	11	11	22	11 22	11 22	11	11	22	22 11 11	22	12 1	1 12	12 22	11	22	11 22	11 1	2 12	11	22 11	12	12
pop BETA1681, GREECE 55	11	12	22	11 *		11	12	22	12	12	12 22	13	12	22	24 12	11	12	11	11	11	11 12	11 22	12	11	22	22 11 11	22	13 1	1 12	12 22	11	22	11 23	11 1	2 12	12	12 11	12	12
pop BETA2071, ITALY 35	11	11	22	12	11	11	22	22	22	12	12 22	23	12	22	22 22	12	12	11	11	22	11 12	11 22	11	*	22	22 11 11	23	11 1	1 12	12 *	11	22	11 23	11 1	2 12	13	22 11	12	12
pop BETA1723, ITALY 55	11	22	22	11	12	11	22	22	12	12	12 11	12	12	12	33 22	11	12	11	12	11	11 11	11 22	22	11	11 *	11 *	33	11 1	2 22	12 22	12	22	11 22	11 1	1 12	12	12 11	11	12
pop BETA1795,THE NETHERLANDS 55	11	11	22	11	22	11	22	22	22	12	12 22	23	12	22	44 22	11	12	11	11	22	11 22	11 22	2 11	11	22	22 11 11	22	11 1	1 22	12 22	11	22	11 22	11 1	2 12	11	22 11	12	12
pop BETA2040,THE NETHERLANDS 55	11	22	22	11	12	11	22	22	22	12	11 22	23	12	22	22 22	12	12	11	12	22	11 12	11 22	2 11	12	22	12 11 11	23	11 1	1 12	12 22	11	22	11 22	11 1	2 12	12	22 11	13	12
pop BETA222, POLAND 55	11	12	22	11	22	11	12	22	22	12	11 22	23	12	22	33 11	11	22	11	11	22	12 22	11 22	12	11	22	22 11 11	33	11 1	1 22	12 22	11	22	11 23	11 1	2 12	11	22 11	12	12
pop BETA340, ROMANIA 55	11	12	22	11	22	11 *		22	22	12	12 22	23	12	22	22 12	12	22 *		•		11 11	11 22	12	11	22	22 11 11	22	11 1	2 12	12 22	11	22	11 22	11 1	2 12	12	12 11	12	11
pop BETA334, ROMANIA 45	11	12	22	12	22	22	12	22	22	12	11 22	23	12	12	24 22	12	22	11	11	22	12 22	11 22	2 12	11	22	22 11 11	22	11 1	2 12	12 22	11	22	11 23	11 1	2 12	11	12 11	12	12
pop BETA184, SLOVAKIA 55	11	22	22	12	12	11	11	22	12	12	12 22	23	12	22	22 12	12	22	11	11	22	12 22	11 22	2 12	12	12	22 11 11	23	11 1	1 11	12 22	11	22	11 22	11 1	2 12	11	22 11	11	11
pop BETA336, SLOVAKIA 15	11	11	22	11	12	22	11	23	22	33	12 12	12	11	22	34 22	13	12	11	12	13	11 12	12 22	2 12	12	22 *	11 11	33	22	1 22	12 22	12	22	11 22	11 1	1 12	12	12 11	11	12
pop BETA248, SPAIN 55	11	12	22	11	12	11	11	22	22	33	12 22	23	12	12	24 22	11	12	11	11	11	11 11	12 22	2 22	11	12	22 11 *	33	11 2	2 11	12 22	22	22	11 23	11 1	1 12	12	22 12	11	12
pop BETAT/9, CHINA 55		12	22		22	22	11	22	22	12	12 22	23	12	22	24 11	22	12	11	12	22	12 12	12 22	11	11	22	22 12 11	22	12 1	1 12	12 22	11	22	11 23	12 1	1 12	11	22 11	12	12
pop BETA3818, CUBA 55		11	22		12	11	12	22	22	12	12 22	23	12	22	24 22	22	22		12	22	22	11 22	11		- 11	22 11 11	23		1 11	12 22	11	22	11 23	11 1	2 12	11	12 11	12	12
pop BETATS66, SOVIET UNION 33		12	22		22		-	22	22	10	12 22	23	12	22	33 22	22	22		11.5	22	22 22	11 22	12		22	22 22 11	33	10	22	12 22	11	22	11 23		2 12	10	12 11	10	12
pop BETA903, UNKNOWN 33		22	12		22	22	22	22	22	12	12 22	2.5	12	22	12 12	22	12		10	22	22 12	11 22	13	10	22	22 11 11	2.5	12 1	22	12 22	11	22	11 22	10 1	2 12	12	22 11	12	10
pop BETA2129, 05A 33		22	12		22		22	23	22	12	12 22	23	13	22	24 12	12	12		12	22	22 11	11 22	1 12	12	22	22 11 11	22			12 22	11	12	11 23		2 12	10	12 11	12	12
POP BETA1018, USA 33	11	10	22	11	11	11 4	12	11	22	12	12 22	23	12	11	24 11	12	12	11	11	11	11 11	11 22	2 22	12	12	22 11 11	2.5			12 22	11	22	11 22	10 1	2 12	12	12 11	12	12
DETAILOR CEDALARY			22		22	22.4		10	22.4		12 22				14 14		10		10		22 22			10	22	22 11 22	33			12 22		22			a 14		22 11	1.0	10
pop BETATI //4, GERMAN I 55			22	11	22	22 -		12	12	44	12 22	13 -	12	10	24 12		12	11	12		12 22	11 22	12	12	22	22 11 22	33		22	12 22	11	22	11 23 -	11 1	2 12		22 11	12	12
DETAIL COOPER			22		22	12.4		10	10.4		12 22	12		22	14 14	10	10				11 10				22	22 11 22	22			12 22		22			a 14	10	10 11	1.2	10
non RETA155 RUSSIA 55	11.5		22	- 11	12	11 *		12	22	22	11 22	13	12	22	44 11	12	12		12		12 12	1 22	22	11	22	22 11 8	22	22	12	12 22	12	22	11 22	11	2 12	12	22 11	13	12
non 201 mmPR CMS 44	- 11		22	12	12	11 0		22	22	12.8		22	12	22 4		12	12		12		22 11	. 22		10	22	22 12 11	22	11	12	11 11	11		11 22		2 12		12 11	12	12
non 315mmBR-0 44	- 11		22	12	11	11 *		22	22	12.*	22	23	12	22	12	22	12		12		22 11		11	11	22	22 33 11	22	11 3	12	11 11	11	11	11 23	11	2 12	11	12 22	13	12
non 195mmBR.CMS 44	12	12	22	11	11	11	11	22	22	12.*	22	23	11	22	24 22	22	12	11	11	12	11 11	12 22	22	12	12	22 11 11	22			12 11	11	22	11 23	11 1	2 12	12	12 11	11	11
non BETA368 PORTUGAL 64	11	12	22	12	22	22	12	22	22	12	12 13	13	11	22	13 12	*	12		11	22	12 11	11 22	222	12	11	22 11 22	22	11	22	12 22	22	22	11 33	22	1 12	12	12 12		12
pop NGB14676, DENMARK 66 *		11	22	11	22	11 *	1.4	11	22	12	12 11	11	11	22	33 12	- 11	12		11	22	12 11	11 22	22	12	11	22 11 *	22	44	11	12 22	22	22	11 33	22 1	1 12	14	22 12		12
"a"missing data				1						- 1		- 11							22							1		- 11 - I											

Table S3 Pairwise population  $F_{st}$  values among Groups and Pops. *P* values are shown in parentheses.

## Groups

	Group II	Wild Beet
Group I	0.066 (0.002)	0.306 (0.001)
Group II		0.168 (0.002)

Pops

	Pop B	Pop C	Pop D	Pop E
Pop A	0.000 (0.430)	0.290 (0.028)	0.168 (0.001)	0.190 (0.003)
Pop B		0.172 (0.001)	0.086 (0.001)	0.110 (0.001)
Pop C			0.312 (0.001)	0.278 (0.002)
Pop D				0.126 (0.001)

Table S5 Probabilities of mitotype differentiation for each pair of Groups and Pops calculated using GENEPOP

Pairs	p *
Group I and Group II	0.00
Pop B and Pop D	0.00
Pop B and Pop E	0.00
Pop D and Pop E	0.00

\*Exact G test



Fig S1 Dendrogram of accessions based on the result of UPGMA. Three groups in this dendrogram are shown by black bars.



Fig S2 Plots of posterior probability (vertical axis) for each *K* values (horizontal axis) calculated by STRUCTURE.