

# COMPARATIVE STUDY OF CHROMOSOME VARIATION IN THE JAPANESE AND AMERICAN *TRILLIUM* SPECIES\*

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Plants of the genus *Trillium* (Liliaceae) are distributed in the northern hemisphere of both sides of the Pacific Ocean. The Asian species, *Trillium kamschaticum*, and the North American species, *Trillium ovatum*, which are selected in the present paper, have a disjunction in Sea of Okhotsk, Bering Sea and Gulf of Alaska (Fig. 1).

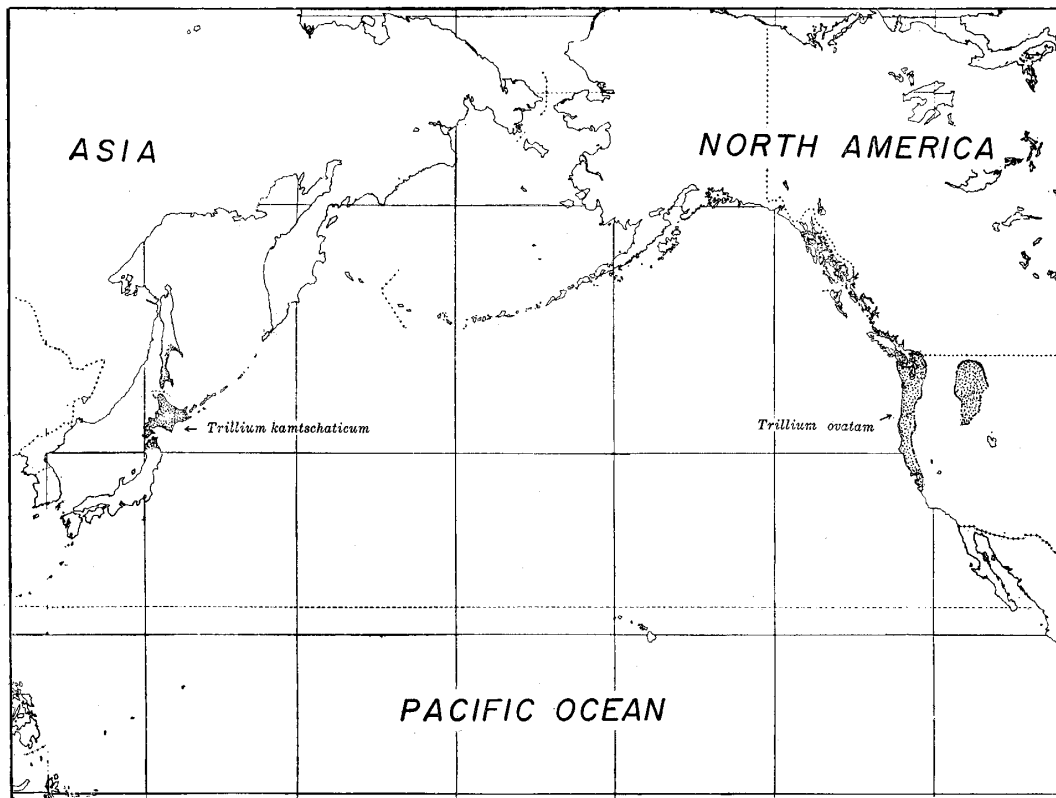


FIG. 1. Distribution map of the Asian species, *Trillium kamschaticum* and American species, *Trillium ovatum*, showing a disjunction across the northern Pacific Ocean.

Both species have ten large somatic chromosomes consisting of two metacentrics, six submetacentrics and two acrocentrics. The metaphase chromosomes exhibit allocyclic patterns by staining according to the Feulgen reaction after the cold treatment (Darlington and La Cour, 1940),

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As the results of population analyses in the Japanese *T. kamtschaticum* and American *T. ovatum* for two decades (Fukuda & Kozuka, 1958, Fukuda, 1969, Fukuda, 1970), the present paper deals with the comparison of chromosome variation between both species and discusses evolutionary significances in both species which have a large disjunction.

### Materials and methods

*Trillium kamtschaticum*, which was selected from the Asian region, is distributed in Tohoku, Hokkaido, Kuril islands and Sakhalin. *Trillium ovatum*, which was selected from the North American region, is distributed in California, Oregon, Washington, Idaho, Montana and British Columbia. Both species belong to the pedicelled flower, which indicate differences in sizes of floral organs. The materials were collected for cytological analyses from the whole distribution area. Cytological observations were made on meristematic cells of the root tips and the ovular tissues after each individual had been kept in a refrigerator or a snow cave at  $0^{\circ}\text{C}\pm 1^{\circ}\text{C}$  for 72–96 hours. Somatic cells were fixed in La Cour 2BE for 15 minutes, hydrolyzed by 1 N HCl at  $60^{\circ}\text{C}$  and stained in Feulgen solution. Squash preparations were made in 45% acetic acid. Chromosomes of both species were classified as A, B, C, D and E by the length of chromosome arms and the positions of centromeres. From the above collected materials population analyses were dealt for 61 populations, chromosome samples 3410 in *T. kamtschaticum*, and for 14 populations, chromosome samples 1028 in *T. ovatum*.

### Results and discussion

#### *Kinds of chromosome patterns in both species:*

In *T. kamtschaticum*, 78 different chromosome patterns were found in chromosome A, 22 patterns in chromosome B, 18 patterns in chromosome C, 32 patterns in chromosome D, 20 patterns in chromosome E, total 170 chromosome patterns (Table 1). On the other hand, in *T.*

TABLE 1. Chromosome variation in the Asian and American *Trillium* species.

Species	Sample number	Chromosome patterns					Total
		A	B	C	D	E	
<i>T. kamtschaticum</i>	3410	78	22	18	32	20	170
<i>T. ovatum</i>	1028	18	58	132	43	46	297

*ovatum*, 18 different chromosome patterns, 58 patterns in chromosome B, 132 patterns in chromosome C, 43 patterns in chromosome D, 46 patterns chromosome E, total 297 chromosome patterns (Table 1). Figure 2 is shown as frequencies for numbers of these chromosome patterns. Chromosome A in *T. kamtschaticum* and chromosome C in *T. ovatum*

are the highest frequency in a whole chromosome variation. On the contrast, chromosome C in *T. kamtschaticum* and chromosome A in *T. ovatum* are the lowest frequency in the variations.

From these data, chromosome variation by a common specific chromosome is not detected at the species level within the same genus. Each variation is independent in each species. A kind of chromosome shows a large variation in a species but the same chromosome indicates the small variation in another species. An interesting fact is that the most variable chromosome in a species is a little variation in the other species. On the other point there is not related apparently to the length of chromosome arms as shown in Fig. 2, the drawings of chromosomes.

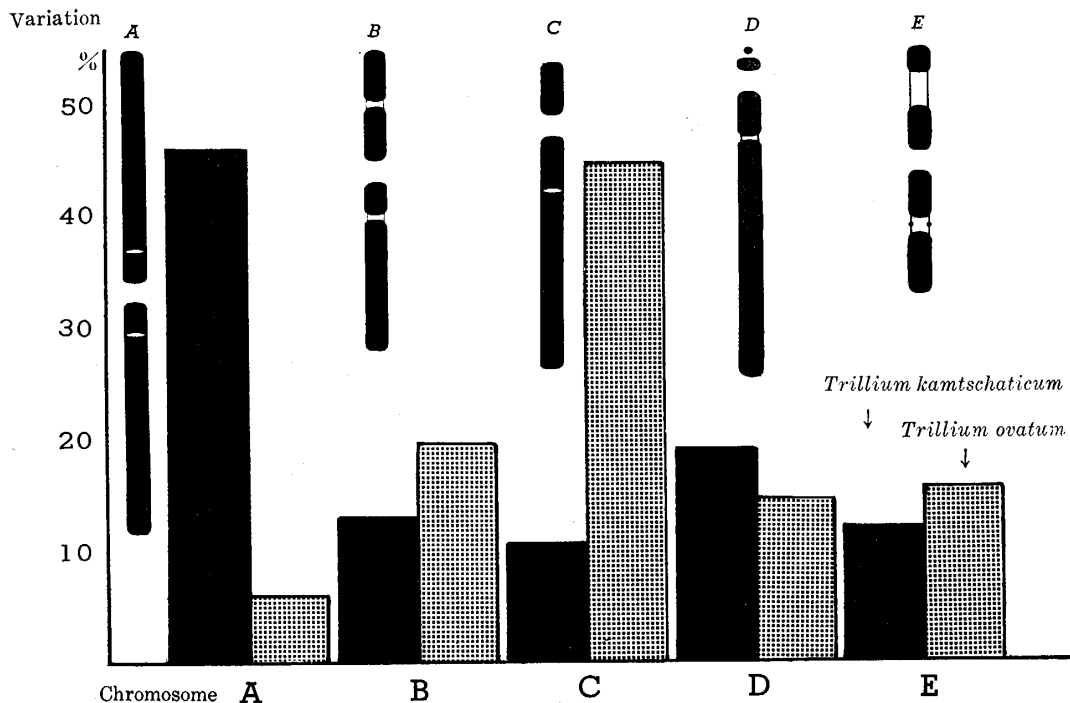


FIG. 2. Frequencies of chromosome variation designated by allocyclic chromosome patterns in *T. kamtschaticum* and *T. ovatum*.

Moreover, an important aspect is that chromosome A in *T. kamtschaticum* and chromosome C in *T. ovatum* are much variable predominantly compared with the other chromosomes. Variations of these chromosomes attain 45% in all variation respectively in each species. Therefore, it is concluded that chromosome variations increase strongly by a special chromosome although the predominant kind of chromosomes is different in each species.

*Distribution of chromosome variation in both species:*

Figure 3 shows the distribution and frequency of chromosome patterns of chromosome A, which is most variable at the species level, in natural populations of *T. kamtschaticum*. The pie diagrams indicate

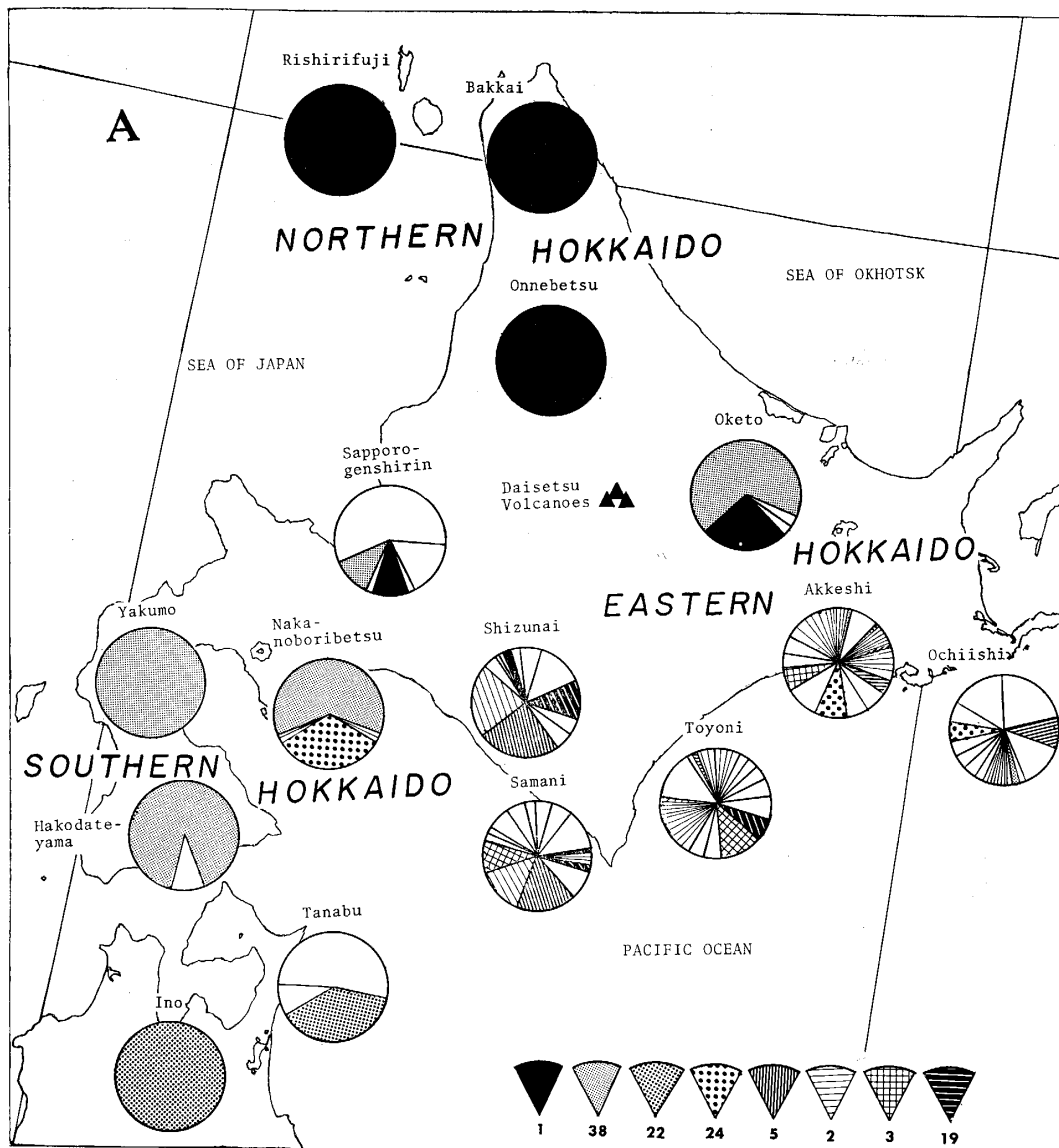


FIG. 3. The distribution and frequency of chromosome patterns of chromosome A in natural populations of *T. kamtschaticum*. Pie diagrams show the frequencies of the contained chromosome patterns indicated at the bottom of the map (white segments include chromosome patterns other than the eight high frequency).

the frequencies of the contained different chromosome patterns in each population. Figure 4 indicates the distribution and frequency of chromosome patterns of chromosome C, which is most variable in the species, in natural populations of *T. ovatum*.

From both data, we recognize some population groups which contain the common chromosome patterns and their same frequencies within the distribution area. This is, population groups in Northern Hokkaido, Southern Hokkaido and Eastern Hokkaido in *T. kamtschaticum*, and population groups in the Pacific Coast Region and the Rocky Mountain Region in *T. ovatum*. These facts mean the existences of races within species

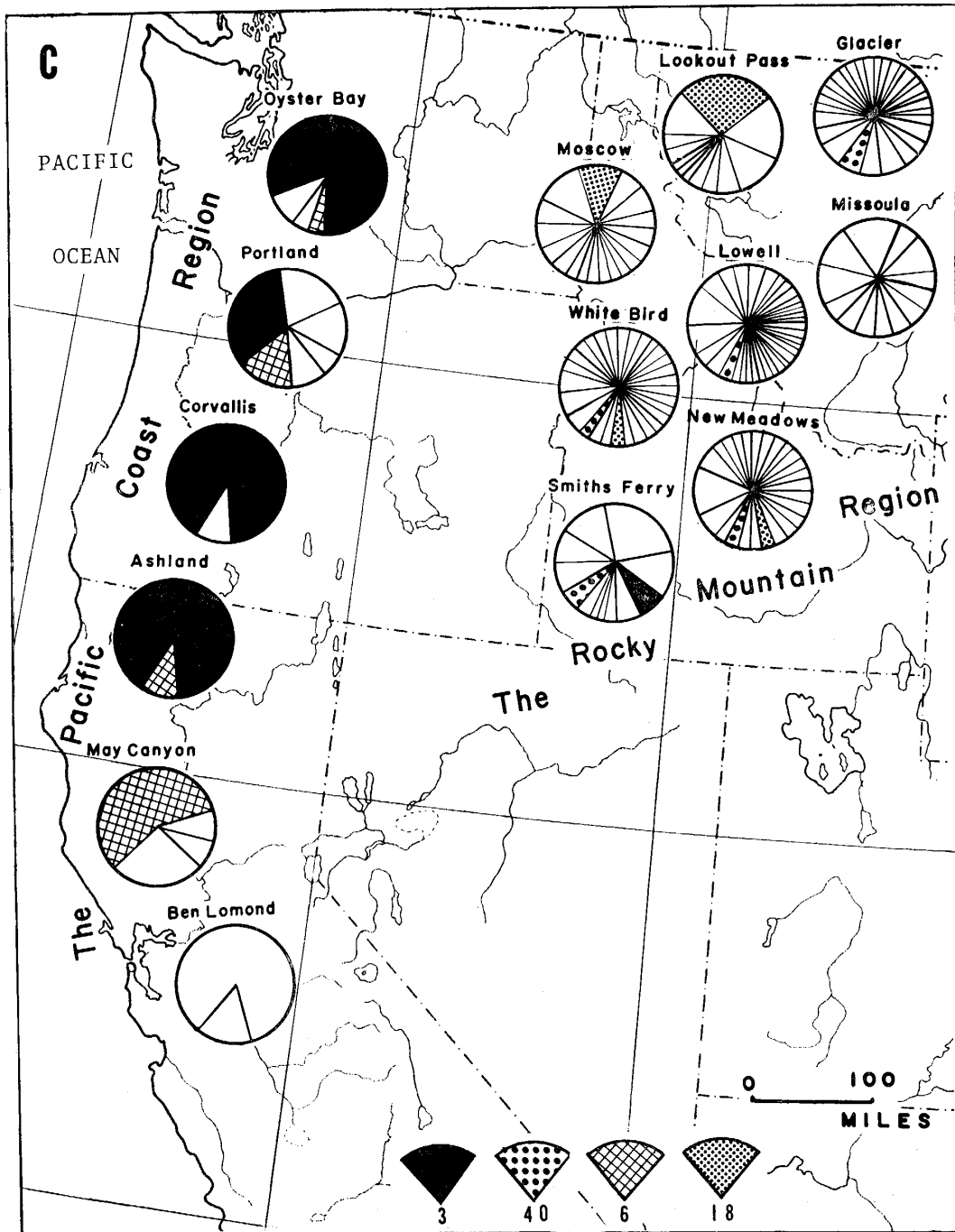


FIG. 4. The distribution and frequency of chromosome patterns of chromosome C in natural populations of *T. ovatum*. For further explanation see Fig. 3.

respectively with addition to morphological data (Fukuda, 1962, Fukuda & Channell, 1974). An interesting problem is that we recognize the race formation in the Japanese *Trillium* species and also in the American *Trillium* species.

*Population structures designated by chromosome pattern in both species:*

Two kinds of population structures are common in *T. kamtschaticum* and *T. ovatum*. One is the homogeneous population structure as shown in Northern Hokkaido and Southern Hokkaido in *T. kamtschaticum* and the Pacific Coast populations in *T. ovatum*. Two is the heterogeneous population structure as shown in Eastern Hokkaido in *T. kamtschaticum* and in the Rocky Mountain populations in *T. ovatum*. Mechanism of the formation of such a different population structure will be discussed in the other paper (Fukuda, 1973, Fukuda, in preparation). It is interesting that both species in the Asian and American regions have a common population structure.

### Summary

The Asian *Trillium kamtschaticum* is distributed in Tohoku, Hokkaido, Kuril islands and Sakhalin. On the other hand, across the Pacific Ocean, the American *Trillium ovatum* occurs in California, Oregon, Washington, Idaho, Montana and British Columbia. Both species are the diploids which have ten somatic chromosomes consisting of two metacentrics, six submetacentrics and two acrocentrics.

As the results of population analyses by alloenzymes, the following subjects were found:

1) In *T. kamtschaticum*, chromosome A is most variable and chromosome C is the smallest variation but, in *T. ovatum*, chromosome C has the largest variation and chromosome A is less variable. These largest variations of both species attain 45 per cent of all variations respectively in each species. It is considered that chromosome variations were prompted predominantly by a special kind of chromosome although the kind of chromosome was different in each species.

2) Both species have two or three races within the species: Northern Hokkaido, Southern Hokkaido and Eastern Hokkaido races in *T. kamtschaticum*, the Pacific Coast and the Rocky Mountain races in *T. ovatum*.

3) These races are characteristic in the population structure: the heterogeneous population structure, Eastern Hokkaido populations in *T. kamtschaticum* and the Rocky Mountain populations in *T. ovatum*, the homogeneous population structure, Northern Hokkaido and Southern Hokkaido populations in *T. kamtschaticum* and the Pacific Coast populations in *T. ovatum*. It seems that the same pattern of speciation has been advancing in the Asian and American regions.

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