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款冬属的核形态(菊科:千里光族)*

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摘 要 研究了款冬属的核形态。染色体间期为简单型与复杂型的过渡型;前期染色体为近基型与中间型的过渡型。染色体较小,核型不对称,具明显的二型性;数目与核型公式为 2n = 60 = 42m + 10sm + 6st + 2t。比较发现款冬的核型明显不同于千里光族中已有的核型记载,其核型特征似乎与它独特的形态特征相联系,具有重要的系统学意义。

关键词 款冬属;千里光族;核形态

KARYOMORPHOLOGY OF TUSSILAGO L. (ASTERACEAE:SENECIONEAE) AND ITS SYSTEMATIC SIGNIFICANCE

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Abstract Investigated in the present paper was the karyomorphology of *Tussilago* L. The interphase nuclei were categorized to be the intermediate type between the simple chromocenter type and complex chromocenter type, and the mitotic prophase chromosomes were classified as the intermediate type between the proximal type and interstitial type. The metaphase chromosomes were rather small, ranging from 2.67μm to 1.05μm and the average length was 1.37μm. The karyotype was formulated as 2n = 60 = 40m + 8sm + 10st + 2t with distinct bimodality. The karyomorphological characteristics of *Tussilago* are disctinct from those of other genera reported in the Senecioneae and seem to be correlated to its unique gross morphology.

Key Words *Tussilago*; Senecioneae; Karyomorphology

Tussilago L., a monotypic genus of the tribe Senecioneae in the Asteraceae, occurs wide-

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ly in Eurasia. Karyomorphological characters are of utmost importance for elucidating the phylogeny and evolution of the Asteraceae[1], especially for the subdivision of the tribe Senecioneae[2,3], but the karyotype of *Tussilago*, except its chromosome number being reported to be 2n = 60 several times from different localities[4~8], has not been reported yet. The karyomorphology of *Tussilago* was reported and its systematic significance was discussed in the present paper.

1 Material and Methods

The roots of *Tussilago farfara* were collected in Xining, Qinghai Province, China. The voucher specimen (Liu Jian - quan 354) was deposited in Northwest Plateau Institute of Biology, the Chinese Academy of Sciences (HNWP).

The root tips were pretreated in the mixture of 0.1 % colchicine and 0.002 mol/L hydroxyquinoline for two hours, and then fixed overnight in the fixative (1:3 glacial acetic acid and absolute alcohol). They were macerated in 1 mol/L HCl at 60 ℃ for five minutes, and stained and squashed in Carbol Fuschin solutions before observation. The karyotype formula was based on the measurements of mitotic metaphase chromosomes. The karyomorphological classifications of the resting and mitotic prophase introduced by Tanaka[9], the symbols for centromeric positions defined by Levan et al.[10], the index of relative length suggested by Kuo[11] and the classification of karyotype asymmetry of Stebbins[12] were followed.

2 Result

In the resting nuclei (Plate I: 1), several darkly herteropycnotic bodies were observed. The boundary of the bodies was rather indistinct and chromatin surrounding appeared to diffuse gradually. Thus the karyomorphology of resting nuclei was the intermediate type between the simple chromocenter type and complex chromocenter type. In the prophase chromosomes (Plate I: 2), the heterochromatic segments were mainly distributed in proximal regions of both arms, but were indistinctly found in distal and interstitial regions. Therefore, the prophase chromosomes were classified as the intermediate type between the proximal type and interstitial type.

The metaphase chromosomes were counted to be 2n = 60 (Plate I: 3), ranging from 2.67μm to 1.05μm in length (Plate I: 4). The average length was 1.37μm. The karyotype was formulated as 2n = 60 = 42m + 10sm + 6st + 2t; no secondary constriction was detected. The relative length was formulated as $2n = 18 = 6L + 14M_2 + 38M_1 + 2S$. The karyotype was categorized as Stebbins' 2B type.

3 Discussion

The chromosome number of 2n = 60 of *Tussilago* is here reconfirmed. In the tribe Senecioneae, the chromosome numbers have been recorded for most genera[2], and two major basic chromosome numbers are found: x = 10 and x = 30. Based on the basic chromosome num-

bers, as well as the morphological characters, two major evolutionary lineages (senecionoid and tussilaginoid) have long been recognized in the tribe Senecioneae[2,3,13~15]. The senecionoid lineage is characterized by chromosome numbers of x = 10 or 20 or numbers derived therefrom, as well as style branches with separate stigmatic lines, upper stamen filaments with swollen collars and anthers often with thickening in the lateral walls of the endothecial cells. In the tussilaginoid lineage, the chromosome numbers are based mostly on x = 30 or numbers derived therefrom, the stigmatic surfaces is entire or nearly so across the inner face of the style branch, the upper stamen filaments are cylindrical and the anthers often have thickenings in the transverse walls of the endothecial cells. *Tussilago*, as well as the genera *Ligularia*, *Parasenecion* and *Farfugium* etc. with x = 30, belongs to the tussilaginoid lineage.

Table 1 Parameters of mitotic metaphase chromosomes of Tussilago farfara

NO	RL	AR	T	IRL	No	RL	AR	T	IRL
1	1.45 + 4.84 = 6.29	3.34	st	1.89	16	1.50 + 1.69 = 3.19	1.13	m	0.97
2	1.21 + 4.11 = 5.32	3.40	st	1.60	17	1.45 + 1.60 = 3.05	1.10	m	0.91
3	1.31 + 2.90 = 4.21	2.21	sm	1.26	18	1.35 + 1.60 = 2.95	1.19	m	0.89
4	1.69 + 2.42 = 4.11	1.43	m	1.23	19	1.26 + 1.64 = 2.90	1.30	m	0.87
5	1.26 + 2.56 = 3.82	2.03	sm	1.19	20	1.21 + 1.69 = 2.90	1.40	m	0.87
6	1.60 + 2.13 = 3.73	1.33	m	1.12	21	1.16 + 1.74 = 2.90	1.50	m	0.87
7	0.82 + 2.71 = 3.53	3.30	st	1.06	22	1.06 + 1.79 = 2.85	1.69	m	0.86
8	1.26 + 2.18 = 3.44	1.73	sm	1.03	23	1.21 + 1.64 = 2.85	1.36	m	0.86
9	1.11 + 2.27 = 3.38	2.05	sm	1.02	24	1.11 + 1.74 = 2.85	1.57	m	0.86
10	1.50 + 1.84 = 3.34	1.23	m	1.00	25	1.06 + 1.74 = 2.80	1.64	m	0.84
11	1.45 + 1.84 = 3.24	1.27	m	0.99	26	1.00 + 1.79 = 2.79	1.79	sm	0.84
12	1.40 + 1.84 = 3.24	1.31	m	0.97	27	1.26 + 1.50 = 2.76	1.19	m	0.83
13	1.55 + 1.69 = 3.24	1.09	m	0.97	28	1.21 + 1.50 = 2.71	1.24	m	0.81
14	0.20 + 3.04 = 3.24	15.0	t	0.97	29	1.21 + 1.45 = 2.66	1.19	m	0.80
15	1.50 + 1.69 = 3.19	1.06	m	0.97	30	1.21 + 1.26 = 2.47	1.04	m	0.74

RL: relative length; AR: arm ratio; T: type; IRL: index of relative length

However, in his systematic revision of the Chinese Asteraceae, Ling[16] rejected these two evolutionary lineages. He thought the genera of the tussilaginoid lineage are not a natural group and treated the tussilaginoid genera in three subtribes: Subtrib. Tephroseridinae, Ligulariinae and Tussilagininae. The subtribe Tussilagininae (s. s.) includes only two genera: *Tussilago* and *Petasites*, and is closer to his subtribe Crassocephalinae of the senecionoid lineage (with x = 10) than to his subtribes Liguriinae (x = 30) and Tephroseridinae (x = 23, 24); the latter two subtribes together with *Tussilago* and *Petasites* comprise the natural tussilaginoid lineage according to Robinson et al.[2], Bremer[3] and Jeffrey[13].

The karyotype analyses in the Senecioneae are only limited to a few genera occurred in Japan[17,18]. The studied genera can be ascribed to the above two evolutionary lineages: *Senecio* and *Erechtites* with x = 10 belonging to the senecionoid lineage and *Ligularia*, *Parasenecio* and *Farfugium* with x = 30 belonging to the tussilaginoid lineage. Their observations indicated there rarely existed karyotype differentiation among the studied genera even between the groups with rather different basic numbers: x = 10 and x = 30. All karyotypes consist of median, submedian and subtelenic chromosomes without bimodality. The chromosome lengths are relatively large varying between 3～7μm. Compared with these genera (*Senecio*, *Erechtites*, *Ligularia*, *Parasenecio* and *Farfufium*), *Tussilago* differs karyomorphologically from them in the rather small chromosomes (2.67～1.05μm), bimodal and rather asymmetrical karyotypes. According to Stebbins[12] and compared with the outgroup (Astereae, a tribe closely related to the Senecioneae), these karyomorphological characteristics should be derived. They seem to be correlated with the advanced morphology of *Tussilago*: trimorphological flowers and flowers precocious. To a extent, the present observation seems to support the treatment provided by Ling(1997) that *Tussilago* and *Petasites* should be separated from the other genera of the tussilaginoid lineage. But another possibility is that there might exist an early karyotype differentiation among the genera of the tussilaginoid lineage. However, up to now, no karyotype information is available for *Petasites* and most genera of tussilaginoid lineage. Therefore, until a more extensive survey of karyomorphology on the tribe Senecioneae is completed, it is still unclear whether *Tussilago* and *Petasites* should be recognized at the subtribe level (Tussilaginiae s. s. as circumscribed as by Ling[16]) unrelated to the other tussilaginoid genera or retained as a early diverging branch of the tussilaginoid lineage (Tussilaginiae s.l.). In other words, it can not be determined whether the genera of the tussilaginoid lineage comprise a monophylegenetic group or not. We hope molecular systematic studies of the tribe Senecioneae currently underway can provide additional information to assist in solving the above questions.

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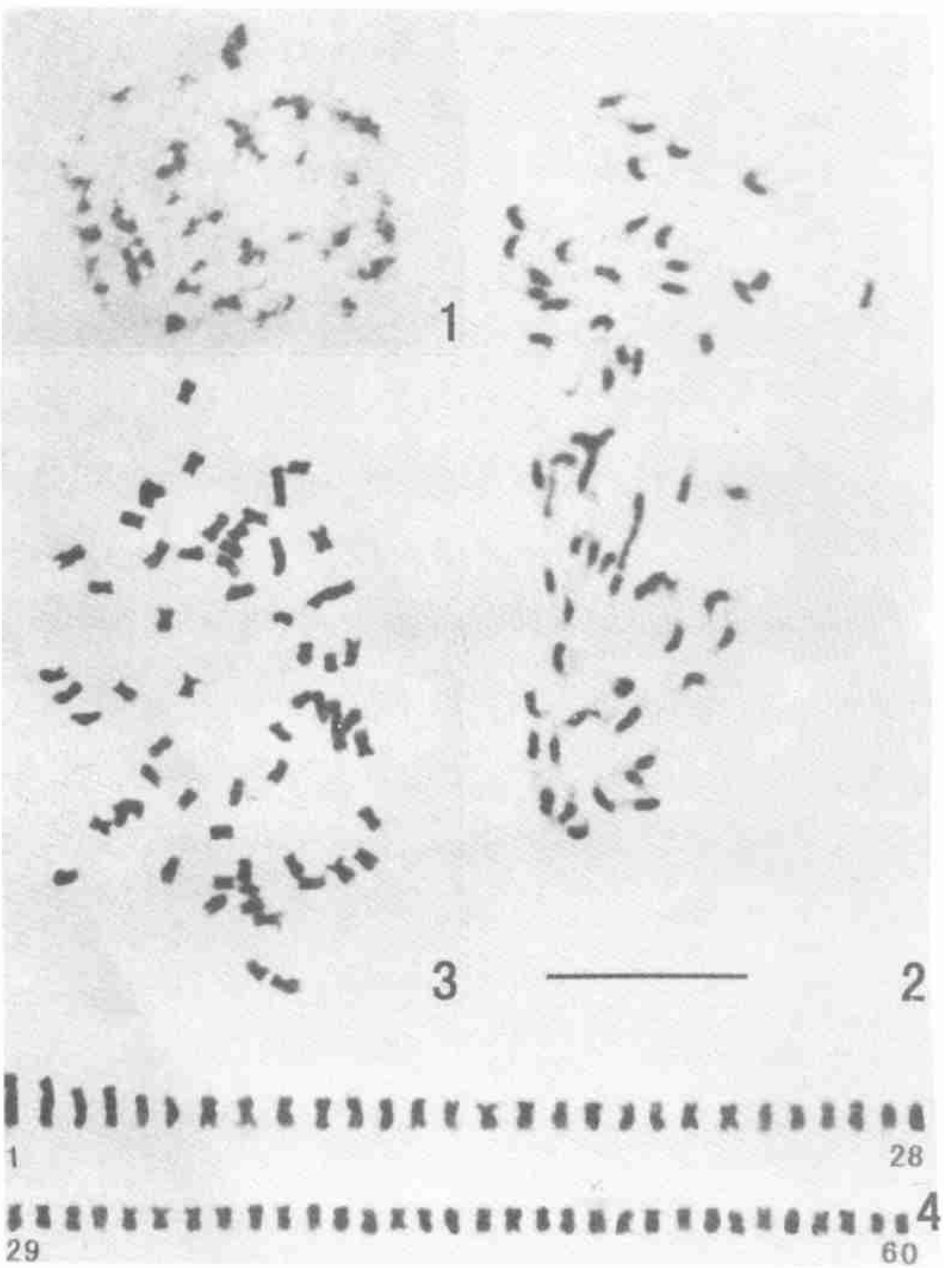
Explanation of plates

1. The resting nuclei; 2. The prophase chromosome; 3. The metaphase chromosomes;
4. Karyotype. - Bar = 10μm



See explanation at the end of text