

高原生物学集刊

ACTA BIOLOGICA PLATEAU SINICA

第十三集 No. 13

中国科学院西北高原生物研究所 编辑

1995—1997



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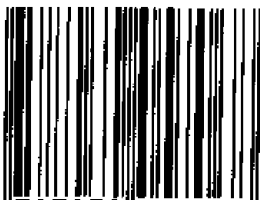
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四川无心菜属一新种

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A NEW SPECIES OF *ARENARIA* L. FROM SICHUAN, CHINA

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摘 要

在编写《中国植物志》26卷石竹科无心菜属时, 所用崔友文教授遗留于标本上的一新种——海子山老牛筋 *Arenaria haitzeshanensis* Y. W. Tsui, 虽然1993年吴征镒教授在《横断山区维管植物》上册已发表, 但仅有学名没有特征记载而成为裸名 (nomen nudum), 现将特征记述如下。

关键词: 无心菜属; 海子山老牛筋

海子山老牛筋 新种 图1: 1—7

Arenaria haitzeshanensis Tsui ex C. Y. Wu sp. nov.

Haec species *A. capillaris* Poir. et *A. acicularis* Williams ex Keissler affinis, sed rhachidibus foliis non nis longiusculis, multivillosis autem aglandulosis, sepalis petalis longioribus, 6—7 mm. longis valde insignis.

Herba perennis pulvinata, 6—10 cm. alta. Radix conica, lignea, atro-brunnea. Caules dense caespitosi. Folium basale lineare, 2—5 cm. longum, circ. 1 mm. latum, basi latiorum apice actum; folia caulina 2—3-jugata, subulata vel lineari-subulata, 1—2 cm. longa, 1—2 mm. lata, basi latiora, apice pungentia, margine anguste membractae, dorso protuberante 1-nervia. Cyma 1—3 flora, rhachidibus dense villosa. Bractae lanceolatae, 6—7 mm. longae, basi latiore, apice pungentes, margine membractae. Sepala

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图1 1—7. 海子山老牛筋: 1. 全株; 2. 叶放大; 3. 萼片; 4. 花展开; 5. 雄蕊、花瓣和萼片;
6. 雌蕊; 7. 种子。(阎翠兰绘)

Fig. 1 1—7. *Arenaria haitzeshanensis*: 1. Habitus; 2. Folium ampliatum; 3. Sepalum; 4. Flos patens; 5. Stamen, petalum and Sepalum; 6. Pistillum; 7. Semen.

lonceolata, 6—7 (8) mm. longa, basi crassi uscula, apice acuta, margine anguste membranacea, dorso 1—3 nervia. Petala alba, ovata, calycibus 3/5 longiora. Ovarium ovoideum circ. 2mm. longum, stylis 3, 2—3 mm. longis.

W. Sichuan: Dege, Haizishan, alt. s. m. 3 800 m, alpine meadow, Sichuan Exped. D-7 475 (Typus in Herb. WUG conservatus)

Xizang: Jiangda, Qinghai-Xizang Exped. 12477.

多年生垫状草本，高6—10厘米。根圆锥形，木质化，黑褐色。茎紧密丛生。基生叶线形，长2—5厘米，宽约1毫米，基部较宽，顶端锐尖；茎生叶2—3对，钻形或线状钻形，长1—2厘米，宽1—2毫米，基部较宽，顶端具刺状尖；边缘窄膜质，具突起的1脉。花序聚伞形，具1—3花，花序轴密被长毛；苞片披针形，长6—7毫米，基部较宽，顶端具刺状尖，边缘膜质；萼片披针形，长6—7(8)毫米，基部加厚，顶端锐尖，边缘窄膜质，具1—3脉；花瓣白色，卵形，长约为萼片的3/5；子房卵圆形，长约2毫米，花柱3，长2—3毫米。

本种花序轴长度仅略超过叶长，上面多长毛而无腺毛；萼片长6—7毫米，超过较短的花瓣，而既不同于毛叶老牛筋 *Arenaria capillaris* Poir. 也不同于针叶老牛筋 *A. acicularis* Williams ex Keissler.

四川西部：德格，海子山，生于高山草甸，海拔3 800米，四川调查队德字7 475（模式，存西北植物所标本室）。

西藏：江达，青藏考察队12477。

薰倒牛的细胞学和形态解剖学研究

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摘 要

首次报道了薰倒牛植物的染色体数目并进行了核型分析, 薰倒牛的染色体数目为10, 基数是5, 为2倍体。核型公式 $K(2n) = 2x = 10 = 2m + 8sm$, 未见随体, 属于2A核型。通过石蜡切片对薰倒牛的根、茎、叶和花做了解剖学研究, 观察到了茎中维管束有异常次生结构, 叶上表皮一层细胞排列不整齐, 栅栏组织致密, 气孔分布于下表皮等旱生结构。并对其形态—生态学适应作了探讨。

关键词: 薰倒牛; 细胞学; 核型分析; 解剖学; 形态-生态学适应

薰倒牛属 (*Biebersteinia* Stephan ex Fisch.) 共有5个种, 是牻牛儿苗科 (Geraniaceae) 中的一个特殊类群, 仅薰倒牛 (*B. heterostemon* Maxim.) 1种产于青藏高原东北部, 其余4种产于欧洲、西亚、中亚至我国西藏西部, 显然为地中海—中亚分布类型。由于其特殊的形态特征和孢粉学特征, Bortenschlager (1967) 认为薰倒牛属应提升为科级分类单位, 并认为它同蔷薇科委陵菜族 (Potentilleae) 相近, 而远不同于牻牛儿苗科其它类群。薰倒牛为一年生草本植物, 仅分布于我国青海、甘肃、宁夏、新疆、四川和西藏, 为青藏高原特有植物, 生长于1600—3200米的路边、山坡等地。藏药名为明见赛宝, 苦、辛、寒、治痈疔、丹毒、喉痛、胃痛、全身水肿和中风等症。张晓峰等 (1995) 从中提取了2种新的天然产物, 其中之一为N-3-甲基-2-丁烯基豚, 有镇痛、降压, 并有一定增强免疫功能的作用。然而, 由于薰倒牛分布的局限性, 使其一直未能得到系统和细致的研究。本文拟对薰倒牛的形态解剖学和细胞学作一初步研究, 为讨论该属植物的分类地位提供资料, 并讨论其形态结构与生态适应的关系。

一、材料和方法

薰倒牛采自西宁植物园后山, 海拔2300米的干旱山坡。

本文1995年11月9日收到。

1. 细胞学观察

取部分幼花经 0.1%秋水仙碱处理 4 小时,卡诺(3:1)固定液固定,70%乙醇保存,供压片用。

将幼花在解剖镜下剥出子房壁,以浓盐酸-乙醇(1:1)解离液在室温下解离 10 分钟,水洗后用改良苯酚品红染色液染色过夜,压片镜检,选取 50 个有中期分裂相的细胞,计数染色体数目,选取分散较好的分裂相进行显微摄影,按李懋学等(1985)和 Levan et al.(1964)的标准进行核型分析,以染色体长度排序编号。

2. 解剖学观察

全草各部分均分割为小块,FAA 固定液固定,70%乙醇(0—4℃)保存,供切片用。常规石蜡切片法制片,番红-固绿对染,切片厚度 7—10 微米。加拿大树胶封片。用 Olympus 显微镜观察并照相。

染色体玻片标本和切片的永久封片标本均保存于中国科学院西北高原生物研究所细胞学实验室,薰倒牛凭证标本存于中国科学院西北高原生物研究所植物标本馆。

二、实验结果及讨论

1. 核型分析

经显微观察,统计 50 个具有较好的细胞中期分裂相的细胞染色体数目均为 10,染色体基数为 5,为二倍体。

对显微照片(图版 1:A)进行测量,计算,结果见表 1。核型公式为 $K(2n) = 2x = 10 = 2m + 8sm$,未见随体。其中只有第 4 条染色体为中部着丝点的,其余均为近中部。染色体组总长度为 9.167 微米,染色体绝对长度变动于 1.57—2.00 微米之间;最长染色体和最短染色体的比为 1.20,小于 2.00;臂比大于 2.00 的染色体百分数为 0.40,按 Stebbins (1971)的标准为 2A 型。

表 1 薰倒牛的核型分析结果
Table 1 The karyotype analysis result of *B. heterostemon*

序号 Number	相对长度 Relative length	臂比 Arm Ratio	类型 Classification
1	6.91+14.91=21.82	2.16	sm
2	7.27+13.64=20.91	1.88	sm
3	5.45+14.54=19.99	2.67	sm
4	8.18+10.91=19.09	1.33	m
5	6.37+11.82=18.18	1.86	sm

薰倒牛的染色体基数是 5 和牻牛儿苗科其它属的染色体基数不同 (*Erodium* $x=9$ 或 10; *Geranium* $x=7$; *Pelargonium* $x=9$ 或 11),也和蔷薇科委陵菜族各属的染色体基数

(基本为7)不同,由于其特殊的形态特征和孢粉学特征, Bortenschlager (1967)把薰倒牛属提升为科级分类单位,并认为它同蔷薇科委陵菜族相近,而远不同于牻牛儿苗科其它类群。从染色体数目来看把薰倒牛属独立成科是有道理的。

2. 形态解剖学特征

一年生草本,高30—150厘米。根细圆柱状,直立,周皮较厚,红褐色,木质化发达,未见韧皮部和形成层(图版I:B)。全体有棕褐色头状并具有分泌道的蜜腺毛(图版I:C)和白色单细胞的长柔毛(图版I:D)。腺毛可分泌难闻的黏稠物质。茎表皮由3—4层细胞构成,排列比较整齐;表皮内主要由薄壁组织构成;维管束分2轮排列,束与束之间有薄壁细胞构成的束间区域(髓射线)。维管束由韧皮部,1层形成层和木质部3部分构成,外韧式。(图版I:E、F),茎中维管束的这种排列方式是一种异常次生结构。叶互生,三回羽状深裂,小裂片条状披针形;上下表皮均分布有疏微柔毛,上表皮由一层大小不同的细胞构成,细胞呈波浪状排列,其上极少见到气孔;叶肉组织有栅栏组织和海绵组织的分化,栅栏组织细胞一层,排列致密,叶绿体小,沿着栅栏组织细胞的壁排列,海绵组织细胞排列疏松,胞间隙发达;气孔主要分布于下表皮,气孔下有较大的气孔腔(图版II:G、H)。顶生圆锥花序,长达40厘米,花黄色,整齐多数,萼片5片,短渐尖,长4—5毫米,花瓣5枚,淡黄色,倒卵形,略短于萼片,顶端波状。雄蕊2轮,5+5,共10枚,子房上位,5心皮5室(图版II:K)。柱头顶端相连成环,花柱分离(图版II:J)。心皮基部合生,蒴果不开裂,内含1粒种子。在子房基部有无分泌道的花蜜腺(图版I:I),花蜜腺里充满了薄壁组织。

从观察结果可以看出,薰倒牛茎中存在异常次生结构,即维管束分2轮排列。有关这种结构已有一些报道,杨培军等(1993)在沙蓬(*Agriophyllum squarrosum*)中发现其轴中普遍存在异常次生结构,他们认为包埋在厚壁或薄壁组织中的多轮异常维管束能较好的避免干旱,是沙蓬充分适应沙生环境的结果。薰倒牛生长于1600—3200米的路边、河谷及山坡,生境条件极为干旱,在茎中出现异常次生结构,是它对干旱环境的一种适应。另外,薰倒牛叶片的形态结构特征如表皮上分布有疏微柔毛,上表皮细胞大小不一,排列不整齐,栅栏组织细胞排列紧密等也是对干旱环境的一种适应。Openheimier (1960)就曾经指出叶表皮细胞排列不规则是旱生植物的常见特征。另外,薰倒牛气孔主要分布在下表皮、叶两面具表皮毛等特征又可防止水分散失,由此可见,薰倒牛是一个较为典型的旱生物种。

在薰倒牛叶片海绵组织中有十分发达的空隙腔,是该植物对高山缺氧环境的适应,关于植物体内存在有发达的通气组织的现象,王为义(1985)就曾经有过报道,认为是高山植物普遍存在的一种特异性结构,它有利于储藏气体,是植物适应高原环境的结果。

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CYTOLOGICAL AND MORPHO-ANATOMICAL STUDIES OF *BIEBERSTEINIA HETEROSTEMON* MAXIM.

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The cytology and anatomy of *B. heterostemon* Maxim. were studied. The results showed that the chromosome number is $2n=10$ and it is a diploid plant, and that its karyotype formula is $K(2n) = 2x=10=2m+8sm$, belonging to 2A type. It was also showed that structures of its root, leaf and stems were of the characteristics which adapt to dry environment and the high altitude, such as abnormal secondary structure in the stem, a layer irregular cells in the upper epidemis, tight palisade cells and the stomatas mainly in the lower epidemis. We think that the species is a xerophyte.

Key words: *Biebersteinia heterostemon* Maxim.; Cytology; Karyotype analysis; Plant anatomy; Morpho-ecology adaptability

**THE KARYOTYPES AND CHROMOSOME NUMBERS
IN NINE SPECIES OF *GENTIANA* FROM
ALPINE MOUNTAINS OF WESTERN CHINA**

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Abstract

The karyotypes and the chromosome numbers in nine species of the genus *Gentiana* (Tourn.) L. from the alpine mountains of western China are reported in the present paper. All the chromosome data for these species in this paper are recorded for the first time. In *Gentiana yunnanensis* Franch. the karyotype formula and the chromosome complement of relative length are $K(2n) = 14 = 12m + 2M = 8M_2 + 6M_1$; in *G. aristata* Maxim. $K(2n) = 18 = 14m + 4M = 8M_2 + 10M_1$; in *G. haynaldii* Kanitz $K(2n) = 18 = 16m + 2sm = 8M_2 + 10M_1$. The karyotypes of three species all belong to Stebbins' type 1A and are symmetrical or subsymmetrical with low asymmetry indices (A_1 , A_2 and A_s , k%). In *G. burkii* H. Smith $K(2n) = 32 = 26m + 6sm = 14M_2 + 16M_1 + 2S$ and in *G. vernayi* Marquand $K(2n) = 26 = 24m + 2sm = 2L + 12M_2 + 8M_1 + 4S$. Their karyotypes belong to Stebbins' type 2A or 1B respectively and are asymmetrical with high asymmetry indices (A_1 , A_2 and A_s , k%). The chromosome numbers are reported for four following species: *G. atunsiensis* W. W. Smith $2n = 36$, *G. rigescens* Franch. ex Hemsl. $2n = 36$, *G. pseudoaquatica* Kusnez. $2n = 40$, and *G. squarrosa* Ledeb. $2n = 76$. The karyotype evolution is distinctly correlated with geographical distribution progression. The more leaves the distribution centre, the more occur polyploidy species.

Key words: *Gentiana*; chromosome number; karyotype; polyploid; geographical distribution.

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Gentiana, a large genus including about 361 species, is widely distributed all over the world except in Africa. There are 247 species in China. Since last half century, *Gentiana* has been studied cytologically. However, most studies are concentrated on the accumulation of chromosome number counts, and only a few on karyology, such as those by Shigenbu (1984) and Yuan & Kupfer (1993). The karyotypes of five species and the chromosome number counts of four species are recorded for the first time in the present paper.

Materials and Methods

The materials used in this study were seeds of the Gentians. The seeds and the voucher specimens were collected at the same places of the field, and the specimens all were conserved in the herbarium of Northwest Plateau Institute of Biology, the Chinese Academy of Sciences (HNWP).

The seeds were germinated in petri dishes on wet filter paper at room temperature. Root tips were pretreated in 0.002 mol/L 8-hydroxyquinoline for 15—20 hours at 4°C and then fixed with carnoy's solution (100% alcohol : glacial acetic acid = 3 : 1) for at least four hours. After washing out the fixer completely with water, the root tips were macerated in 1 mol/L HCL at 60°C for 4—5 minutes, stained and squashed in a dilute solution of Carbol's fuchsing.

The chromosome numbers were counted from examined 50—100 cells for each species. The detailed karyotype analyses were microphotographed and measured from at least five cells. The observations of the chromosomes were made at mitotic metaphase.

The terminologies used for centromere positions are those defined by Leven et al. (1964). The calculated method of chromosome complement of relative length (I. R. L.) used by Kuo et al. (1972), the classification of karyotype asymmetry of Stebbins (1971), and the intrachromosomal asymmetry index (A_1) and the interchromosomal asymmetry index (A_2) proposed by Romero Zarco (1986) were followed.

Results

The measurements of the chromosomes in five species of *Gentiana* are listed in Table 1 and the karyotype analyses of these species in Table 2. The somatic chromosomes and karyograms are illustrated in Plate I and I.

The results are described as follows:

1. *Gentiana yunnanensis* Franch. (Sect. *Microsperma* T. N. Ho)

The somatic chromosomes are $2n=14$, $2x$. The karyotype consists of six pairs of metacentric chromosomes and one pair of exact metacentric chromosomes so the karyotype formula is $K(2n)=14=12m+2M$. The chromosome complement of relative length has four pairs of longer chromosomes and three pairs of shorter chromosomes. It can be formulated into $2n=14=8M_2+6M_1$. The length sum of the genome is of $15.22\mu\text{m}$ with