ANNEXURE
## ANNEXURE 1

### Reagents required for cytological procedures:

<table>
<thead>
<tr>
<th>Name of Chemicals</th>
<th>Concentration</th>
<th>Preparation</th>
</tr>
</thead>
<tbody>
<tr>
<td>8-Hydroxyquinoline</td>
<td>0.002 M</td>
<td>0.029 g of 8-Hydroxyquinoline was weighted and added to 100 ml of distilled water in dark coloured reagent bottle. Solution was kept overnight at room temperature to dissolve the crystals completely and then stored 4°C.</td>
</tr>
<tr>
<td>pDB (para-Dichlorobenzene solution)</td>
<td>Saturated</td>
<td>In a dark-coloured reagent bottle, 100 ml distilled water was taken to which few crystals of para-Dichlorobenzene were added and stirred continuously until the crystals completely dissolved. More crystals were added until the solution became saturated visually confirmed by excess crystals. Then the solution was stored at 4°C.</td>
</tr>
<tr>
<td>Carnoy’s fluid</td>
<td>1:3</td>
<td>100 ml of the solution was prepared by mixing 25 ml of glacial acetic acid with 75 ml of absolute ethanol. The solution was kept in reagent bottle and stored at room temperature.</td>
</tr>
<tr>
<td>Acetic acid</td>
<td>45%</td>
<td>45 ml glacial acetic acid was mixed with 55 ml distilled water and the solution was stored at room temperature in reagent bottle.</td>
</tr>
<tr>
<td>HCl (Hydrochloric acid)</td>
<td>1 N</td>
<td>9 ml of 35% HCl was diluted with distilled water to a final volume of 100 ml and the solution was kept in reagent bottle at room temperature.</td>
</tr>
<tr>
<td>Aceto-orcein</td>
<td>2%</td>
<td>In a 250 ml conical flask 100 ml 45% acetic acid solution was added and was heated to simmer. 2 g orcein powder was weighted and added to it solution, and stirred continuously with a glass rod. The solution was kept simmering gently till the dye dissolves. Then it was cool down to the room temperature and filtered in a reagent bottle using funnel and filter paper.</td>
</tr>
<tr>
<td>Aceto-orcein: HCl</td>
<td>9:1</td>
<td>To the prepared aceto-orcein stain 1N HCl was added in 9:1 (aceto-orcein:HCl) ratio.</td>
</tr>
</tbody>
</table>
1 g basic fuchsin powder was gradually dissolved in 200 ml boiling distilled water. It was then cooled down to 50°C to 58°C. The solution was then filtered in a dark coloured reagent bottle and the filtrate was cooled to 26°C. To the filtrate 30 ml 1N HCl and 3g potassium metabisulphite were added and the mouth of the container was tightly sealed. The container was stored in cool dark chamber. After 24 hours the solution turned faint straw colour. The staining solution was then kept in a dark airtight bottle and stored in refrigerator for future use.

### ANNEXURE 2:

**Reagents required for molecular marker based study:**

<table>
<thead>
<tr>
<th>Name of Chemicals</th>
<th>Concentration</th>
<th>Preparation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Tris-Cl</td>
<td>1 M, pH 8.0</td>
<td>12.11 g of Tris base was dissolved to 80 ml of double distilled water and adjusted to pH8 using 1 N HCl. After dissolution the volume of the solution was adjusted to 100 ml, autoclaved and stored for further use.</td>
</tr>
<tr>
<td>EDTA, disodium salt dihydrate (Ethylene diamine tetraacetic acid disodium salt, dihydrate)</td>
<td>0.5 M pH 8.0</td>
<td>To 80 ml double distilled water, 18.61 g of disodium EDTA.2H₂O was added and adjusted to pH8 using initially sodium hydroxide pellets and then its 1 N solution. The final volume of the solution was adjusted to 100 ml, autoclaved and then stored for further use.</td>
</tr>
<tr>
<td>NaCl (Sodium Chloride)</td>
<td>5 M</td>
<td>29.2 g of sodium chloride was dissolved in 80 ml of double distilled water. The final volume of the solution was then adjusted to 100 ml, autoclaved and stored for further use.</td>
</tr>
<tr>
<td>Cetrimide (CTAB) (N-cetyl-N, N, N-trimethyl ammonium bromide) for molecular biology (Himedia, India)</td>
<td></td>
<td>Purchased and added 2% w/v in the extraction buffer.</td>
</tr>
<tr>
<td>Chemical</td>
<td>Concentration</td>
<td>Action</td>
</tr>
<tr>
<td>---------------------------</td>
<td>---------------------</td>
<td>---------------------------------------------</td>
</tr>
<tr>
<td>PVP 40 (polyvinyl pyrrolidine) (SRL, India)</td>
<td>1% w/v</td>
<td>Added to the extraction buffer</td>
</tr>
<tr>
<td>2-Mercaptoethanol for molecular biology (Merk, Germany)</td>
<td>0.2% v/v</td>
<td>Added to the extraction buffer</td>
</tr>
<tr>
<td>Extraction buffer</td>
<td></td>
<td>Consisted of 1M Tris-HCl (pH 8.0), 0.5 M EDTA (pH 8.0) and 5M NaCl. All reagents were autoclaved and stored at room temperature. Just before use, the buffer was warmed to 65°C, CTAB, 2% w/v and PVP 40, 1.0% w/v were added and allowed to dissolve by gentle intermittent swirling. Prior to homogenisation 2-Mercaptoethanol, 0.2% v/v was added to the buffer solution.</td>
</tr>
<tr>
<td>Phenol:Chloroform: Isoamylalcohol (Sisco Research Laboratories Pvt. Ltd., India)</td>
<td>(25:24:1)</td>
<td>Purchased and used</td>
</tr>
<tr>
<td>Ammonium acetate</td>
<td>7.5 M</td>
<td>77 g ammonium acetate was dissolved in 80 ml of double distilled water. The volume of the solution was then made up to 100 ml, filter sterilized and stored for further use.</td>
</tr>
<tr>
<td>Ethanol for molecular biology</td>
<td>70%</td>
<td>70 ml of absolute ethanol was added to 30 ml of double distilled water to prepare 100 ml solution.</td>
</tr>
<tr>
<td>RNase (GeNei™, Merck Genei, Mumbai, India)</td>
<td>10 mg ml⁻¹</td>
<td>Purchased and used</td>
</tr>
<tr>
<td>TBE Buffer</td>
<td>5 X</td>
<td>54 g of Tris base, 27.5 g of boric acid and 20 ml of 0.5 M EDTA (pH 8) was dissolved in 800 ml of double distilled water and the volume of the solution was adjusted to 1000 ml, and stored at room temperature for further use.</td>
</tr>
<tr>
<td>Agarose (medium EEO) (Himedia, India)</td>
<td></td>
<td>Purchased and used</td>
</tr>
<tr>
<td>Item</td>
<td>Concentration/Composition</td>
<td>Use</td>
</tr>
<tr>
<td>----------------------------------------------------------------------</td>
<td>------------------------------------------------------------------------------------------</td>
<td>----------------------------------------------------------------------</td>
</tr>
<tr>
<td>Ethidium bromide solution</td>
<td>10 mg ml(^{-1})</td>
<td>10 mg of Ethidium bromide powder was added to 1 ml of sterilized double distilled water and stirred on magnetic stirrer. The solution stored in dark bottle for future use.</td>
</tr>
<tr>
<td>dNTP (dATP, dCTP, dGTP, dTTP)</td>
<td>10 mM</td>
<td>Purchased and used</td>
</tr>
<tr>
<td>(Applied Biosystems, Carlsbad, California, US)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RAPD Primers (OPERON Technologies Inc., USA and Integrated DNA Technologies, USA)</td>
<td></td>
<td>Purchased and used</td>
</tr>
<tr>
<td>ISSR Primers (Integrated DNA Technologies, USA)</td>
<td></td>
<td>Purchased and used</td>
</tr>
<tr>
<td>ITS primers (Integrated DNA Technologies, USA)</td>
<td></td>
<td>Purchased and used</td>
</tr>
<tr>
<td>Taq DNA Polymerase Buffer A</td>
<td>10 X</td>
<td>Purchased and used</td>
</tr>
<tr>
<td>(GeNei™, Merck Genei, Mumbai, India)</td>
<td>(100 mM Tris-HCl, pH 9 at 25°C; 15 mM MgCl(_2); 500 mM KCl and 0.01% gelatine)</td>
<td></td>
</tr>
<tr>
<td>Taq DNA polymerase (GeNei™, Merck Genei, Mumbai, India)</td>
<td>1.5 U</td>
<td>Purchased and used</td>
</tr>
<tr>
<td>300 bp to 3 kb DNA ladder (Applied Biosystems, Carlsbad, California, US)</td>
<td></td>
<td>Purchased and used</td>
</tr>
<tr>
<td>100 bp DNA ladder (Applied Biosystems, Carlsbad, California, US)</td>
<td></td>
<td>Purchased and used</td>
</tr>
</tbody>
</table>
PUBLICATIONS IN PEER REVIEWED JOURNALS


SEQUENCE SUBMISSIONS IN GenBank

23 different *Allium* species were submitted to GenBank (KT7895597, KT7895596, KU140433, KU140434, KT781693, KU145492, KT781691, KU145490, KT781694, KT895596, KU176880, KU145491, KT895595, KU145494, KT882613, KU145493, KT762156, KT762157, KT762155, KT762158, KU145489, KT781692, KR349330, KU145488)

CONFERENCE PRESENTATIONS


Comparative karyomorphological studies of three edible locally important species of *Allium* from India

Mou Dutta · Maumita Bandyopadhyay

Received: 9 September 2013 / Published online: 2 April 2014
© Archana Sharma Foundation of Calcutta 2014

Abstract Karyomorphological studies of three locally important species of *Allium*, namely, *A. tuberosum*, *A. chinense* and *A. schoenoprasum*, were performed to highlight the chromosomal variations between them, despite the fact that all of them are known as “chives” in commerce, due to their overall morphological similarities. Only critical morphological analyses reveal several important phenotypic dissimilarities between the three species. Karyomorphological investigations show that *A. tuberosum* and *A. chinense* are both 2n=32, and *A. schoenoprasum* is 2n=16. *A. chinense* has maximum karyotype symmetry among the three, and most of its chromosomes are of either median or submedian types. The karyotype of *A. tuberosum* is characterized by the presence of different types of secondary constrictions, while *A. schoenoprasum*, apart from showing the maximum karyotype asymmetry among the three, also reveals the presence of at least one pair of acrocentric chromosomes.

Keywords Karyomorphology · Chives · *A. tuberosum* Rottl. ex Spreng. · *A. chinense* G. Don · *A. schoenoprasum* L.

Introduction

*Allium* L. (Family Alliaceae) is one of the largest genera of the monocotyledons, comprising of some 750 species [6], including both wild and cultivated plants [16]. Members of this genus are widely distributed in the Temperate and Alpine regions of the Northern Hemisphere, with centers of diversity in Southwest or Central Asia, Eastern Asia and North America [17]. In India, 35–40 species of *Allium* L. are distributed in the Western Himalayas (Jammu and Kashmir, Uttarakhand, Himachal Pradesh) and in the Eastern Himalayan region (Darjeeling hill tracts of West Bengal, Sikkim and the North Eastern States) [16, 21].

*Allium* includes many economically important species, and different species are regularly used as food, or are exploited for their medicinal and horticultural merit. Onion (*A. cepa*), Japanese bunching onion (*A. fistulosum*), chives (*A. schoenoprasum*), leek (*A. porrum*) and garlic (*A. sativum*) are some of the most important edible *Allium* crops in the world [17, 21]. In fact, onion ranks second in value after tomato on the list of cultivated vegetable crops worldwide [11]. In India too, common onion (*A. cepa*), garlic (*A. sativum*), shallots (*A. ascalonicum*) and leek (*A. porrum*) feature among the well-known vegetable crops [21]. In addition to these species, several locally available *Allium* species are also cultivated in different parts of India [16]. These include *Allium tuberosum* Rottl. ex Spreng., *Allium chinense* G. Don and *Allium schoenoprasum* L. Nomenclature of *Allium* species, both in scientific and in commercial terms, is a controversial issue due to overall morphological similarities. This problem is compounded by variations in local names, seasonal flowering and use of only detached parts like leaves and/or bulbs for human use, all of which make the taxonomic identification very difficult. The present study deals with the karyomorphology of three species of *Allium*, namely, *A. tuberosum*, *A. chinense* and *A. schoenoprasum*. All these three *Allium* species are vegetable crops of local economic importance, having enough morphological similarities to be grouped under the common name “chives”. According to the classification of Friesen et al. [6], *A. chinense* and *A. schoenoprasum* belong to the Subgenus Cepa, under Section Sacculiferum and Section Schoenoprasum respectively, while *A. tuberosum* belongs to the Subgenus Butomissa under Section Butomissa.

*Allium tuberosum* or Garlic Chives, extensively cultivated in China, Japan, Korea, Vietnam and Taiwan [26], is semi-domesticated and cultivated only in certain localities in India.
Fresh and dried leaves of *A. tuberosum* are used as condiments, as well as medicinal herbs by locals in Uttarakhand [16]. *Allium chinense* or Chinese chives or rakkyoo, another extensively cultivated crop in East Asia, is grown in kitchen gardens of Meghalaya and Arunachal Pradesh. Whole plants are sold in the local markets around North Eastern India as condiments [17]. *Allium schoenoprasum* or English chives are important Central European spice plants. The leaves and flowers are used to flavour and garnish dishes, and the stems used as appetizers. This species is found in the wild in Ladakh Himalaya and in Kashmir, and has restricted commercial cultivation in India [17].

The main aim of this study was karyomorphological characterization of the three species. It is reported that study of karyotypic differences is important in understanding the nature of plant variations at the population to generic level [24]. Our present investigation deals with karyomorphological analysis of chromosomes from somatic cells of the three different types of *Allium*, all commonly called “chives”. The study revealed significant differences in chromosome number, size and karyotype symmetry and would provide additional support for identification of species at chromosome level.

**Material and methods**

*Plant material studied:* *Allium tuberosum* Rottl. ex Spreng. plants were available in the Experimental Garden, Department of Botany, University of Calcutta (Accession I), and seeds were bought from Sutton and Sons Seeds, Kolkata (Accession II). These seeds were germinated and the seedlings grown in the Experimental Garden, Department of Botany, University of Calcutta. Whole plants of *Allium chinense* G. Don were collected from Shillong, Meghalaya (Accession I) and also from National Bureau of Plant Genetic Resources, Niglat, Bhowali, Uttarakhand (Accession II). Accession I of *Allium!* ![Image](https://example.com/1) was successfully established in the Experimental Garden, Department of Botany, University of Calcutta. *A. tuberosum* and *A. chinense* plants were maintained in pots in the Experimental Garden of University of Calcutta throughout the year. Fresh roots were harvested from these potted plants for cytological studies. Seeds of *Allium schoenoprasum* L. were bought from Plant World Seeds, London, UK (Accession I) and also from Sutton and Sons Seeds, Kolkata (Accession II). These seeds were germinated during December–January, but the seedlings didn’t survive beyond a month and could not be transplanted to the field. Fresh roots were harvested from the germinated seedlings for cytological studies. The plant specimens were identified by comparisons with relevant references and the voucher specimens were submitted to the Calcutta University Herbarium (CUH). A detailed list of plant accessions and their sources is included in Table 1.

**Morphological study** Whole plants and seeds of collected material were studied and described using standard taxonomic descriptors [14, 28].

**Mitotic study** For studying karyotype details, young root-tips from 20 randomly selected plants for each species were taken. Root tips 0.5–1 cm in length, were initially washed in water, then pre-treated in saturated solution of 0.002 % 8-hydroxyquinoline and *para*-dichlorobenzene solution (8 °C, 3–4 h) and fixed in 3:1 absolute ethanol: glacial acetic acid (10 °C for 12–16 h). The root tips were stained in 2 % aceto-orcein and 1(N) HCl mixture (9:1) (room temperature, 45 min), after brief heating if required, and finally squashed in 45 % acetic acid on grease-free slides, after macerating in 45 % acetic acid (5–10 min, room temperature). Detailed karyomorphological data for each species is based on 15 independent plates from at least five different root tips.

**Karyomorphological study** Well scattered metaphase plates (with properly condensed chromosomes) were observed under microscope (Carl Zeiss, Primo star) and photographed using AxioCamERc5s Camera (Carl Zeiss). Chromosome images were analysed using software packages (Zeiss Axiovision LE 4.3) and the images in pixel unit were converted to micrometer with reference to a standard scale (stage micrometer). For detailed karyotype analysis values of measurements such as long arm (L), short arm (S), arm ratio (r) and total length of chromosomes and value of relative chromatin (VRC=∑TL/n), were calculated. Chromosomes were classified according to Levan et al. [13] with centromeric index of Median constriction (M) (>47.5–50.0), median region constriction (m) (>37.5–47.5), submedian region constriction (sm) (>25.0–37.5), subterminal constriction (st) (>12.5–25.0) and terminal (t) (>2.5–12.5). Categorization of karyotype asymmetry was performed according to the classification proposed by Stebbins [29]. Based on Paszko [22] the coefficients of variation of chromosome length (CVCL = standard deviation of chromosome length/mean chromosome length x100), coefficients of variation of centromeric index (CVCI = standard deviation of centromeric index/mean centromeric index x100) and asymmetry index (AI=CVCL×CVCI/100) were calculated.

**Results**

Detailed morphological and karyomorphological analysis of *A. tuberosum, A. chinense* and *A. schoenoprasum* were done in the present study. All these three species are sold in the markets under the common name “chives”, creating confusion among buyers by the virtue of their morphological similarity. Detailed study, however, shows they have both distinct
morphological and karyological characters. The chromosome numbers and detailed numerical data on the karyotype parameters studied for all the three species are summarized in Tables 2 and 3. The mitotic metaphase plates, karyograms and ideograms of the species studied are depicted in Fig. 1.

Allium tuberosum Rottl. ex Spreng. or garlic chives Herbs (14–45 cm); bulbs cylindrical, swollen (2–4 cm); scales fibrous, profusely rooting at base; bulbs in a group remain attached to a elongated or rhizome-like common stem; leaves (15–30 cm in length) 3–6 in number per bulb, green, basal, linear, flat, cross-section of leaf crescent shaped; seeds obovoid (3×2 mm), blackish brown, coarsely reticulate.

Karyomorphological study revealed that root tips of both the Accessions of A. tuberosum consistently showed 2n=32. The chromosome size of both the varieties of A. tuberosum ranged from 8 to 18 μm. Value of relative chromatin (VRC) of Accession I was 26.31 μm and the value of relative chromatin (VRC) of Accession II was 26.06 μm (Table 2). Asymmetry index (AI) value, which was derived from the mean data related to chromosome length and centromeric index of both the populations studied, was 4.12 (Table 3). The mean CVc(t) value was 22.1 (Table 3). On the basis of proportion of chromosomes (0.53) with arm ratio lesser than 2:1 and ratio of longest to shortest chromosome (2.2), the karyotype falls into 2B category of Stebbins chart of chromosome asymmetry [29]. The karyotype formula of Accession I was 4 M+14 m+2 sm+2 m:sm+3 m:st+3 m:t+4 st:t and Accession II was 4 M+9 m+4 sm+3 st+4 m:m+7 m:st+1 mt. The mean karyotype formula was resolved into 4 M+11.5 m+3 sm+1.5 st+2 m:m+1 m:sm+5 m:st+2 m:t+2 st:t. As reported earlier [27], based on overall morphology (chromosome length and centromeric index) 32 chromosomes (Fig. 1A) of Accession I formed eight quadruples. While two groups are homomorphic (III and VIII), others are heteromorphic (I, II, IV, V, VI, VII) (Fig. 1a, a+). Somatic chromosome complement of A. tuberosum reveals the presence of different types of secondary constrictions namely m:m, m:sm, m:st, m:t, st:t.

Allium chinense G. Don or Chinese chives Small herbs (25–30 cm); bulbs clustered, ovoid (2–3 cm), elongated, swollen at basal end, tapering and curved at the end from which leaves arise, bulbs produced from single bulb remain attached to a common stem; scales not fibrous, formed by sheaths of leaf bases; leaves (10–20 cm in length) 2–6 in number per bulb, bright green, linear, basal, slender, hollow and thin walled, leaves in cross-section show 3 to 5 angles; seeds are reportedly not produced [14, 28].

The total somatic chromosome number of both the Accessions of A. chinense was 2n=32. The chromosome size of

<table>
<thead>
<tr>
<th>Table 1</th>
<th>Allium sp. studied with accession number and place of collection</th>
</tr>
</thead>
<tbody>
<tr>
<td>Taxa</td>
<td>Accession</td>
</tr>
<tr>
<td>Allium tuberosum Rottl. ex Spreng.</td>
<td>I</td>
</tr>
<tr>
<td></td>
<td>II</td>
</tr>
<tr>
<td>Allium chinense G. Don</td>
<td>I</td>
</tr>
<tr>
<td></td>
<td>II</td>
</tr>
<tr>
<td>Allium schoenoprasum L.</td>
<td>I</td>
</tr>
<tr>
<td></td>
<td>II</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Table 2</th>
<th>Comparative Karyotype analysis of three species of Allium</th>
</tr>
</thead>
<tbody>
<tr>
<td>Species</td>
<td>Somatic chromosome number (2n)</td>
</tr>
<tr>
<td>Allium tuberosum (Accession I)</td>
<td>32</td>
</tr>
<tr>
<td>Allium tuberosum (Accession II)</td>
<td>32</td>
</tr>
<tr>
<td>Allium chinense (Accession I)</td>
<td>32</td>
</tr>
<tr>
<td>Allium chinense (Accession II)</td>
<td>32</td>
</tr>
<tr>
<td>Allium schoenoprasum (Accession I)</td>
<td>16</td>
</tr>
<tr>
<td>Allium schoenoprasum (Accession II)</td>
<td>16</td>
</tr>
</tbody>
</table>

*VRC value of relative chromatin
**Table 3** Karyomorphological characteristics in the studied species of *Allium*

<table>
<thead>
<tr>
<th>Species</th>
<th>Range SC(^a) - LC(^b) (μm)</th>
<th>Ratio LC(^b)/SC(^a)</th>
<th>Proportion of chromosomes with arm ratio &lt;2:1</th>
<th>Karyotype category (according to Stebbins, 1971)</th>
<th>CL(^c) Mean(±SD)</th>
<th>CI(^d) Mean(±SD(^e))</th>
<th>CV(_{CL})(^f)</th>
<th>CV(_{CI})(^g)</th>
<th>AI(^h)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Allium tuberosum</em></td>
<td>8–18</td>
<td>2.2</td>
<td>0.53</td>
<td>2B</td>
<td>13.4±2.5</td>
<td>38.8±8.6</td>
<td>18.65</td>
<td>22.1</td>
<td>4.12</td>
</tr>
<tr>
<td><em>Allium chinense</em></td>
<td>9–17.5</td>
<td>1.95</td>
<td>0.72</td>
<td>2A</td>
<td>13.4±2.6</td>
<td>43.35±5.6</td>
<td>19.40</td>
<td>12.9</td>
<td>2.38</td>
</tr>
<tr>
<td><em>Allium schoenoprasum</em></td>
<td>6.75–13.52</td>
<td>2.0</td>
<td>0.87</td>
<td>2B</td>
<td>9.97±2.1</td>
<td>40.8±10.6</td>
<td>21.06</td>
<td>25.9</td>
<td>5.45</td>
</tr>
</tbody>
</table>

\(^a\) SC the shortest chromosome, \(^b\) LC the longest chromosome, \(^c\) CL mean length of chromosomes, \(^d\) CI mean centromeric index, \(^e\) SD standard deviation, \(^f\) CV\(_{CL}\) component expressing the relative variation in chromosome length, \(^g\) CV\(_{CI}\) component expressing the relative variation in centromeric index, \(^h\) AI Asymmetry Index

*A. chinense* Accessions I and II ranged from 9 to 17.5 μm. Value of relative chromatin (VRC) of Accession I was 27.38 and 26.89 μm in Accession II (Table 2). Chinese chives had the lowest asymmetry index (AI) value among the three species of chives studied, which at 2.38 (Table 2), indicated maximum karyotypic symmetry. The CV\(_{CI}\) value (12.9) was also lowest among the three, indicating minimum difference between centromeric indices of the chromosome complements. On the basis of proportion of chromosomes with arm ratio (0.72) lesser than 2:1 and ratio of longest to shortest chromosome (1.95) the karyotype falls into 2A category of Stebbins’ chart of chromosome asymmetry [29]. The karyotype formula of *A. chinense* was found to be 4 M+20 m+6 sm+2 sm:t in Accession I and 6 M+16 m+4 sm+2 st+1 M:st+3 m:st in Accession II. Thus, the mean karyotypic formula were resolved to be 5 M+18 m+5 sm+1 st+0.5 M:st+1.5 m:st+1 sm:t. Based on overall morphology (chromosome length and centromeric index) 32 chromosomes (Fig. 1B, b) of Accession I formed eight quadruples. While four groups are homomorphic (II, III, VI and VII) other four groups are heteromorphic (I, IV, V and VIII) (Fig. 1b+). So the study shows that most of the chromosomes of *A. chinense* have either median (M) or median region constriction (m) (Fig. 1b+).

![Fig. 1](image)

Fig. 1 Mitotic metaphase plates of (A) *Allium tuberosum* (Accession I) showing 2n=4x=32 chromosomes, (B) *Allium chinense* (Accession I) showing 2n=4x=32 chromosomes, (C) *Allium schoenoprasum* (Accession I) showing 2n=16 chromosomes, and a,b,c and a+, b+, c+ represented by their respective karyograms (bar=10 μm), and ideograms (bar=5 μm), respectively. *Heteromorphic groups

© Springer
**Allium schoenoprasum** L. or English chives Herbs (20–35 cm) [28]; bulbs cylindrical (2–4 cm), clustered, scales membranous; leaves (10–20 cm in length) 1–3 in number per bulb, green, linear, fusiform, leaf cross-section was smoothly round; seeds blackish, orbicular (2.5–3.5×2 mm).

Both the Accessions of *A. schoenoprasum* showed the total chromosome number 2n=16 (Fig. 1C), though the chromosome sizes differed significantly. The chromosome size of Accession I ranged from 9.5 to 19 μm while the chromosome size of Accession II ranged from 4.02 to 8.04 μm (Table 2). Value of relative chromatin (VRC) of Accession I was 28.12 μm and the value of relative chromatin (VRC) of Accession II was 14.87 μm (Table 2). Among the three species studied, *A. schoenoprasum* had the highest asymmetry index (5.45) derived from the mean data of the populations studied, indicating highest karyotypic heterogeneity. The CVCI (25.9) derived from the mean data was also highest among the three (Table 3), indicating maximum difference between centromeric indices of the chromosome complements. On the basis of proportion of chromosomes with arm ratio (0.87) lesser than 2:1 and ratio of longest to shortest chromosome (2.0) the karyotype falls into 2B category of Stebbins’ chart of chromosome asymmetry [29]. Karyotype analysis of Accession I (Fig. 1c, c+) revealed the sixth pair of chromosomes was acrocentric with secondary constriction on the short arm. Additional secondary constrictions were also present on metacentric chromosomes of fifth and eighth pair (Fig. 1c, c+), as reported [1, 7]. The karyotype formula of Accession I was 2 M+8 m+1 m:st+3 m:t+2 t:t. The karyotype formula of Accession II was 4 M+8 m+2 sm+1st+1st:t. Thus in Accession II, only the eighth pair was acrocentric with secondary constriction. No other chromosome pair with secondary constriction was found as reported by Cai and Chinnappa [2] and Garrido et al. [7]. The mean karyotype formula was resolved into 3 M+8 m+1sm+0.5 st+0.5 m:st+1.5 m:t+0.5 st+t+1 t:t. The chromosomes of Accession I formed eight pairs based on overall morphology (chromosome length and centromeric index). While five groups are homomorphic (I, III, IV, VI and VIII) others are heteromorphic (II, V and VII) (Fig. 1c, c+). In *A. schoenoprasum* although the maximum number of chromosomes are of median type, all the other three types of primary constrictions like sm, st and t were also found (Fig. 1c, c+).

**Discussion**

All the three species of *Allium* discussed in this paper, are herbs with bulbs (approximately 2 to 4 cm) clustered together, with leaves (approximately 3–6 in number) originating from each bulb. Based on these gross morphological similarities, the three species are all sold in the open market under the common name ‘chives’. But, in fact, they are three different species having many morphological and karyological differences as discussed here.

A closer assessment of the bulbs reveal that the group of bulbs in *A. tuberosum* remain attached to an elongated, rhizome-like stem, which is absent in both *A. chinense* and *A. schoenoprasum*. The scales of bulb of *A. tuberosum* are fibrous but scales of *A. chinense* are not, while those of *A. schoenoprasum* are membranous. Both *A. chinense* and *A. schoenoprasum* have slender, hollow and thin walled leaves, but *A. tuberosum* have flat leaves.

Karyotypically all the three species are different. According to earlier reports, *A. tuberosum* is a unique autotetraploid species with 32 chromosomes in the somatic cells, of which seven sets are metacentric and one set sub-metacentric chromosomes with satellite [3, 4]. There are records of naturally occurring diploids (2n=16) [19, 32] and tetraploids (2n=4x=32) [9, 15, 25, 26, 30], as well as a double hypoploid (2n=4x=30) [12, 27] and hypotetraploid (2n=4x=31), along with a haploid plant (2n=48) [26]. Experimentally produced octaploids (2n=61–64) were also reported [12]. Our analysis also showed that both the Accession I (Fig. 1A) and II of *A. tuberosum* studied had 32 chromosomes belonging to metacentric, sub-metacentric and subtelocentric types. Metaphase plates studied also showed presence of chromosomes with different types of secondary constrictions, for example, namely m:m, m:sm, m:st, m:t, st:t. The asymmetric index and CV CI values lies in-between those of *A. chinense* and *A. schoenoprasum*, indicating moderate level of karyotype symmetry.

*A. chinense* or Chinese chives or scallion or rokkyo, another tetraploid species, also has 32 chromosomes [2] and the populations studied have lowest asymmetric index and CV CI values among the three. Our mitotic metaphase study showed that *A. chinense* had the highest karyotypic symmetry with minimum difference between centromeric indices. In fact, it was seen that majority of its chromosomes were metacentric, and only four or six chromosomes being submetacentric (Fig. 1B, b, b+). This observation was similar to the report of Ogura et al. [18]. Metacentric and sub-metacentric chromosomes with secondary constrictions were also found as reported by Wufeng et al. [31] who recorded populations of *A. chinense* with various karyotypic formulas like 2n=4x=32, 24 m+8sm(SAT), 28 m(SAT)+4sm, 24 m(SAT)+4sm+4st and variant chromosome numbers 2n=3x=21, 2m+3sm. *A. chinense* with variant number of chromosomes, 2n=24 and 2n=33 were also reported [5, 8].

*A. schoenoprasum* had 16 chromosomes, showing maximum asymmetric index and CV CI values denoting lowest karyotypic symmetry among the three species studied, with maximum difference between centromeric indices. Earlier reports point out that the characteristic feature of the karyotype of *A. schoenoprasum* was the presence of two acrocentric...
chromosomes [2]. Secondary constrictions were found only on the acrocentric chromosomes [2] or also on two other pairs [1]. Two Accessions of *A. schoenoprasum* were studied, of which Accession I (Fig. 1C, c, c+) was identified to the karyotype reported by Bougourd and Parker [1] while the Accession II resembled that reported by Cai and Chinappa [2] and by Bougourd and Parker [1]. It is on record that there are variable numbers of chromosomes with nucleolar-organiser regions in different Accessions of *A. schoenoprasum* [1]. In our study, we found that Accession I had three pairs of chromosomes with secondary constrictions (Fig. 1C, c, c+), while Accession II had only one pair of chromosomes with secondary constrictions, though the typical acrocentric chromosome with secondary constriction was present in both the populations. Though B chromosomes have been previously reported in *A. schoenoprasum* [2], the Accessions we studied did not show any.

Thus, the present study sheds light on the distinct karyotype patterns of the three species of *Allium*, namely *A. tuberosum*, *A. chinense*, *A. schoenoprasum*. The primary difference among the three is the ploidy level. It is known that the genus *Allium* displays a range of ploidy, varying between aneuploidy to 16X polyploids [23], the basic chromosome numbers being *x* = 7, 8 or 9 [10, 23]. *A. tuberosum* and *A. chinense* are autotetraploids, though variants are also reported. Our studies also revealed that both the species have 32 chromosomes each, though the karyotype in *A. chinense* is more symmetric with all median and sub-median chromosomes, in contrast to *A. tuberosum* which shows the presence of chromosomes with median constriction, median region constriction, submedian constriction and subterminal constrictions. *Allium schoenoprasum* has the least number of chromosomes among the three, but the 16 chromosomes make up a karyotype with very low symmetry. This karyotype was typified by the presence of a pair of acrocentric chromosomes, which distinguishes it from other diploid *Allium* species. Mean chromosome length was the least in *A. schoenoprasum*, while both *A. tuberosum* and *A. chinense* have longer chromosomes of almost of identical sizes.

In the earlier accepted classification of Hanelt et al. [10], all the three species studied were grouped under the Subgenus *Rhiziridium*, which could be the justified owing to their obvious morphological similarities. *A. schoenoprasum* was placed under Section *Schoenoprasum* of the same which was characterized by the smallest genome size. Ohri et al. [20] have argued that the small genome size is an evolutionary advancement in the species to facilitate its wide ecological distribution, and to help in ecological specialization. The high level of karyotypic asymmetry that we have found in the two populations of *A. schoenoprasum*, along with the significant difference in the value of relative chromatin, can be argued to be due to different levels of adaptive divergences among the populations. *A. chinense* was placed under Section *Sacculiferum*, and characterized by its geographical isolation, 3-angled leaf structure and late flowering [20]. It can be argued that this restricted geographical distribution and low adaptive pressure helped in the attainment of a symmetric karyotype in this species with chromosomes showing only median and submedian type of constrictions and also lesser number of chromosomes with secondary constrictions, which is a derived character from an ancestral state with many chromosomes with secondary constrictions. *A. tuberosum* was placed under Section *Butomissa*, and showed very similar 2C DNA values to *A. chinense*. In our study, though the chromosome numbers of both these species are similar, *A. tuberosum* has a more asymmetric karyotype with many more chromosomes showing secondary constrictions, which may be due to the wider distribution of this species in comparison to *A. chinense*. Friesen et al. [6] later redefined the classification of *Allium*, and reorganised Hanelt et al.’s [10] Subgenera *Rhiziridium* and *Allium* into seven monophyletic groups. Under this system, *A. tuberosum* was classified under Section *Butomissa* of the newly created Subgenus *Butomissa*, while *A. chinense* and *A. schoenoprasum* were put under Section *Sacculiferum* and Section *Schoenoprasum* respectively, both under the newly created Subgenus *Cepa*. The authors contended that monophyly of the groups was the prime consideration, along with morphological and serological characters in their classification, though their karyotypes are quite similar. We also find that characters like rhizome like common stem and bulb tunics are very distinct in *A. tuberosum* in contrast to the other two, justifying the former’s categorization into a separate subgenus in the new system.

Thus, we can infer that karyomorphological considerations help not only in authentic identification of different species, but also augment our understanding of the intra-generic relationships and the structural changes that lead to the diversification of the genus.

Acknowledgments Maumita Bandyopadhyay acknowledges the Young Scientist Project, Science and Engineering Research Board, Department of Science and Technology, Government of India, for financial assistance. Authors also thank Dr. KS Negi, NBPGR, Bhowali, for *Allium chinense* plant material.

References


Karyomorphological study and report of B chromosome in *Allium griffithianum* Boiss. from India

Mou Dutta · Maumita Bandyopadhyay

Received: 25 February 2014 / Published online: 19 August 2014
© Archana Sharma Foundation of Calcutta 2014

**Abstract** The chromosomal characteristics of *Allium* L. have intrigued scientists on account of variation in basic chromosome number (x) ranging from 8 to 11, occurrence of polyploidy and presence of B chromosomes. The present study provides karyotypic details *Allium griffithianum* and presence of B chromosome in the species, the being a first report. The root-tip mitosis in this species showed presence 16 chromosomes, but 30 % of cells also showed occurrence of an additional B chromosome. The chromosome size ranged from 8.45 μm to 18.46 μm. The B chromosome size ranged between 2.4 and 2.7 μm in the mitotic metaphase plates. The mean karyotype formula was deduced to be 4.5 M+7.5 m+1sm+1st+2 m (SAT)+1B.

**Keywords** *Allium griffithianum* Boiss. · Karyomorphology · B chromosome

**Introduction**

The chromosomal characteristics of *Allium* L. have intrigued scientists since the early 20th century, and the members of the genus show very interesting chromosome characters, i.e., basic chromosome number (x) ranging between 8 and 11, polyploidy and presence of B chromosomes. B chromosomes have been described as dispensable elements that do not recombine with the standard chromosome set (A chromosomes), and whose inheriance is non-Mendelian and irregular [10]. Supernumerary B chromosomes are found extensively in both plants and animals, especially in those which have large genomes [1]. Though their role in augmenting the survival of natural populations is still open to controversy, it cannot be denied that the widespread presence of B chromosomes in the plant and animal kingdoms imply their importance in the genome characterisation and evolution of the species concerned [10]. Blagojević et al. [1] reported that at least 34 species of *Allium* show B chromosomes and different authors have correlated numbers of B chromosomes in different species of *Allium*, with geographical distribution, culture conditions and age of the plant concerned [2–4, 17]. The present study focuses on the karyotype analysis of *Allium griffithianum* Boiss., emphasizing on the presence of a B chromosome, which to the best of our knowledge has not been reported earlier. According to Negi [12], plants of *A. griffithianum* are frequent in the wild, in temperate and alpine zones, up to 1,500–3,500 m altitude in the Western Himalayas. Earlier Pandita and Mehra [15] had reported that *A. griffithianum* found in Kashmir Himalayas had shown 32 chromosomes at mitotic metaphase stages. Gohil and Kaul [7] also reported the mitotic chromosomes number in *A. griffithianum* to be 2n=32. Ohri et al. [13, 14] and Friesen et al. [6] reported 2n=16 in *A. griffithianum* from the IPK, Gatersleben collection of *Allium*. We report the karyotype analysis of *A. griffithianum* collected from Uttarakhand, India which is deviant from the earlier reports from India with respect to their chromosome number and the presence of a B chromosome.

**Materials and methods**

Plant material studied

Whole plants of *A. griffithianum* Boiss. (Accession number IC 14272) were collected from National Bureau of Plant Genetic Resources, Regional Station, Niglat, Bhowali, Uttarakhand, where they were maintained in the germplasm collection of *Allium*.
Mitotic study

For studying karyotypic details, young root–tips were randomly selected from plants taken from the field of collection. Root tips 0.5–1 cm in length, were initially washed in water, then pre-treated in saturated solution of 0.002 M 8-hydroxyquinoline and para-dichlorobenzene solution (8 °C, 3–4 h) and fixed in 3:1 absolute ethanol: glacial acetic acid (10 °C for 12–16 h). The root tips were stained in 2 % aceto–orcein and 1(N) HCl mixture (9:1) (room temperature, 45 min) and finally squashed in 45 % acetic acid on grease–free slides, after macerating in 45 % acetic acid (5–10 min, room temperature). Data for karyotype analysis of A. griffithianum is based on at least 25 independent plates from ten root tips and data for B chromosomes is based on unbiased observations of over hundred division stages from several root tips belonging to different plants.

Karyomorphological study

Well scattered metaphase plates (with properly condensed chromosomes) were observed under microscope (Carl Zeiss, Primostar) and photographed using AxioCamERc5s Camera (Carl Zeiss). Chromosome images were analysed using software packages (Zeiss Axiovision LE 4.3) and the images in pixel unit were converted to micrometer with reference to a standard scale (stage micrometer). For detailed karyotype analysis, values of measurements such as length of long arm (LA), length of short arm (SA), total length of chromosome (TL = LA + SA), standard deviation of chromosome length (SDCL), mean chromosome length (XCL), mean centromeric index (CI = SA/TL × 100), mean centromeric index (XCI), mean centromere index (XCI), value of relative chromatin (VRC = ΣTL/n) were calculated. Karyotype asymmetry was evaluated using Huziwara’s total form percent (TF%) and Zarco’s intra- and inter-chromosomal asymmetry indexes (A1 and A2) [5, 9, 19]. Classification of karyotypes in relation to their degree of asymmetry according to Stebbins was calculated [18]. The coefficients of variation of chromosome length (CVCL), chromosome index (CVCI) and asymmetric index (AI) were also calculated based on Paszko [16]. Chromosomes were classified according to Levan et al. [11].

Results

Morphological and karyomorphological analysis of A. griffithianum Boiss.

The plants of A. griffithianum were collected from wild, subsequently identified and catalogued by Dr. K.S. Negi and

Table 1 Numerical data on the karyotype parameters of the haploid chromosome complement of Allium griffithianum Boiss.

<table>
<thead>
<tr>
<th>Chromosome pair</th>
<th>Long arm (μm)</th>
<th>Short arm (μm)</th>
<th>Total length (μm)</th>
<th>Centromeric position</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>8.61±0.24</td>
<td>7.01±1.95</td>
<td>18.46±2.86</td>
<td>m (SAT)</td>
</tr>
<tr>
<td>2</td>
<td>8.14±0.02</td>
<td>7.74±0.38</td>
<td>15.88±0.41</td>
<td>M</td>
</tr>
<tr>
<td>3</td>
<td>7.99±0.10</td>
<td>6.69±0.12</td>
<td>14.68±0.02</td>
<td>m</td>
</tr>
<tr>
<td>4</td>
<td>8.28±0.59</td>
<td>5.58±0.10</td>
<td>13.86±0.59</td>
<td>m</td>
</tr>
<tr>
<td>5</td>
<td>8.365±1.63</td>
<td>3.805±1.03</td>
<td>12.16±1.40</td>
<td>sm*</td>
</tr>
<tr>
<td>6</td>
<td>6.22±0.01</td>
<td>5.72±0.00</td>
<td>11.94±0.01</td>
<td>M</td>
</tr>
<tr>
<td>7</td>
<td>5.53±0.62</td>
<td>5.07±0.34</td>
<td>10.6±0.96</td>
<td>M</td>
</tr>
<tr>
<td>8</td>
<td>4.35±0.13</td>
<td>4.1±1.187</td>
<td>8.45±1.32</td>
<td>M</td>
</tr>
<tr>
<td>B</td>
<td>–</td>
<td>–</td>
<td>2.5±0.15</td>
<td>–</td>
</tr>
</tbody>
</table>

*The two chromosomes belonging to this group vary in nature of primary constriction in all the metaphase plates studied, one having submedian region constriction and the other subterminal constriction. The mean centromeric index value falls within the range of submedian region constriction according to Levan et al. [11].

Table 2 Karyomorphological characteristics of Allium griffithianum Boiss.

<table>
<thead>
<tr>
<th>Range SC-LC (μm)</th>
<th>Ratio LC/SC</th>
<th>Proportion of chromosomes with arm ratio &lt;2:1</th>
<th>Karyotype category (according to Stebbins, 1971)</th>
<th>CL (μm) Mean(±SD)</th>
<th>CI Mean (±SD)</th>
<th>CVCL</th>
<th>CVCI</th>
<th>AI</th>
<th>VRC (μm)</th>
<th>TF%</th>
<th>A1</th>
<th>A2</th>
</tr>
</thead>
<tbody>
<tr>
<td>8.45–18.46</td>
<td>2.1</td>
<td>0.87</td>
<td>2B</td>
<td>12.41±2.7</td>
<td>43.30±6.83</td>
<td>21.79</td>
<td>15.78</td>
<td>3.4</td>
<td>24.8</td>
<td>43.36</td>
<td>0.6</td>
<td>0.21</td>
</tr>
</tbody>
</table>

SC the shortest chromosome, LC the longest chromosome, CL Mean length of chromosomes, CI Mean centromeric index, SD Standard deviation, CVCL component expressing the relative variation in chromosome length, CVCI component expressing the relative variation in centromeric index, AI: Asymmetry index (CVCL× CVCI / 100), VRC* value of relative chromatin, TF% Total form percent, A1: intrachromosomal asymmetry index, A2: interchromosomal asymmetry index.

© Springer
maintained in the Field Gene Bank, Bhowali. The morphological characteristics of the plants studied were compared to earlier reports of the same collection [12].

*Allium griffithianum* Boiss., syn. *A. rubellum* M. Bieb., or Jamboo are small herbs (25–30 cm); bulbs small (2.5–3 cm), cylindrical, swollen; covered with red fibrous outer sheath, profusely rooting at base; leaves (15–20 cm) 3–6 in number per bulb, green, narrow, cross-section of leaf half rounded half flattish; flowers 1.5–2 cm, pedicels long, unequal, tepals white, 6 in number, midvein present, filaments free, ovary globose, style linear [12].

The chromosome numbers, numerical data on the karyotype parameters and karyomorphological characteristics studied are summarized in Tables 1 and 2, respectively. The mitotic prophase, metaphase and anaphase plates with B chromosomes are depicted in Fig. 1. A well scattered mitotic metaphase plate, karyogram and idiogram representing the same plate, are depicted in Fig. 2. Karyomorphological study revealed that all the root tips of *A. griffithianum* consistently showed 2n=16, with 30 % cells showing an additional unpaired B chromosome. The chromosome size ranged from 8.45 μm to 18.46 μm, while the B chromosome size ranged between 2.4 and 2.7 μm (Table 1) in the mitotic metaphase plates. On the basis of proportion of chromosomes (0.87) with arm ratio lesser than 2:1 and ratio of longest to shortest chromosome (2.1), the karyotype falls into 2B category of Stebbins’ chart of chromosome asymmetry [18]. Value of relative chromatin (VRC) was found to be 24.8 μm. The total form percent or average centromeric index (TF%) derived from the total length of short arms in chromosome set and total chromosome length in set was 43.36 [9]. The intrachromosomal asymmetry index (A1) calculated from mean length of short and a long arm in every homologous pair was 0.6. The interchromosomal asymmetry index (A2) calculated from standard deviation and the mean chromosome length was 0.21 [19]. Asymmetry index (AI) value [16], which was derived from the mean data related to chromosome length and centromeric index, was 3.4 (Table 2).
maximum numbers of chromosomes were with median (M or m) constrictions (Table 1). The mean karyotype formula from 25 individual metaphase plates was deduced to be 4.5 M + 7.5 m + 1 sm + 1 st + 2 m (SAT) + 1 B. The secondary constriction was present at the subterminal (st) position on two chromosomes with median (m) primary constriction.

**Discussion**

*Allium griffithianum* is a small herb with red fibrous outer sheath and half rounded half flatish cross–section of leaves typical of the subgenus *Allium* [8]. According to earlier reports of Ohri et al. [13, 14] and Friesen et al. [6], *A. griffithianum* showed 16 chromosomes in its mitotic metaphase, while Gohil and Kaul [7] and Pandita and Mehra [15] reported 2n = 32 chromosomes in *A. griffithianum*. Pandita and Mehra [15] reported *A. griffithianum* from Kashmir as an autotetraploid species having all 32 chromosomes with metacentric (M or m) constrictions and TF% value of 43.36. Our study revealed that the population of *A. griffithianum* studied had 2n = 2x = 16 chromosomes with metacentric (M, m), submetacentric (sm), and subterminal (st) constrictions. The karyotype formula (4.5 M + 7.5 m + 1 sm + 1 st + 2 m (SAT) + 1 B) derived from our analysis also showed a predominance of chromosomes with median (M or m) constrictions. One noteworthy feature of the karyotype was that two chromosomes from every metaphase plate studied were not metacentric, and among these two, one was always submetacentric and the other always subterminal in nature. Predominance of metacentric chromosomes was also reflected by Zarco’s [19] A1 value (0.6) and thus the karyotype was categorized under Stebbins’ category 2 of asymmetry [18]. Two chromosomes with secondary constrictions were consistently found in all the metaphase plates studied. A two–times difference in length observed between the shortest (8.45 μm) and the longest chromosome (18.46 μm) explains the 0.21 A2 value of Zarco [19]. The karyotype thus falls under Stebbins’ [18] category B of asymmetry. According to Paszko [16] higher AI index indicates higher levels of karyotype asymmetry. High TF% value (43.36) and low AI index value (3.4) (Table 2) thus indicates moderately symmetrical karyotype in *A. griffithianum*. Huziwara’s [9] TF% value (43.36) was also in accordance to that of Pandita and Mehra [15]. Although there are no previous reports of B chromosomes in *A. griffithianum*, 30 % of the cells studied in either of prophase, metaphase, anaphase and telophase stages showed presence of one B chromosome (Fig. 1). The size of B chromosomes ranges from 2.4 to 2.7 μm (Table 1) which is almost 1/3 of the size of the smallest chromosomes of *A. griffithianum* (8.45 μm) studied, as is usually the case in the other plants as well [17]. It is known that presence of B chromosomes not only impart fitness to the species in difficult growing conditions, but its presence can also prove to be an evolutionary advantage. A detailed study on the origin or effect of B chromosome in *A. griffithianum* was not done in the present study. But it may be argued that since the plants of *A. griffithianum* studied were collected from alpine and temperate regions of Western Himalayas, the presence of the B chromosome may provide an adaptive advantage to the plants growing under such harsh conditions. The adaptive significance of B chromosomes in *A. griffithianum* in the natural population thus needs further investigation.

**Acknowledgments** Maumita Bandyopadhyay acknowledges the Young Scientist Project, Science and Engineering Research Board, Department of Science and Technology, Government of India, for financial assistance. Authors acknowledge MTA with NBPG and also thank Dr. K. S.Negi, NBPGR, Bhawal, for sampling *Allium griffithianum* plant material.

**References**

Novel cytogenetic resources of wild Allium (Amaryllidaceae) from India

Mou Dutta · Kuldeep Singh Negi · Maumita Bandyopadhyay

Received: 22 September 2014 Published online: 28 February 2015 © Archana Sharma Foundation of Calcutta 2015

Abstract India is home to around 40 species of Allium, out of which a majority are found in the wild in the higher reaches of the Eastern and Western Himalayas. Changing environmental conditions and various anthropogenic interventions have threatened the existence of many of these wild species, most of which are not cytologically characterized. In this paper, novel cytotypes of Allium carolinianum and Allium fasciculatum are reported for the first time from India. Detailed cytological investigations revealed tetraploidy in A. carolinianum (2n=4x=32) and in A. fasciculatum (2n=4x=40). The karyotype of A. carolinianum is more symmetrical, with majority of the chromosomes having median/median region constrictions [16 M(2SAT)+10 m+2sm+3st+1 t] and falls in 2B category of Stebbins’s chart of chromosome asymmetry, while that of A. fasciculatum was found to be asymmetrical, with chromosomes having mostly submedian and subterminal constrictions [1 M+3 m+16sm(2SAT)+18st(2SAT)+2 t], categorized in 3B category of Stebbins’s chart of chromosome asymmetry.

Keywords Allium · Wild · Karyomorphology · Tetraploid · Asymmetry index · Novel cytotypes

Introduction

For a long time, the wild relatives of cultivated plants were relegated to obscurity with all research efforts being concentrated only on their economically important domesticated counterparts. In the last decade or so, it has become obvious that these plants are the true repositories of ‘novel’ genes, which their cultivated relatives have lost due to repeated inbreeding and intensive cultivation practices. This is true for the wild relatives of cultivated Allium L. species too. The genus Allium has around 750 species [15] and is placed under Tribe Allieae, Sub-family Allioideae, Family Amaryllidaceae, Order Asparagales in the recent APG III classification [1]. Well known members of Allium like Allium cepa L. (onion), A. ascalonicum L. (shallot), A. sativum L. (garlic), A. porrum L. (leek), A. tuberosum Rottl. ex Spreng (garlic chives), A. chinense G. Don (Chinese chives) and A. fistulosum L. (Japanese bunching onion) are cultivated all over the World and are important contributors to the agro-economy of many developing countries like India. Like many other crops, the cultivated Allium species too are plagued by the lack of genetic variability, presence of very narrow genetic bases, despite having large genomes, and severe inbreeding depression. In the current scenario of rapid depletion of natural flora due to anthropogenic interventions, a concerted effort should be made to study the wild species of Allium, so that their potential as sources of agronomically important genes can be properly exploited. Many wild species, like A. roylei Streak, A. vavilovii Popov & Vved, A. galanthum Kar. and Kir., and A. fasciculatum Rendle, also have significant contribution to Allium breeding, being progenitors of novel hybrids, and thus to the global food and health needs [14].

Out of 35 to 40 species reported from India [2] 7 to 9 are cultivated and rest are wild [13]. Wild Alliums are distributed both in the Western Himalayas (Jammu and Kashmir, Uttarakhand, Himachal Pradesh) and in the Eastern Himalayan...
regions (Darjeeling hill tracts of West Bengal, Sikkim and the North Eastern States) [13, 18] which have two endemic species i.e., A. stracheyi Baker and A. wallichii Kunth [18]. Most of the wild Allium species, A. wallichii, A. victorialis L., A. griffithianum Boiss, A. ursinum L., A. roylei and A. carolinianum DC are medicinally important and utilised locally. Over-exploitation of these wild Alliums, without back-up conservation strategies, has made some wild Allium species rare, for example, A. roylei and A. carolinianum. Over-exploitation of these wild Alliums, without back-up conservation strategies, has made some wild Allium species rare, for example, A. roylei, A. carolinianum, A. griffithianum and A. ursinum. The present study deals with cytological investigations of the wild Alliums from India, very little is known about their cytological status, which is in part due to their restricted distribution in the alpine Himalayas.

A detailed study of important cytological parameters like chromosome numbers and size, chromosome morphology, karyotype characters are necessary prerequisites to genetically characterize any plant species. The present study deals with cytological investigations of the wild Allium carolinianum and the predominantly wild (though occasionally cultivated) Allium fasciculatum. A. carolinianum, locally known as “Pharan” or “Lahsooniya”, is frequent on the stony slopes and drier areas in alpine zones of North-West Himalayas in India [13]. Bulbs and young leaves are cooked as vegetables and dried leaves are used as condiment by the locals. A. fasciculatum plants, although common in Bhutan, are also found in wild in Sikkim and Arunachal Pradesh of India. They are locally known as “Zap” and are used as vegetables. We report the karyomorphological analysis of the novel cytotypes of wild A. fasciculatum and A. carolinianum, for the first time from India.

**Methods**

**Plant material**

Rooted plants of A. carolinianum (Accession number IC 353527) and A. fasciculatum (Accession number NG 3176) were collected from alpine regions of Uttarakhand, and from Sikkim and Arunachal Pradesh, respectively, morphologically characterized, and maintained in the field germplasm collection of Allium at the National Bureau of Plant Genetic Resources, Regional Station Niglal, Bhowali, Uttarakhand [13, 18].

**Mitotic study**

For mitotic study, young root-tips, 0.5–1 cm in length, were washed in water, then pre-treated in 0.002 M 8-hydroxyquinoline or para-dichlorobenzene solution (8 °C, 3–4 h), and fixed in 3:1 absolute ethanol: glacial acetic acid (10 °C for 12–16 h). The root tips were stained in 2 % acet-orcein and 1(N) HCl mixture (9:1) (room temperature, 45 min) and finally squashed in 45 % acitic acid on grease-free slides, after macerating in 45% acetic acid (5–10 min, room temperature). Data for karyotype analysis of the investigated two species are based on at least ten independent plates from five root tips.

**Karyomorphology**

Well scattered metaphase plates (with properly condensed chromosomes) were selected under microscope (Carl Zeiss, Primostar) and photographed using AxioCamERc5s Camera (Carl Zeiss). Chromosome images were analysed using software packages (Zeiss Axiovision LE 4.3) and the images in pixel unit were converted to micrometer with reference to a standard scale (stage micrometer). Detailed chromosomal analyses were done as reported earlier by Dutta and Bandyopadhyay [3, 4]. For detailed karyotype analysis, chromosome number and values of measurements such as length of long arm (LA), length of short arm (SA), total length of chromosome (TL=LA+SA), standard deviation of chromosome length (SC), mean chromosome length (XCL), centromeric index (CI=SA/TL×100), standard deviation of centromeric index (SIC), mean centromeric index (XIC), value of relative chromatin (VRC=ΣTL/n) were calculated. Karyotype asymmetry was evaluated using Huziwara’s [9] total form percent (TF%) and Zarco’s [25] intra- and inter-chromosomal asymmetry indexes (A1 and A2). Classification of karyotypes in relation to their degree of asymmetry according to Stebbins [23] was calculated. The coefficients of variation of chromosome length (CVCL), chromosome index (CVCI) and asymmetric index (AI) were calculated based on Paszko [19] Chromosomes were classified according to Levan et al., [12]. Photo karyograms and idiograms were prepared on the basis of chromosome size and the nature of centromeric index.

**Results**

Morphological and karyomorphological analysis of species in the present study

The plants were collected from wild, subsequently identified and catalogued by Dr. K.S. Negi and maintained in the Field Gene Bank, Bhowali. The morphological characteristics of the plants studied were compared to earlier reports of the same collection [13].

The chromosome numbers, numerical data on the karyotype parameters and karyomorphological characteristics studied are summarized in Tables 1 and 2 respectively. Well scattered mitotic metaphase plates, karyograms and ideograms representing the same plate, are depicted in Figs. 1 and 2.
**Allium carolinianum**

Herbs (15–40 cm), bulbs brownish, oblong or narrowly ovoid (3–4×1.5 cm), scales fibrous, papery, leaves 4–6, flat, thick, obtuse at apex, umbel globose or hemispherical, tepals purple to pink.

Karyomorphological study revealed that all the root tips of *A. carolinianum* consistently showed 2n=4x=32. The chromosome size ranged from 5.47 to 12.86 μm, in the mitotic metaphase plates. On the basis of proportion of chromosomes (0.81) with arm ratio lesser than 2:1 and ratio of longest to shortest chromosome (2.35), the karyotype falls into 2B category of Stebbins’ chart of chromosome asymmetry [23]. Value of relative chromatin (VRC) was found to be 14.20 μm. The total form percent or average centromeric index (TF%) derived from the total length of short arms in chromosome set and total chromosome length in set was 42.75 [9]. The intrachromosomal asymmetry index (A₁) calculated from mean length of short and a long arm in every homologous pair was 0.22. The interchromosomal asymmetry index (A₂) calculated from standard deviation and the mean chromosome length [25] was 0.19. Asymmetry index (AI) value [19] which was derived from the mean data related to chromosome length and centromeric index, was 5.49 (Table 2). Most of the chromosomes had median (M or m) constrictions (Table 1). Secondary constriction was present at the subterminal (st) or terminal position on four chromosomes with submedian (sm) or subterminal (st) primary constrictions (Figs. 1 and 2). The mean karyotype formula from ten individual metaphase plates was deduced to be 16 M(2SAT)+10 m+2sm+3st+1 t.

**Allium fasciculatum**

Herbs (10–30 cm), bulbs ovoid (3×2 cm), or insignificant, surrounded with coarse parallel fibres, roots many, fleshy, fusiform or cylindric, leaves 5–8, basal, linear, umbels globose, numerous flowers, spathe broadly ovate, tepals white.

Karyomorphological study revealed that all the root tips of *A. fasciculatum* consistently showed 2n=4x=40. The chromosome size ranged from 6.86 to 20.07 μm, in the mitotic metaphase plates. On the basis of proportion of chromosomes (0.1) with arm ratio lesser than 2:1 and ratio of longest to shortest chromosome (3.2), the karyotype falls into 3B category of Stebbins’ chart of chromosome asymmetry [23]. Value of relative chromatin (VRC) was found to be 20.54 μm. The total form percent or average centromeric index (TF%) derived from the total length of short arms in chromosome set and total chromosome length in set was 27.26 [9]. The intrachromosomal asymmetry index (A₁) calculated from mean length of short and a long arm in every homologous pair was 0.61. The interchromosomal asymmetry index (A₂) calculated from standard deviation and the mean chromosome length [25] was 0.28. Asymmetry index (AI) value [19] which was derived from the mean data related to chromosome length and centromeric index, was 10.87 (Table 2). Most of the chromosomes had subterminal (st) and submedian constrictions (Table 1). Secondary constriction was present at the subterminal (st) or terminal position on four chromosomes with submedian (sm) or subterminal (st) primary constrictions (Figs. 1 and 2). The mean karyotype formula from ten individual metaphase plates was deduced to be 1 M+3 m+16sm(2SAT)+18st(2SAT)+2 t.

**Discussion**

It has been reported that only 10% of the 750–780 species of *Allium* known, are [5, 6, 14]. A majority of the wild *Allium* species are believed to harbor unexploited genes coding for agronomic traits, including productivity, disease resistance

---

**Table 1** Comparative karyotype analysis of two novel polyploid cytotypes of *Allium*

<table>
<thead>
<tr>
<th>Species</th>
<th>Somatic chromosome number (2n)</th>
<th>Ploidy level</th>
<th>Karyotype formula</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Allium carolinianum</em></td>
<td>32</td>
<td>4x</td>
<td>16 M(2SAT)+10 m+2sm+3st+1 t</td>
</tr>
<tr>
<td><em>Allium fasciculatum</em></td>
<td>40</td>
<td>4x</td>
<td>1 M+3 m+16sm(2SAT)+18st(2SAT)+2 t</td>
</tr>
</tbody>
</table>

**Table 2** Karyomorphological characteristics in two novel polyploid studied species of *Allium*

<table>
<thead>
<tr>
<th>Species</th>
<th>Range SC-LC (μm)</th>
<th>Ratio LC/SC</th>
<th>Proportion of chromosomes with arm ratio&lt;2:1</th>
<th>Karyotype category according to Stebbins’</th>
<th>VRC (μm)</th>
<th>TF%</th>
<th>A₁</th>
<th>A₂</th>
<th>AI</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Allium carolinianum</em></td>
<td>5.47–12.86</td>
<td>2.35</td>
<td>0.81</td>
<td>2B</td>
<td>14.20</td>
<td>42.75</td>
<td>0.22</td>
<td>0.19</td>
<td>5.49</td>
</tr>
<tr>
<td><em>Allium fasciculatum</em></td>
<td>6.21–20.07</td>
<td>3.20</td>
<td>0.1</td>
<td>3B</td>
<td>20.54</td>
<td>27.26</td>
<td>0.61</td>
<td>0.28</td>
<td>10.87</td>
</tr>
</tbody>
</table>

**Abbreviations:** SC the shortest chromosome, LC the longest chromosome, VRC value of relative chromatin, A₁ intrachromosomal asymmetry index, A₂ interchromosomal asymmetry index, AI Asymmetry index (CV<sub>Ch</sub>×CV<sub>CI</sub> / 100), CV<sub>Ch</sub> component expressing the relative variation in chromosome length, CV<sub>CI</sub> component expressing the relative variation in centromeric index.
and secondary metabolism. Allium species show variation in several cytological characters like basic chromosome number, ploidy level and genome size. The somatic chromosome number ranges from 2n=16–64, the basic chromosome number being x=7, 8, 9, 10 and 11. The ploidy level also varies from 2x to 8x [5, 15, 16].

Despite being one of the few cytologically very well studied genera, the genetics of Allium is still not well understood, due to their large and complex genomes. Detailed cytological analysis is a prerequisite in our understanding of such large and complex genomes, which can further help in conservation and utilization of these important genetic resources. In India, not much of cytological information about the wild Alliums is available. Our cytological investigations revealed, two novel cytotypes, a tetraploid A. carolinianum (2n=4x=32) and a tetraploid A. fasciculatum (2n=4x=40), both of which are first reports from India.

Although many karyological surveys of the genus Allium are being undertaken, published and indexed, there are no published reports of chromosome study on A. fasciculatum and A. carolinianum from India. Authors like Zakirova and Nafanailova [26], Yang and Wu [24], Ohri and Pistrick [16], Hongguan et al. [7], Oyuntselsetseg et al. [17] have reported cytology of A. carolinianum populations from other parts of
Asia. Reports on the cytology of *A. fasciculatum* population from China were communicated by Huang et al. [8], Jie-Mei et al. [10], Hongguan et al. [7].

*A. carolinianum* belongs to subgenus *Polyprason* of genus *Allium* and the basic chromosome number of this group is reported to be \(x = 8\) [5]. The present cytological analysis revealed that, the population of *A. carolinianum* studied, has 32 chromosomes in each mitotic metaphase cell. The estimated asymmetry index (AI) value 5.49 denoted a moderately symmetrical karyotype. The interchromosomal asymmetry index \((\text{AI}_1)\) was 0.19, with chromosome length varying between 5.47 and 12.86 μm. TF% and \(\text{AI}_1\) of the species were 42.75 and 0.22 respectively, verifying the predominance of chromosomes with median constriction in the karyotype. The karyotype of *A. carolinianum* is more symmetrical among the two species studied and falls into 2B category of Stebbins’s chart of chromosome asymmetry [23]. Previous cytological reports of *A. carolinianum* include those of Hongguan et al. [7], who reported that these plants from Qinghai-Tibetan Plateau had mitotic chromosome number of \(2n=16\), and deduced that its basic chromosome number should be \(x = 8\). They reported the karyotype formula of the species as 14 M+2sm(2SAT) and the asymmetry of karyotype as 2A according to Stebbins’s table of chromosome asymmetry [23]. Yang and Wu [24], Huang et al. [8] and Ohri and Pistrick [16] also reported \(2n=16\) in *A. carolinianum*, thus confirming its diploid nature. Zakirova and Nafanailova [26] reported the tetraploid nature of *A. carolinianum* (\(2n=32\)) from a population in south Kazakhstan. Recently Quntsetseg et al. [17] reported \(2n=32\) for *A. carolinianum* from Mongolia which consists of 28 metacentric and 2 pairs of acrocentric chromosomes the latter with very small diffuse satellites. The population of *A. carolinianum* that we studied from India is cytologically very similar to the tetraploid population reported from Outer Mongolia, with 32 chromosomes and a predominance of metacentric chromosomes [16 M(2SAT)+10 m+2sm+3st+1 t]. We believe that this tetraploid cytotype of *A. carolinianum* is either a spontaneous auto-tetraploid originating from a diploid ancestor like the Chinese population (which share gross chromosomal similarities, except the ploidy) or the remnant of a now geographically disjunct part of the Kazakhstan or Mongolia tetraploid population. This is also the only report of chromosome number of *A. carolinianum* from India from the best of our knowledge.

We studied the cytological parameters of a novel tetraploid cytotype of *A. fasciculatum* from India, the first of its kind ever reported, and the only report from India. The somatic chromosome of *A. fasciculatum* studied was 40 in each mitotic metaphase cell and the asymmetric index (AI) was estimated to be 10.87, denoting high heterogeneity of chromosome length and/or centromeric index. In the investigated population the interchromosomal asymmetry index \((\text{AI}_2)=0.28\) was also high, differing in chromosome length (6.86 to 20.07 μm). TF% and \(\text{AI}_1\) of the species were 27.96 and 0.61 respectively, both the values verifying the predominance of submedian (sm) and subterminal (st) chromosomes in the karyotype. So, the karyotype of *A. fasciculatum* was found to be asymmetrical and falls into 3B category of Stebbins’s chart of chromosome asymmetry [23]. Terminal secondary constrictions were found on four chromosomes. *A. fasciculatum* belongs to the subgenus *Amerallium* and the basic chromosome number of this group is \(x = 10\), 11 [5]. Jie-Mei et al. [10] confirmed that the basic chromosome number of *A. fasciculatum* is \(x = 10\). They reported the karyotypes of three Chinese populations of *A. fasciculatum*, and resolved the karyotype formula of one population (from Dagze of Xizang) to be \(2n=2x=20=4m+10sm+2t(2SAT)+4T\), another population from Xiangcheng of Sichuan to be \(2n=2x=20=10sm+6(2SAT)+4T\) and the third population from Lixiang of Sichuan to be \(2n=2x=20=6m+10sm+2t(2SAT)+2T\). In a later study Hongguan et al. [7] reported that the karyotype formula of *A. fasciculatum* \((2n=2x=20)\) from Lixiang of Sichuan locality was 6 M+6sm+4st+4 t with 1SAT chromosome, presumably collected from the same locality as the third population of Jie-Mei et al. (1998). Another population collected from Xiangcheng of Sichuan locality in Qinghai-Tibetan Plateau, which was the same locality as the second population of Jie-Mei et al. [10] had a karyotype formula of 2 M+8sm+10 t with 2SAT chromosomes. Thus, cytological studies of *A. fasciculatum* populations from same localities (Lixiang and Xiangcheng of Sichuan) but by different groups and at different times reveal difference in the karyotypes, possibly indicating an ongoing karyotypic rearrangement in those populations. Our cytological analysis of *A. fasciculatum* showed a mitotic chromosome number of 40, but the karyotype formula of 1 M+3 m+16sm(2SAT)+18st(2SAT)+2 t was broadly similar to that of the *A. fasciculatum* population from Dagze of Xizang locality [10] and also from Lixiang of Sichuan locality [7]. Thus, it may be argued that the tetraploid population of *A. fasciculatum* studied from India is a spontaneous autotetraploid originating from the diploid Chinese populations, possibly as an adaptation strategy, but detailed meiotic studies are necessary to prove such a hypothesis. Another interesting observation by the previous authors was that the karyotype of *A. fasciculatum* from China was very asymmetrical. The Indian population of *A. fasciculatum* studied also showed asymmetrical karyotype falling under 3B category of Stebbins’s table of chromosome asymmetry [23]. In fact, Huang et al. [8] proposed that *A. fasciculatum* had the most asymmetrical karyotype in the Sect. Bromatorrhiza of the genus *Allium*, which according to Jie-Mei et al. [10] may be due to their fairly recent origin. It may be argued that the *A. fasciculatum* populations reported earlier from China have
restricted distribution, and hence lower chromosome number, while the tetraploid population of \textit{A. fasciculatum} that we studied has a wider distribution range, possibly from Bhutan to Sikkim and Arunachal Pradesh of India. It has been reported earlier that the higher polyploids have greater capability to colonize new habitats, and polyploidization may be an adaptive strategy of the plant to colonize and survive difficult terrains. This argument may be used to explain the occurrence of the tetraploid \textit{A. fasciculatum} populations in alpine Himalayas.

It has been hypothesized that during genome evolution by chromosome rearrangements there may be repeating cycles of asymmetry to symmetry of complements making relationships between karyotypes difficult to deduce based on just the parameter of karyotype symmetry or asymmetry [11]. Again it has been argued that a symmetric karyotype may not always indicate the ’primitive’ nature of the specimen and some other parameters should also be included while making such an assessment [21]. In \textit{Allium}, the general convention is to consider symmetrical, homogeneous karyotypes as primitive, indicative of a stable population growing under minimum stress, while heteromorphic and asymmetrical karyotypes generally represent more advanced and evolving karyotypes that are constantly adapting to prevalent environmental conditions. Peruzzi et al. [20] argued that in Liliaceae the ancestral karyotypes were possibly those which had low CV\textsubscript{Cl} values and relatively high CV\textsubscript{CL} values. Thus, a more comprehensive karyotype analyses of the genus \textit{Allium} is necessary to assess karyotype evolution trends within the genus.

The occurrence of the polyploid populations of the generally diploid species of \textit{Allium} as reported in the present study indicates the continuous genome modifications that the wild \textit{Allium} species undergo. \textit{A. fasciculatum} with asymmetrical karyotype (AI=10.87, 3B) perhaps indicates a still evolving karyotype. Asymmetric index (AI) of \textit{A. carolinianum} karyotype (AI=10.87, 3B) perhaps indicates a still evolving \textit{Allium} evolution. The most interesting facet of this study was that intermediate position in terms of population stability and cytotypic rearrangements and changes as indicated by high spontaneous autotetraploid that is undergoing extensive karyotypic rearrangements there may be repeating cycles of chromosome changes: reliable indicators of the direction of evolution? Chromosome changes in plant evolution. Taxon. 1970;19:172–8.


Numerical taxonomic studies on Indian *Allium* species

Mou Dutta and Maumita Bandyopadhyay*
Plant Molecular Cytogenetics Laboratory, Centre of Advanced Studies, Department of Botany, University of Calcutta, 35, Ballygunge Circular Road, Kolkata 700 019, West Bengal, India.

The taxonomy of *Allium*, is complicated with a great number of synonyms and intrageneric groupings, with disagreements about the subdivision of the genus in the intrageneric level and also in the knowledge of the geographical and evolutionary relationships. Classical taxonomic treatment of the Indian *Allium* too is plagued by the lack of resolution of character states, especially at the intrageneric levels.

Numerical taxonomy groups taxonomic units into taxa by numerical methods based on their character states. The application of numerical taxonomic methods in plant taxonomy offers a series of advantages over classical morpho-taxonomy, most importantly, objectivity. In the present study, an attempt was made to carry out numerical taxonomic studies on *Allium* collected from various parts of India. For the numerical analysis twenty one operational taxonomical units (OTU) were selected based on the selected morphological variations. Characters were coded following accepted norms as dichotomies or presence/absence characters where 0 codes for absence and 1 for presence of the feature or as quantitative characters which are either two- or multistate where the rank is of no significance. The data matrix was subjected to the cluster analysis. The Euclidean distance measured similarity matrix and a dendrogram was constructed by using the complete linkage method with the NTSYSpc-2.02i software. The main groups in the dendrogram produced by the numerical analysis were compared with the recent classification of Friesen et al. (2006) and discrepancies between the two were discussed.

**Key words:** Morphology, numerical taxonomy, operational taxonomical unit (OTU), dendrogram, NTSYSpc-2.02i software

INTRODUCTION

The genus *Allium* includes wide range of morphologically variable species. Species of the genus *Allium* are herbs with tunicate bulbs and onion like or garlic like odour when fresh. Bulbs are solitary or clustered, rhizome may be present or absent. Leaves are sessile, with a closed leaf sheath at base, blade linear or flat, fistulose or solid, angled, v-shaped, semiterete or terete in cross section. Inflorescence is terminal umbel, sometimes with bulbets, enclosed in spathe like bract. Flowers are pedicillate and bisexual. Perianth segments are six in number, free or united. Filaments are usually connate and adnate at base, entire or toothed. Ovary has one or several ovules per locules, septa containing nectaries; style simple; stigma capitate to three lobed. Capsule is loculicidal. Seeds are black, rhomboidal or spheroidal.
These variations in morphological characters makes the taxonomy of *Allium*, based on nectary morphology, inflorescence structure, vegetative anatomy, bulb or rhizome morphology, basic chromosome number, and biogeographic patterns, complicated with a great number of synonyms and intrageneric groupings (Nguyen et al., 2008). No comprehensive monograph of the genus has been compiled since Regél’s in 1875 (Berg et al., 1996). Again Regél accepted only 285 species, but present estimated *Allium* species is 850 (Keusgen et al., 2011; Wheeler et al., 2013; Huang et al., 2014). Moreover, there are many gaps in the morpho-taxonomical treatment of *Allium* due to disagreement about the subdivision of the genus in the intrageneric level and also in the knowledge of the geographical and evolutionary relationships (Berg et al., 1996). In the Regél’s 1875 monograph the genus *Allium* is arranged in six sections depending mainly on morphological characters like presence or absence of rhizome. Several authors like Vvedenskii (1935) based on morphological characters like nature of bulbs, rhizome, leaves, pedicels e.t.c placed the species of U.S.S.R into sections following Regél’s scheme in general. But he omitted the section *Schoenoprasum* transferring the species either into section *Rhizirideum* or into sections *Cepa* Prokh. and *Phyllodon* (Salish.). Hermann (1939) also published a sectional scheme for the species of *Allium* in Europe following Regél’s (1875) scheme. Stearn (1946) circumscribed the species of genus *Allium* of North America and Wendelbo (1969) of Iran and Afghanistan into different sections depending on morphological characters like presence or absence of rhizome mainly. The schemes of sections by all these authors were regional and based on small number of characters. Numerical taxonomic studies on species of subgenus *Rhizirideum* by El-Gadi and Elkington (1977) and subgenus *Mohium* by Badr and Elkinston (1978) were based on relatively large numbers of morphological, cytological and chemical characters. These studies were again restricted on rhizomatous taxa of *Allium* only and not the entire genus. Hanelt et al. (1991) studied 220 species of the genus *Allium* from living collection of the Department of Taxonomy, IPK Gatersleben under various aspects by morphological, geographical, cytological, anatomical, serological and numerical methods. The evaluation was synthesized into an intrageneric classification with 6 subgenera. To avoid taxonomic confusion or ambiguity, molecular phylogenetic analysis of *Allium* has been undertaken by different authors recently. The first approach to structure the genus *Allium* by molecular markers was by Berg et al. (1996). They recognized the subgenera proposed by Hanelt et al. (1991), but found that subgenera *Amerallium* and subgenera *Bromatorrhiza* could not be clearly distinguished. Nguyen et al. (2008) focussed on the Western North American species while Hao et al. (2002) studied the Korean species of *Allium* section *Sacculiferum*. The most comprehensive study was by Friesen et al. (2006) who classified 196 species of the genus into 15 monophyletic subgenera from the living collection of *Allium* at the Department of Taxonomy, IPK Gatersleben, based on nuclear ribosomal DNA ITS sequences. Phylogenetic analysis by Li et al. (2010) reveals that although the genus *Allium* is monophyletic but the subgenera are not. This taxonomic synopsis divides Chinese *Allium* into 13 subgenera and 34 sections.

To the best of our knowledge numerical taxonomic treatment of Indian *Allium* especially wild species is lacking. Taxonomic treatment of Indian *Allium* is needed, due to the fact that intrageneric placement of some Indian species is lacking even in the most accepted classification by Friesen et al. (2006). In this paper numerical taxonomic methods are used to study the relationships of twenty one samples, collected from different parts of India, both cultivated and wild. The study compares seventeen different species based on thirty morphological characters.

**MATERIAL AND METHODS**

In the present investigation 21 O.T.U.s comprise samples of seventeen species collected from different parts of India. The list of samples, accession number and their place of collection are listed in Table 1. Morphological measurements and photographs (Fig. 1) of different parts of the samples were taken in their fields of collection. The plant samples were identified by comparisons with relevant references and proper taxonomic descriptors.

Numerical Analysis was performed using the NTSYSpc version 2.02i programme (Rohlf, 1998) which compares each O.T.U. with every other, calculating a percentage similarity for each pair of O.T.U.s. A hierarchical cluster analysis was done from this similarity matrix which is presented as a UPGMA
dendrogram (Fig. 2). The morphological characters employed in this analysis were coded in three different ways: (1) dichotomies or presence/absence characters, where 0 codes for absence and 1 for presence (2) qualitative characters which are either two or multistate where the rank is of no significance (3) quantitative characters where the O.T.U. with the lowest value is given the code 1 and highest value is given maximum code. Description, types and coding ranges of all thirty morphological characters are given in Table 2. All the characters are given equal weightage.

RESULTS AND DISCUSSION

In the UPGMA dendrogram the distances corresponded to the morphological similarities calculated by simple matching procedure (100% similarity = 1.0). Qualitative and quantitative morphological characters of the studied samples showed a wide range of variation. Marked variations were observed in characters like bulb shape and maximum cross-sectional diameter, nature of rhizome, bulb tunic colour and texture, leaf length and breadth, shape of leaf cross section, tepals colour and size, nature of midvein in tepals, filament size and nature of base. In the present study the 21 O.T.U.s were split into two major groups (I and II) at the 0.25 similarity level in the dendrogram based on the hierarchical cluster analysis (Fig 1). Group I divided into two subgroups (I.1 and I.2). The first subgroup (I.1) includes all the morphotypes of *A. cepa*, *A. ascalonicum*, *A. x cornutum*, *A. fistulosum* and *A. griffithianum* separated at 0.41 similarity level from the second subgroup (I.2) comprising all the morphotypes of *A. sativum* and *A. ampeloprasum*. The *A. cepa* branch of the first subgroup (I.1) split into two small subgroups (one containing *A. cepa* morphotype Nashik red, *A. cepa* morphotype white and *A. cepa* morphotype aggregatum and another *A. ascalonicum* and *A. x cornutum*) at the 0.81 similarity level mainly based on their nature of bulbs (Fig. 2). The morphotypes of the species *A. sativum* were also separated into two small subgroups (one containing *A. sativum* morphotype multiple small cloves, *A. sativum* morphotype multiple large cloves and another only *A. sativum* morphotype one clove) at the 0.85 similarity level mainly based on the number and size of cloves within the same bulb. The second major group (II) also split into two subgroups (II.1 and II.2) at 0.30 similarity level. Subgroup (II.1) includes *A. chinense*, *A. roylei*, *A. carolinianum*, *A. schoenoprasum* and *A. auriculatum* and subgroup (II.2) includes *A. tuberosum*, *A. hookeri*, *A. fasciculatum*, *A. cernuum* and *A. macranthum*. In the latest Angiosperm Phylogeny Group classification, the genus *Allium* is placed under Tribe Allieae, Sub-family Allioideae, Family Amaryllidaceae, Order Asparagales (APG III, 2009). Around 35-40 species of *Allium* are reported in India (Dasgupta, 2006) among which some 7 to 9 species are cultivated in India, others are found in the Himalayas in the wild (Negi, 2006). Wild Alliums are distributed both in the Western Himalayas (Jammu and Kashmir, Uttaranchal, Himachal Pradesh) and in the Eastern Himalayan region (Darjeeling hill tracts of West Bengal, Sikkim and the North Eastern States) (Negi, 2006; Pandey et al., 2008). Morphology of *Allium* is very interesting having wide range of variations. Although various regional revision of the genus *Allium* was done earlier, taxonomic treatment of Indian *Allium* is lacking may be due to their restricted distribution in the high altitude and complicated and controversial intrageneric classification. So, the present study focuses on the numerical taxonomic treatment of twenty one taxa of Indian *Allium* having marked geographical and morphological variations.

The intrageneric circumscription proposed by Friesen et al. (2006) based on morphological and molecular data, segregates the species into subgenera which are in turn grouped as three main evolutionary lines: i. subgenera: *Amerallium*, *Nectaroscordum*, *Microscordum*; ii. subgenera: *Melanocrommyum*, *Caloscordum*; iii. subgenera: *Anguinum*, *Porphyroprason*, *Vvedenskya*. The correspondence of the subgenera/sections of the genus to the main groups and subgroups of the present dendrogram was noted and position of

---

*On Indian Allium species*
Table 1: Accession number, subgenus, section and collection details of *Allium* species studied

<table>
<thead>
<tr>
<th>Accessions</th>
<th>Taxa</th>
<th>Cultivar/ Mornhotvpe/ NBPGR Accession No.</th>
<th>Subgenus/ Section*</th>
<th>Collected from</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cepa 1</td>
<td><em>Allium cepa</em> L.</td>
<td>Nashik Red</td>
<td>Cepa/ Cepa</td>
<td>New Market, Kolkata, West Bengal</td>
</tr>
<tr>
<td>Cepa 2</td>
<td><em>Allium cepa</em> L.</td>
<td>white onion</td>
<td>Cepa/ Cepa</td>
<td>New Market, Kolkata, West Bengal</td>
</tr>
<tr>
<td>Cepa 3</td>
<td><em>Allium cepa</em> L.</td>
<td>aggregatum</td>
<td>Cepa/ Cepa</td>
<td>New Market, Kolkata, West Bengal</td>
</tr>
<tr>
<td>Cepa 4</td>
<td><em>Allium ascalonicum</em> L.</td>
<td>Pran</td>
<td>Allium/ Allium</td>
<td>Bardhaman, West Bengal</td>
</tr>
<tr>
<td>Pran</td>
<td><em>Allium x cornutum</em> Clementi ex Vis.</td>
<td>CUH 20019</td>
<td>Cepa/ Schoenoprasum</td>
<td>Srinagar local Market, Jammu and Kashmir</td>
</tr>
<tr>
<td>MB2</td>
<td><em>Allium fistulosum</em> L.</td>
<td>NIC-20231</td>
<td>Cepa/ Schoenoprasum</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB3</td>
<td><em>Allium schoenoprasum</em> L.</td>
<td>English chives</td>
<td>Cepa/ Schoenoprasum</td>
<td>Sutton and Sons, Kolkata (seeds sourced from Paignton, England)</td>
</tr>
<tr>
<td>MB4</td>
<td><em>Allium chinense</em> G. Don</td>
<td>Chinese chives</td>
<td>Cepa/ Schoenoprasum</td>
<td>Shillong local Market, Assam</td>
</tr>
<tr>
<td>Sat 1</td>
<td><em>Allium sativum</em> L.</td>
<td>multiple small cloves</td>
<td>Allium/ Allium</td>
<td>New Market, Kolkata, West Bengal</td>
</tr>
<tr>
<td>Sat 2</td>
<td><em>Allium sativum</em> L.</td>
<td>multiple large cloves</td>
<td>Allium/ Allium</td>
<td>New Market, Kolkata, West Bengal</td>
</tr>
<tr>
<td>Sat 3</td>
<td><em>Allium sativum</em> L.</td>
<td>one clove</td>
<td>Allium/ Allium</td>
<td>New Market, Kolkata, West Bengal</td>
</tr>
<tr>
<td>Leek 1</td>
<td><em>Allium anepeloprasum</em> L.</td>
<td>Leek</td>
<td>Ameerullium/ Bromathiraza</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 6</td>
<td><em>Allium griffithianum</em> Boiss.</td>
<td>IC-353540</td>
<td>Ameerullium/ Lopioprason</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 7</td>
<td><em>Allium roylei</em> Stearn</td>
<td>IC-353546</td>
<td>Polyprason/ Orieprason</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 8</td>
<td><em>Allium carolinianum</em> DC.</td>
<td>IC-353627</td>
<td>Polyprason/ Falcatifolia</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 9</td>
<td><em>Allium hookeri</em> Thwaites</td>
<td>HN-2800</td>
<td>Polyprason/ Orieprason</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 10</td>
<td><em>Allium fasciculatum</em> Rendle</td>
<td>SN05</td>
<td>Ameerullium/ Bromathiraza</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 11</td>
<td><em>Allium macranthum</em> Baker</td>
<td>NNMK-3236</td>
<td>Ameerullium/ Lopioprason</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 12</td>
<td><em>Allium cernuum</em> Roth.</td>
<td>IC-353540</td>
<td>Butomissa/ Butomissa</td>
<td>Experimental Garden, Department of Botany, University of Calcutta</td>
</tr>
<tr>
<td>MB 13</td>
<td><em>Allium tuberosum</em> Rottl. ex Spreng.</td>
<td>Garlic chives</td>
<td>Ameerullium/ Lopioprason</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
<tr>
<td>MB 14</td>
<td><em>Allium auriculatum</em> Kunth</td>
<td>IC-353533</td>
<td>Cyathophora/ Coleoblastus</td>
<td>NBPGR, Bhowali, Uttarakhand</td>
</tr>
</tbody>
</table>

*According to Friesen et al. (2006), Li et al. (2010) and USDA, ARS, GRIN.

The species like *A. auriculatum*, *A. x cornutum* (Pran), *A. fasciculatum* and *A. macranthum* were discussed.

**Sub-group I.1**

The sub-group I.1 corresponds to the subgenus/section *Cepa/Cepa* (Friesen et al., 2006), includes all the morphotypes of *A. cepa*, *A. ascalonicum*, *A. x cornutum*, *A. fistulosum* and *A. griffithianum*. All these species share many common morphological features like ovoid shaped bulb, scarious or membranous bulb tunic texture, linear, fistulose leaves, globose umbel, white tepals, exserted stamens. Placement of *A. griffithianum* (subgenus/section *Allium/Avulsea*) in this sub-group (I.1) may be due to the gross morphological similarities with *A. cepa*. Although there is no mention about the position of *A. x cornutum* in the Friesen et al. (2006) classification, this species is placed in same subgroup (I.1) and branch along with *A. cepa* with 82% similarity.

Interestingly *A. chinense* (section: *Sacculiferum*) and *A. schoenoprasum* (section: *Schoenoprasum*) both belonging to subgenus *Cepa* (Friesen et al., 2006) are separated from sub-group I.1 based primarily on distinct morphological characters like narrowly ovoid bulb, membranous white tunic of bulb and purplish tepals. Although *A. schoenoprasum*, *A. chinense* and *A. cepa* were placed in the same subgenus *Cepa* by Friesen et al. (2006) bias towards morphological data
Fig. 2: Morphological Characters, types and coding ranges of characters of O.T.U.s

<table>
<thead>
<tr>
<th>No</th>
<th>Morphological characters</th>
<th>Character types*</th>
<th>Coding Range</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Maximum cross-sectional diameter</td>
<td>3</td>
<td>1-6</td>
</tr>
<tr>
<td>2</td>
<td>Rhizome present/absent</td>
<td>1</td>
<td>0-2</td>
</tr>
<tr>
<td>3</td>
<td>Number of bulbs attached to the same rhizome/same stem base</td>
<td>3</td>
<td>1-6</td>
</tr>
<tr>
<td>4</td>
<td>Number of cloves produced by one bulb</td>
<td>3</td>
<td>0-5</td>
</tr>
<tr>
<td>5</td>
<td>Outer tunic colour</td>
<td>2</td>
<td>1-5</td>
</tr>
<tr>
<td>6</td>
<td>Outer tunic texture</td>
<td>2</td>
<td>1-3</td>
</tr>
<tr>
<td>7</td>
<td>Shape</td>
<td>2</td>
<td>1-4</td>
</tr>
<tr>
<td>8</td>
<td>Nature of roots</td>
<td>2</td>
<td>1-3</td>
</tr>
<tr>
<td>9</td>
<td>Number of leaf sheathing one scape</td>
<td>3</td>
<td>1-5</td>
</tr>
<tr>
<td>10</td>
<td>Lamina length</td>
<td>3</td>
<td>1-5</td>
</tr>
<tr>
<td>11</td>
<td>Shape</td>
<td>2</td>
<td>1-4</td>
</tr>
<tr>
<td>12</td>
<td>Diameter (fistulose leaf) or breadth (laminar leaf)</td>
<td>3</td>
<td>1-5</td>
</tr>
<tr>
<td>13</td>
<td>State of leaf tip</td>
<td>2</td>
<td>1-3</td>
</tr>
<tr>
<td>14</td>
<td>Nature of leaf surface (rough/smooth)</td>
<td>2</td>
<td>1-2</td>
</tr>
<tr>
<td>15</td>
<td>Cross-section shape</td>
<td>2</td>
<td>1-10</td>
</tr>
<tr>
<td>16</td>
<td>Number of scapes produced by one bulb</td>
<td>3</td>
<td>1-3</td>
</tr>
<tr>
<td>17</td>
<td>Length from bulb base to umbel</td>
<td>3</td>
<td>1-5</td>
</tr>
<tr>
<td>18</td>
<td>Number</td>
<td>3</td>
<td>1-3</td>
</tr>
<tr>
<td>19</td>
<td>Shape</td>
<td>2</td>
<td>1-3</td>
</tr>
<tr>
<td>20</td>
<td>Pedicel length, mean of several pedicels in one umbel</td>
<td>3</td>
<td>1-6</td>
</tr>
<tr>
<td>21</td>
<td>Number of flowers per umbel, mean of ten umbels</td>
<td>3</td>
<td>1-7</td>
</tr>
<tr>
<td>22</td>
<td>Perianth colour</td>
<td>2</td>
<td>1-5</td>
</tr>
<tr>
<td>23</td>
<td>Perianth segment shape</td>
<td>2</td>
<td>1-4</td>
</tr>
<tr>
<td>24</td>
<td>Nerves on perianth segments</td>
<td>2</td>
<td>0-3</td>
</tr>
<tr>
<td>25</td>
<td>Outer segment length, mean of ten segments</td>
<td>3</td>
<td>1-6</td>
</tr>
<tr>
<td>26</td>
<td>Inner segment length mean of ten segments</td>
<td>3</td>
<td>1-6</td>
</tr>
<tr>
<td>27</td>
<td>Mean outer filament length</td>
<td>3</td>
<td>1-6</td>
</tr>
<tr>
<td>28</td>
<td>Mean inner filament length</td>
<td>3</td>
<td>1-6</td>
</tr>
<tr>
<td>29</td>
<td>Filament teeth</td>
<td>1</td>
<td>0-3</td>
</tr>
<tr>
<td>30</td>
<td>Stigma shape</td>
<td>2</td>
<td>1-3</td>
</tr>
</tbody>
</table>

*1=Presence/absence characters, 2=Qualitative characters, 3=Quantitative characters

alone can separate them in different clades as was seen in the present study.

**Sub-group I.2**

The second sub-group (I.2) corresponds to subgenus/
section *Allium/Allium* and includes all the morphotypes of *A. sativum* and *A. ampeloprasum*. Both the species have obscure rhizome, white, papery bulb tunic, flat leaf, acute leaf apex, presence of ooth flowers and bulbets in umbel, white tepals. This corresponds directly with the circumscription of Friesen *et al.* (2006).

**Sub-group II.1**

In this sub-group, *A. roylei* (subgenus/section *Polyprason/Oreiprason*) and *A. carolinianum* (subgenus/section: *Polyprason/Falcatifolia*) are placed. *A. roylei* and *A. carolinianum* have rhizomes, membranous/papery bulb tunic, hemispherical umbel, purplish to pink tepals, exserted filaments. *A. roylei* has ovoid bulb, linear, acute apex leaf and base of filament toothed like *A. cepa*, while *A. carolinianum* has oblong bulb, flat obtuse apex leaf and base of filaments entire. Though a member of subgenus *Cyathophora, A. auriculatum* is placed in the sub-group II.1 due their linear leaves with circular cross section, purple coloured tepals and inserted filaments like *A. schoenoprasum*. This species also shares characters with *A. tuberosum* like presence of rhizome, elongate bulb, fibrous bulb tunics and many flowered umbel. Thus, sub-group II.1 is a mixed group drawing members of subgenera *Polyprason, Cepa, and Cyathophora* based on their...
morphological similarities.

Sub-group II.2

This sub-group broadly corresponds to subgenus Amerallium of Friesen et al. (2006). *A. hookeri, A. fasciculatum, A. macranthum* and *A. cernuum* of subgenus Amerallium belongs to sections Bromatorrhiza and Lophioprason respectively due to the absence of rhizome, cylindric bulb and profusely growing thick roots. Although the tepals colour in *A. macranthum* is purplish with prominent nerves the other three have white tepals with very faint nerves. These differences explain the separation of *A. macranthum* in a different branch from the rest of the three at 0.41 similarity level. Cytological and molecular studies were not carried out in the present experiment. All the studied seventeen different Indian species, three varieties of *A. cepa* and three varieties of *A. sativum* were categorised by numerical taxonomy based on morphological data only and is broadly similar to Friesen’s et al. (2006) scheme. Verifying the present findings by cytological and molecular genetics characterization will be worthwhile for the taxonomic treatment of Indian *Allium*.

According to Friesen et al. (2006) *Butomissa* is a small group. Among the accessions of the present study only *A. tuberosum* (subgenus/section *Butomissa/Butomissa*) represent this group. In the present dendrogram *A. tuberosum* is placed under sub-group II.2 along with *A. hookeri, A. fasciculatum, A. macranthum* and *A. cernuum* due cylindrical bulb, flat leaves, hemispherical umbel, profusely rooting bulb, white tepals and inserted filaments. *A. tuberosum* is separated in a different branch at 0.51 similarity level.

**REFERENCES**


GenBank: KT895597.1

Allium cepa cultivar Nashik red 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT895597

FASTA Graphics

Go to:

LOCUS KT895597 677 bp DNA linear PLN 11-NOV-2015
DEFINITION Allium cepa cultivar Nashik red 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT895597
VERSION KT895597.1 GI:949326664
SOURCE Allium cepa (onion)
ORGANISM Allium cepa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Alliioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 677)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 677)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
  Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
  Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES
misc_RNA 1..677
| /organism="Allium cepa"
| /mol_type="genomic DNA"
| /cultivar="Nashik red"
| /db_xref="taxon:4679"
| /country="India: Kolkata"
| /altitude="9 m"
| /collection_date="01-Oct-2014"
| /collected_by="Mou Dutta and Maumita Bandyopadhyay"
| /identified_by="Maumita Bandyopadhyay"
| /note="authority: Allium cepa L."
| /contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
ORIGIN
1 ggaaggatct ttgtagagtt ccttctcgaa caactgtgaa attgtactca tacccgtcga
gggaaggatct ttgtagagtt ccttctcgaa caactgtgaa attgtactca tacccgtcga
61 gaactacgta ttgtgcggt tagcacttgc gtgtgtttgga tgggtttcat ttgctgcctt
catgtttgct tcaattgaag taagatgtag agtagaacta agaaaccggc acggtttgtg
tttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
Allium cepa 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank

Allium cepa 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KU140433.1

FASTA

Go to:

LOCUS KU140433 711 bp DNA linear PLN 08-MAR-2016
DEFINITION Allium cepa 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KU140433
VERSION KU140433.1 GI:1002637584
KEYWORDS .
SOURCE Allium cepa (onion)
ORGANISM Allium cepa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Aliiaceae; Alliaceae; Allium.
REFERENCE 1 (bases 1 to 711)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 711)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT #Assembly-Data-START#
  .Assembly Method: Cap3 Sequence Assembly Programme v. 1999
  .Sequencing Technology: ABI 3500 Genetic Analyzer
   #Assembly-Data-END#
FEATURES source 1..711
   /organism="Allium cepa"
   /mol_type="genomic DNA"
   /cultivar="Chanchi Pyaz (Bengali)"
   /isolation_source="multiple cloves"
   /db_xref="taxon:4679"
   /chromosome="2n=18"
   /country="India: Kolkata"
   /altitude="9 m"
   /collection_date="10-Jan-2015"
   /collected_by="Mou Dutta and Maumita Bandyopadhyay"
   /identified_by="Maumita Bandyopadhyay"
   /note="authority: Allium cepa L."
   /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
   /note="contains 18S ribosomal RNA, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence."
ORIGIN 1 tccgtagttg aacctgccaag aggatctttg tagatgtctt ttcgcaaca ctgtagaat
   61 gtactatac cctgctgaga atcagatatt gtcgcctatt acctgctggt gttgtgat
   121 gtttcttctt ctgctttcct atggagatt gattgtag gattgtggt
   181 accgcctggtg ttcctgtgc ctgctgctcc gcctgctcct ccctgcatt
   241 gcgtcctgct atccacagtg gcttgcagtc gactctgggc aatgctgatt atggctctcg
   301 tctgctgctt gcgatgctg aatacgag aa atggatcct ttcgctgc crttatgctg gttgtgctg
   361 atctgatgc ttcgctgctt gcgatgctgc gcctgctcct cctgcatt
   421 gcctgctgcct gcctgctgct gctgccctc acctactgtg cctgctgctg
   481 gctgctgcct gcctgctgct cctgcatt cctgctgcct gcctgctgcgc
   541 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
   601 aggatgcct ccagcctgtt accatacctt ctcagttgct tctagttgct
   661 aacgtccgct aacctgctg cgtctcttc gacacccgc gttgtgtaag c

1/2
Allium ascalonicum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KU140434.1

FASTA Graphics

Go to:

LOCUS        KU140434                  615 bp     DNA      linear    PLN 08-MAR-2016
DEFINITION   Allium ascalonicum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION    KU140434
VERSION      KU140434.1
KEYWORDS     .
SOURCE       Allium ascalonicum
ORGANISM     Allium ascalonicum
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
             Amaryllidaceae; Alilioideae; Alliaceae; Allium.
REFERENCE    1 (bases 1 to 615)
             Dutta, M., Haque, I. and Bandypadhyay, M.
             Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 615)
             Dutta, M. and Bandypadhyay, M.
             Direct Submission
JOURNAL      Submitted (12-NOV-2015) Department of Botany, University of
             Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT      # # Assembly-Data-START#
             Assembly Method:: Cap3 Sequence Assembly Programme v. 1999
             Sequencing Technology:: ABI 3500 Genetic Analyzer
             # # Assembly-Data-END#
FEATURES     source 1..615
             /organism="Allium ascalonicum"
             /mol_type="genomic DNA"
             /db_xref="taxon:1476995"
             /country=India: Bardhaman"
             /altitude=9 m"
             /collection_date="10-Oct-2014"
             /collected_by="Maumita Bandypadhyay"
             /identified_by="Maumita Bandypadhyay"
             /note="authority: Allium ascalonicum L."
             <i>misc_rRNA</i>
             /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
ORIGIN       1 ttgtgaatgtt acctacattg tgtgagaaact cgtgagaact cgtgagaact
tgtctcactt tgaagtaaga gtagattag
tgtctcactt tgaagtaaga gtagattag
tgtctcactt tgaagtaaga gtagattag
tgtctcactt tgaagtaaga gtagattag
tgtctcactt tgaagtaaga gtagattag
tgtctcactt tgaagtaaga gtagattag
tgtctcactt tgaagtaaga gtagattag
121 aataaatgca cccgcagcgt tgggaggagc gctttgagtt gatgattag
181 tttttttctttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
### GenBank: KT781693.1

**Allium cornutum voucher CUH:20019 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence**

**GenBank: KT781693**

**FASTA**

**Go to:**

**LOCUS** KT781693  612 bp  DNA  linear  PLN 11-NOV-2015

**DEFINITION** Allium cornutum voucher CUH:20019 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

**ACCESSION** KT781693

**VERSION** KT781693.1  GI:949326509

**KEYWORDS**

**SOURCE** Allium cornutum

**ORGANISM**

- Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.

**REFERENCE**

- 1 (bases 1 to 612)  
  **AUTHORS** Dutta,M. and Bandyopadhyay,M.  
  **TITLE** Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences  
  **JOURNAL** Unpublished

- 2 (bases 1 to 612)  
  **AUTHORS** Dutta,M. and Bandyopadhyay,M.  
  **TITLE** Direct Submission  
  **JOURNAL** Submitted (18-SEP-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India

**COMMENT** 

```
##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
```

**FEATURES**

- source
  - Location/Qualifiers
    - 1..612
      - /organism="Allium cornutum"
      - /mol_type="genomic DNA"
      - /specimen_voucher="CUH:20019"
      - /db_xref="taxon:138319"
      - /country="India: Srinagar"
      - /altitude="1585 m"
      - /collection_date="09-Sep-2014"
      - /collection_by="Maumita Bandyopadhyay and Mou Dutta"
      - /identified_by="Maumita Bandyopadhyay"
      - /note="authority: Allium x cornutum Clementi ex Vis."
      - 1..612
      - /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

**misc RNA**

```
1 aaatgttact cataccggtc gagaactaag tattttgcgc gttacacttt gcgcgttgtg
61 gatggtgtcct cttcgcct cttccttctt ctcacattga agtaagaaat gagatataaa
121 taagaaacct gcacggtttg tgcccaaagg ttgttgggttá gaaaagcttg ccacattttt
181 agttgcttct ttgtcttttt ctcaggcttc cgttgactc cgggaacctg tattaagggt
241 cttcgccttc ctauagaaacct gcacgactggt gtaattgcttc gtagcctatt ccctaaaagct
301 aacccctcctg ctttttaagtt cagtttgccgc tcggagccat twggtttagtt cgcscctgt
361 ttggtgccttg tcgcttgctag ctcctaaacc ccccccctag tcggtgagtt cgggtggtg
421 gattgccttt ccgtccctcttt atgtcccccc tattggtttg tggattggtc gcgttcttct
481 ccgcgctcct tattatcgtt ggtttttcag tggtaaaacct gagatgtcc cagatgcgcc gaggagtcct
541 acgcagacag tatacagtat gaaacatttt tcgacgctat gccttagttg cagatgcgcc
601 acatatgcccc acc
```

//

Allium x proliferum voucher N/RP/SSM-2799 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KU145492.1

FASTA Graphics

Go to:

LOCUS KU145492  626 bp  DNA  linear  PLN 09-FEB-2016
DEFINITION  Allium x proliferum voucher N/RP/SSM-2799 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KU145492
VERSION KU145492.1  GI:985651436
KEYWORDS .
SOURCE Allium x proliferum
ORGANISM Allium x proliferum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1  (bases 1 to 626)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2  (bases 1 to 626)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..626
/organism="Allium x proliferum"
/mol_type="genomic DNA"
/specimen_voucher="N/RP/SSM-2799"
/db_xref="taxon:88846"
/country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
/altitude="1706 m"
/collection_date="10-Oct-2014"
/collection_by="Maumita Bandyopadhyay and Mou Dutta"
/note="authority: Allium x proliferum (Moench) Schrad."
/misc_RNA
1.626
/note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
ORIGIN
1 acagctgtga attgtaccca tacccgtcga gaactacgta ttgtgcggt tagcacttgc
61 gctgtttgga tgggttccat ttgctgcctt catctttgct tcaattgaag taagaagtag
121 agtagaaata agaaaccggc acggtttgtg cccaggactg ttgttgttgg aaagcttgcc
181 atcattttga tgtgcttttg ttattccagt gagcgtctga atgactcctg ggaatggata
241 tcttggctct cgtgtcgatg aaaaacgtan cgaaatgcga cacttggtgt gaattgcaga
301 atcccgtgaa ccatctagtc tttgaatgca agttgcgctc gaggccatta ngttgagagc
361 acgtctgttt gggcgtcatg cctccattca ttctaaccac ccacctagtg agtgatggcg
421 gatgtggaga ttgaccctcc gtaccataat ggtgcggttg gtttaagtga atgttgtcgt
481 taggtctacg cgcggcgaat ggtgtatcga gttaacacac gatgtctcta actgcgtcca
541 ggagtcctac gcacgatgta acaataatgt gaaaccattt tcgacgtatg ccttagttgc
601 aagctcggaa catgacccca gatcag
//

Allium fistulosum voucher NIC-20231 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

**GenBank: KT781691.1**

**FASTA**

```plaintext
GenBank

11/14/2015

Allium fistulosum voucher NIC-20231 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT781691.1

FASTA

Go to:

LOCUS KT781691 701 bp DNA linear PLN 11‐NOV‐2015
DEFINITION Allium fistulosum voucher NIC‐20231 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT781691
VERSION KT781691.1 GI:949326505
KEYWORDS .
SOURCE Allium fistulosum (Welsh onion)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 701)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 701)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (18‐SEP‐2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly‐Data‐START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly‐Data‐END##
FEATURES location/qualifiers
misc_RNA <1..>701
/organism="Allium fistulosum"
/mol_type="genomic DNA"
/specimen_voucher="NIC‐20231"
/db_xref="taxon:35875"
/country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhad" /altitude="1706 m" /collection_date="10‐Oct‐2014" /collected_by="Maumita Bandyopadhyay and Mou Dutta" /identified_by="Kuldeep Singh Negi"

note="authority: Allium fistulosum L."

1.agggttccac tgccggaaga tcatctttaga gttcccttccc gaacaactgc gatattgtac
61 tcctaccgct cagaaactac gtattttggt ggttagactc tgggtggtgtt ggaatggggtc
121 catttgtgct cttcatcttt gttccaatgt aagtaagaag tagatgataa ataaagaacc
181 gggcagtttt gttccaaagct gtatttggtt tggagacat gcacattgt tagattgttct
241 tgtttatttc cattgagct cttaaagact ccttgcaagt gatatctttg tctctggtgct
301 gcatgaagac tcatgcaagg ggcacactgc gtgttagaag tcgacttccc csaacaccct
361 aggctctttg aaggtcagct ggtcatgcgtt gcagct gcagct gccagcgtt gcagct
421 cgctgcttttt gttctttcatt cccgaccaag cagctatact tagctggt ggatggcggg
481 agttgcagag tgcacccctgg tgcctttact gttggtttgg ttaagttgaa tgtttggtt
541 agtttgacctgc gcggcagagt gtgtgacctc ttaacaacag atgtcctttt ctgctgctg
601 gacgtcctc cagactgtaa cactactgta aacaaccctct gcagctgggct ttagttgcaaa
661 gttcgaaaca tgcacccagag ccagatgag a

Allium schoenoprasum voucher MB3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

GenBank: KU145490.

FASTA

```
LOCUS KU145490 661 bp DNA linear PLN 09-FEB-2016
DEFINITION Allium schoenoprasum voucher MB3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KU145490
VERSION KU145490.1 GI:985651434
KEYWORDS .
SOURCE Allium schoenoprasum
ORGANISM Allium schoenoprasum
eyukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioidae; Allieae; Allium.
REFERENCE 1 (bases 1 to 661)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 661)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES Location/Qualifiers
  source 1..661
    /organism="Allium schoenoprasum"
    /mol_type="genomic DNA"
    /specimen_voucher="MB3"
    /db_xref="taxon:74900"
    /country="India: Sutton and Sons, Kolkata"
    /collection_date="20-Oct-2014"
    /collected_by="Mou Dutta"
    /note="authority: Allium schoenoprasum L."
    /misc_RNA 1..661
      /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN
1 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
61 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
121 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
181 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
241 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
301 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
361 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
421 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
481 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
541 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
601 cctgcggaag gatcattgta gattttcctt ttgcgaacaac tgcgaaattg ttctcatacc
661 c
```

Allium chinense voucher MB 4 internal transcribed spacer 1, partial sequence; and 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence

LOCUS KT781694 600 bp DNA linear PLN 11-NOV-2015
DEFINITION Allium chinense voucher MB 4 internal transcribed spacer 1, partial sequence; and 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence.
ACCESSION KT781694.1 GI:949326511
KEYWORDS .
SOURCE Allium chinense
ORGANISM Allium chinense
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 600)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 600)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (18‐SEP‐2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly‐Data‐START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly‐Data‐END##
FEATURES Location/Qualifiers
misc_RNA <1..600

//

Allium sativum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

GenBank: KT895596.1

FASTA

```
LOCUS KT895596             669 bp   DNA   linear   PLN 11-NOV-2015
DEFINITION Allium sativum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT895596
VERSION KT895596.1
GI:949326663
KEYWORDS .
SOURCE Allium sativum (garlic)
ORGANISM Allium sativum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 669)
AUTHORS Dutta, M. and Bandyopadhyay, M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 669)
AUTHORS Dutta, M. and Bandyopadhyay, M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT 
  Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
  Sequencing Technology :: ABI 3500 Genetic Analyzer
FEATURES Location/Qualifiers
  source 1..669
    /organism="Allium sativum"
    /mol_type="genomic DNA"
    /db_xref="taxon:4682"
    /country="India: Kolkata"
    /altitude="9 m"
    /collection_date="10-Oct-2014"
    /collected_by="Mou Dutta and Maumita Bandyopadhyay"
    /identified_by="Mou Dutta and Maumita Bandyopadhyay"
    /note="authority: Allium sativum L."
misc_RNA -----------
  /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
ORIGIN
  1 cggaaggatc atttgtcagt tccttttcga acagttgtga aattgtgctc atacccgacg
  61 agtactagtc ttgtgtgcct cttattgtgc acgtgtgctt gcggcttccct ttggtgtcgc
  121 ttctgtgttc ttttatttgaa gtttattttt gagacacaggt cacagtttgt
  181 gcgaagggc gtattattttg gattgtcagt ccattcttgg gattttgctt gccatcttctt
  241 agcagacagc tgaattgtgc atacattgtgc ctctgtgtgc atagaaagac
  301 taagcctggct ccgacacagt tgtgaattgtgc cagaatccctg gatgcagtgaatcagtgcct
  361 gcacaggtgc cccagagcga tttagttcag tcggcttgcct tttggtgtccct ctttacagcggc
  421 tctctatcct gccctctgtc gcagttgtgc attttgcttg atggatgtgccgt atcctctttc
  481 ctttcttgct cttaattgct gttatttgg atagatttgc cgtggctgtc tatattcgagc
  541 gcgcggtttg tccggtgtta acgcagaggt ttcttattgc gttcctgtag cacagcatgagc
  601 gacctagcac tagctaaacc gatttttttg gatttttttg gattgctgtcg cggccatgagc
  661 cctcagatc
```

Allium sativum cultivar Agrifound Parvati 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

GenBank: KU176880.1

FASTA

```
>LOCUS KU176880 670 bp DNA linear PLN 08-MAR-2016
>DEFINITION Allium sativum cultivar Agrifound Parvati 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION KU176880
VERSION KU176880.1
GI:1002637586
KEYWORDS
SOURCE Allium sativum (garlic)
ORGANISM Allium sativum
Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Alilioideae; Alliacea; Allium.
REFERENCE 1 (bases 1 to 670)
AUTHORS Dutta, M., Haque, I. and Bandyopadhyay, M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 670)
AUTHORS Dutta, M., Haque, I. and Bandyopadhyay, M.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
#Assembly-Data-END##
FEATURES source
Location/Qualifiers

misc RNA

/<1..>670

//
```

NCBI is phasing out sequence GI numbers in September 2016. Please use accession.version! Read more...

**Allium sativum voucher Sat 3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence**

GenBank: KU145491.1

**FASTA**

```plaintext
LOCUS      KU145491        678 bp    DNA    linear    PLN 09-FEB-2016
DEFINITION Allium sativum voucher Sat 3 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KU145491
VERSION   KU145491.1
GI:985651435

KEYWORDS .

SOURCE     Allium sativum (garlic)

ORGANISM  Allium sativum
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;
           Amaryllidaceae; Allioideae; Allieae; Allium.

REFERENCE 1  (bases 1 to 678)
AUTHORS    Dutta,M. and Bandyopadhyay,M.
TITLE      Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL    Unpublished

REFERENCE 2  (bases 1 to 678)
AUTHORS    Dutta,M. and Bandyopadhyay,M.
TITLE      Direct Submission
JOURNAL    Submitted (14-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India

COMMENT    Assembly Method : Cap3 Sequence Assembly Programme v. 1999
            Sequencing Technology : ABI 3500 Genetic Analyzer
            ##Assembly-Data-START##
            Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
            Sequencing Technology :: ABI 3500 Genetic Analyzer
            ##Assembly-Data-END##
            ORIGIN 1 tagggaacc tgggaagga tcatttgtga gttctttttt gcacagttg gaaatgtgc
d1 tcataccpca cagagtactc tggttggtgc tatagtgcga tgcgtgtct tgggggttc
d2 cctitgtgct cctcgtgtgt gtttatttg aaggggagc aagacggag aataaggac
d3 gcacaggtt gtcacagag cagattttg tggagtctag tcgacagtt tggattgtgc
d4 ttgtgtctatt ctctgaggac tctctggct ttcaggtcgc gagaatccg ccctttttgt
d5 cgagctagt gctgagctgg ggatgtgagc tgcgactcct gagaaggtcg gtttggc
d6 cggaccag tggccaggg ctgctttgg ttcaggtctc gattttggtt cctcgtcatt
d7 gacgagttc atgcataggt cagccaggg ccatttaggtc atgcagctt gttttggc
d8 tctcgtatag gctgagctgg ggatgtggagc tgcgacccct gagaaggtcg gttttggc
d9 cggaccag tggccaggg ctgctttgg ttcaggtctc gattttggtt cctcgtcatt
d10 gacgagttc atgcataggt cagccaggg ccatttaggtc atgcagctt gttttggc

            //
```

Allium ampeloprasum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT895595.1

FASTA Graphics

Go to: }

LOCUS KT895595 678 bp DNA linear PLN 11-NOV-2015
DEFINITION Allium ampeloprasum 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT895595
VERSION KT895595.1 GI:949326662
KEYWORDS .
SOURCE Allium ampeloprasum (leek)
ORGANISM Allium ampeloprasum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 678)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 678)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (10-OCT-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT #Assembly-Data-START#
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
#Assembly-Data-END#
FEATURES source 1..678
/organism="Allium ampeloprasum"
/mol_type="genomic DNA"
/db_xref="taxon:4681"
/country="India: Kolkata"
/altitude="9 m"
/collection_date="10-Oct-2014"
/collection_by="Mou Dutta and Maumita Bandyopadhyay"
/identified_by="Maumita Bandyopadhyay"
/note="authority: Allium ampeloprasum L."
/misc_RNA <1..>678
/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
ORIGIN
ggaaggatca ttgtagagtt ccttttcgaa tagttgtgaa attgtgctca tactcgacga
gtactacgtg tt tgtgctat tagtgcatgc gtagtcttgg tgggttccct ttgctgcct
ttgtgttgct ttatttaaag tg aaatgaag agcagaaata agacaccggc acagtttgtg
ccaaggacag ttactgttgg agtgccattgc catctttttg atgtgctttg tgctgttcta
gcgagcatct gaatgactcc tggcaatgga tatcttggct ctcgtgtcga tgaagaacgt
agcgaaatgc gacacttggt gtgaattgca gaatcccgtg aaccatcgag tctttgaatg
dagagttgcgc acgaggccat taggtcgagt gcacgtctgt ttgggcgtca tgtatagcgt
cattccaatc tcccacatgc gatgagtgtg gtttgggtka tgatgggtat ggagaatgac
ttccgtgct ttaattgtat ggtaggttta agtgattgtc gtggccaggt atatgcgagg
cgaatggtgt atcgagttaa cacacagtnt ccttaatcgct cttcatgaga cctaggcagt
dtcagatcag acggggcg //
Allium ampeloprasum voucher IC-353526 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT882613.1

FASTA

GenBank

ORIGIN
1 cctgcggaag gatcattgtn gagttccttt tcgaacaatt gtgaaattgt gctcataccc
61 gacgagtact atgtgtttgt gctgttagtg catgcgttgt cttggcgggt tcccttttgc
121 tgccttttgtg ttgctttatt tgaagtgaaa cgaagagcag aaataagaca ccggcacagt
181 ttgtgccaag gacagttatt gttggagtgc attgccatct ttttgatgtg ctttgtgcta
241 ttctagcgag cgtctgaatg actcctggca atggatatct tggctctcgt gtcgatgaag
301 aacgtagcga aatgcgacac ttggtgtgaa ttgcagaatc ccgtgaacca tcgagtcttt
361 gaatgcaagt tgcgcacgag gccattaggt cgagtgcacg tctgtttggg cgtcatgtat
421 agcgtcattc caatttccca cgtgggacga gtgcgttttg ggtgatgatg gatatggaga
481 atgaccttcc gtgctttaat tgtgcggtag gtttaagtga ttgtcgttgc caggtatatg
541 cgaggcgaat ggtgtgtcga gttaacgcac gatgtctcta atcgcgtccg tgagacctag
601 gcatgactta gcaataatcg aaaccgattt cgatgtttgc tttggtagca agctcgaacc
661 atgacctc
Allium griffithianum voucher IC-353540 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KU145493.1

FASTA Graphics

Go to:

LOCUS KU145493    713 bp DNA linear PLN 09-FEB-2016
DEFINITION Allium griffithianum voucher IC-353540 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION KU145493
VERSION KU145493.1 GI:985651437

KEYWORDS .

SOURCE Allium griffithianum

ORGANISM Allium griffithianum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.

REFERENCE 1 (bases 1 to 713)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 713)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India

COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##

FEATURES Location/Qualifiers
misc_RNA 1..713
/origin="Allium griffithianum"
/mol_type="genomic DNA"
/specimen_voucher="IC-353540"
/db_xref="taxon:138324"
/country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
/altitude="1706 m"
/collection_date="10-Oct-2014"
/collection_by="Maumita Bandyopadhyay and Mou Dutta"

/organism="Allium griffithianum"

misc_RNA 1..713

/orientation="" /note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN

1 ctccgttag tgaaacctgc gatgagactg tcgagggtct cttttgagaa aatgtgaa aatcaccacat cccgagcttg ggggagcccg gggcataagc aatgagggg aatgagggg
61 tgtgaccc atcaccgac tgcgagcttg ggggagcccg gggcataagc aatgagggg aatgagggg
121 tgtgtcttt ggggagcccg gggcataagc aatgagggg aatgagggg
181 aacgagcttg ggggagcccg ggcgagcttg ggggagcccg gggcataagc aatgagggg aatgagggg
241 tgtgagctt ggcgagcttg ggggagcccg gggcataagc aatgagggg aatgagggg
301 gtgtctttg ggggagcccg gggcataagc aatgagggg aatgagggg
361 cttctggct ggggagcccg gggcataagc aatgagggg aatgagggg
421 ggggagcccg gggcataagc aatgagggg aatgagggg
481 tggcagcgg ccctgagcttg ggggagcccg gggcataagc aatgagggg aatgagggg
541 gtcggagcttg ggggagcccg gggcataagc aatgagggg aatgagggg
601 tggcagcgg ccctgagcttg ggggagcccg gggcataagc aatgagggg aatgagggg
661 cttctggct ggggagcccg gggcataagc aatgagggg aatgagggg

//
Allium roylei voucher IC-353546 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT762156.1

FASTA

GenBank

11/20/2015

Allium roylei voucher IC-353546 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT762156.1

FASTA Graphics

Go to:

LOCUS KT762156 639 bp  DNA  linear  PLN 14-NOV-2015
DEFINITION Allium roylei voucher IC-353546 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT762156
VERSION KT762156.1 GI:949699409
KEYWORDS
SOURCE Allium roylei
ORGANISM Allium roylei
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 639)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 639)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT #Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
#Assembly-Technology-END#
FEATURES source
 Location/Qualifiers
 1..639
 /organism="Allium roylei"
 /mol_type="genomic DNA"
 /specimen_voucher="IC-353546"
 /db_xref="taxon:48874"
 /country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
 /altitude="1706 m"
 /collection_date="10-Oct-2014"
 /identified_by="Kuldeep Singh Negi"
 /note="authority: Allium roylei Stearn"
 1..639
 /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
misc_RNA

ORIGIN
1 aactgtaaat gtccttacat ccgctcgaaga tctcgtattt ttgctcctag cactctgctt
 61 gttgctgtag gttccttcttg cgtccttcat cttgtgtctaa attgtagagtt gtagttggtt
121 aagaagagg gaccttggcag aagcggcgaa ttccttcgca ggttcgccaaga tgctgctgctt
181 atttttaagcccc tattccgtagt gcttctctgtag acctctggagc aaggctcctag
241 ttggctgtagg cggcggc gacccggcag aatgtccacaa agctgctgagc aaggctcctag
301 ccccgtgctac atgcttccttc ggtgcttccttc cgggctctttag cttggagcttc
361 gatgctgctac ccgctcgaaga ttccttcgca ggttcgccaaga tgctgctgctt
421 gatgctgctac ccgctcgaaga ttccttcgca ggttcgccaaga tgctgctgctt
481 aactgtaaat gtccttacat ccgctcgaaga tctcgtattt ttgctcctag cactctgctt
541 aactgtaaat gtccttacat ccgctcgaaga tctcgtattt ttgctcctag cactctgctt
601 cttgcttccttc cggcggc gacccggcag aatgtccacaa agctgctgagc aaggctcctag

//

Allium carolinianum voucher IC-353627 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT762157.1

FASTA

```
LOCUS KT762157 716 bp DNA linear PLN 14-NOV-2015
DEFINITION Allium carolinianum voucher IC-353627 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT762157
VERSION KT762157.1 GI:949699410
SOURCE Allium carolinianum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 716)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 716)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..716
/organism="Allium carolinianum"
/mol_type="genomic DNA"
/specimen_voucher="IC-353627"
/db_xref="taxon:105480"
/country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
/altitude="1706 m"
/collection_date="10-Oct-2014"
/identified_by="Kuldeep Singh Negi"
/note="authority: Allium carolinianum DC."
/misc_RNA 1..716
/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
/ORIGIN 1 tccgtagg gacctgcgga aggatcatg tagagtccc tttgaaacat tttgaactt 61 tattcatc ccagtagatg tagtctggg tctcggtagc aactctgcta tttttaggg 121 ttctacttc gctgccatat gatctgattg gacttttcttg aatatggaa 181 cctggtcgc cttgatttcg gctttagatc aatgccatac tttagtggg 241 ttctttcgg ttcatatag gtttagggg atctctgcca atctgttctt ctgttctgt 301 tgtctctg agatcatgac aatgcggcag cttggttgca tttgatgaa ttttagtggg 361 tgtctctg atctcatgag gctctgatg gcagcagctc tcggatgttg cgcttggg 421 ctctgattc tctctctgct tcagagca caaaccaaaa cctgagggt cacttttcttg 481 gttgctgtgata tggctctccct gcttataagtt ttgggtcattt gttcattctg atctgttttg 541 tgggctgtgga cgcggcagat ggtgatgca gtttaaaccag catttctcttc aatgcgcttg 601 gctcgacttt cgctctggtt gcggcaagtt tcagctgggg gctcaggttc gctcaggttc 661 gctcggcaat gatgcggcgc gcgtggtatc gggtatgactt gttgattttg tgcctggcttg
```
Allium hookeri voucher HN-2800 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT762155.1

FASTA Graphics

Go to:

LOCUS KT762155 654 bp DNA linear PLN 14-NOV-2015
DEFINITION Allium hookeri voucher HN-2800 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT762155
VERSION KT762155.1 GI:949699408
SOURCE Allium hookeri
ORGANISM Allium hookeri
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 654)
  AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
  TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 654)
  AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
  TITLE Direct Submission
JOURNAL Submitted (14-SEP-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
  Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
  Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES Location/Qualifiers
  source 1..654
    /organism=Allium hookeri"
    /mol_type="genomic DNA"
    /specimen_voucher="HN-2800"
    /db_xref="taxon:105303"
    /country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
    /altitute="1706 m"
    /collection_date="10-Oct-2014"
    /collected_by="Maumita Bandyopadhyay and Mou Dutta"
    /note="authority: Allium hookeri Thwaites"
    /misc_RNA <1..>654
      /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"
ORIGIN
1 ctctcagagat tgaagaacat tagacatattta cctctcgagt aagcgtagttt tgctgatgca
36 tcttcgcttt ctagaggtgt gtcccatttgg cgcctccagc ttgctttatt caaggtaaga
121 agggacgccc gaataaagacc cgggctgttc tgcgcctcaag gcagttgatgt ttgggatgatc
181 actgccttct catcttcttt ggtgttattc ttgctttatt gcaggttgaat gcatgactct
241 tggcaacgga tatctaggct ctcgcgtcga tgaagaacgt agcgaaatgc gatacttggt
301 gtgaattgca gaatcccgtg aaccatcgag tctttgaacg caagttgcgc ctaagaccat
361 caggtcaagg gcacgtctgc ttgggcctca cgcctttgcgt cactytgcgc cmmccmagct
421 camaccmtta tatgggtatw gkkatgctgg gatgtggatg atgtggatgat gctgcttttaa
481 ctggcgagct ttaaagtaa tttgctcttc taggtttttc tgggcatgtggttgcagtga
541 ttataacatc aacccataac gatgtttgca tttttgcaag cttcggaccat gacctcagtc acgc

//
Allium fasciculatum voucher SN05 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KT762158.1

FASTA

LOCUS KT762158 679 bp DNA linear PLN 14-NOV-2015
DEFINITION Allium fasciculatum voucher SN05 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KT762158
VERSION KT762158.1 GI:949699411
SOURCE Allium fasciculatum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 679)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 679)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES source 1..679
/organism="Allium fasciculatum"
/mol_type="genomic DNA"
/specimen_voucher="SN05"
/db_xref="taxon:743500"
/country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
/altitude="1706 m"
/collection_date="10-Oct-2014"
/collection_by="Maumita Bandyopadhyay and Mou Dutta"
/identified_by="Kuldeep Singh Negi"
/author="Allium fasciculatum Rendle"
/starts=1/ends=679
/make one sequence
/make one sequence
.Contained in Genbank accession KT762158.1
/misc_RNA

ORIGIN 1 cctncggaag gatcattgtc gagtccctct tcaagagatt gagaacatgt agcatttaac
d6tccaggtca acgttagtttt gcgattgcac tttctgctttc tagatggatg tccttttgtc
e121 gccttcagct tgctttattc aaggtaagaa ggagagcggg aataagaccc cggcgtggtt
t181 cgcgccaagg actgttgttg ttggagtgca ctgccttctt tttgttgtgc ggtgtattct
u241 cctactagtg tgagaatatg catgactctt ggcaacggat atctaggctc tcgcgtcgat
i301 gaagaacgta gcgaaatgcg atacttggtg tgaattgcag aatcccgtga accatcgagt
l361 cttttgtaac gcgagcgcc cgcagcagc cgcagcagc cgcagcagc cgcagcagc cgcagcagc
1421 gccttgcccgt ctctatgag cggaccgg cgaagcgcg cccccc

//
Allium cernuum voucher IC-353525 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KU145489.1

FASTA

LOCUS KU145489 644 bp DNA linear PLN 09-FEB-2016
DEFINITION Allium cernuum voucher IC-353525 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KU145489
VERSION KU145489.1

KEYWORDS .
SOURCE Allium cernuum
ORGANISM
          Eurkarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Monilophyta; Liliopsida; Asparagales; Amaryllidaceae; Alioidae; Alieae; Allium.
REFERENCE 1 (bases 1 to 644)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 644)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES source
    Location/Qualifiers
    1..644
    /organism="Allium cernuum"
    /mol_type="genomic DNA"
    /specimen_voucher="IC-353525"
    /db_xref="taxon:70754"
    /country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
    /altitude="1706 m"
    /collection_date="10-Oct-2014"
    /collected_by="Maumita Bandyopadhyay and Mou Dutta"
    /note="authority: Allium cernuum Roth."
    /misc_RNA:<1..>644
    /note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN
1 acagtgtgaa ttgtgctcat acccgacgag tactacgtgt ttgtgctatt agtgcatgcg
d1 ttgttctgcc aggatccctt ttgctgcctt cgtgttgctt tatttgaagt gaaacgaaga
g1 gcagaaataa gacaccggca cagtttgtgc caaggacagt tattgttgga gtgcattgcc
h1 atcgttttga tgtgctttgt gctattctag cgagcatctg aatgactcct ggcaatggat
i1 atcttggctc tcgtgtcgat gaagaacgta gcgaaatgcg acacttggtg tgaattgcag
j1 aatcccgtga accatcgagt ctttgaatgc aagttgcgca cgaggccatt aggtcgagtg
k1 cacgtctgtt tgggcgtcat gtatagcgtc attccaatct ccctcatgcg acgagtgcat
l1 tttgggttat gatggatatg gagaatgacc ttccgtgctt taattgtatg gtaggtttaa
m1 gtgattgtcg ttgccagtta tatgcgaggc gaatggtgtg tcgagttaac gcacgatgtc
n1 tctaatcgcg tccatgagac ctaggcatga cttagcacta gctaaaaccg atttcgatgt
u1 ttgctttcgt agcaggctcg gaccatgacc tcagatcaga cggc

//

Allium tuberosum internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence

GenBank: KT781692.1

FASTA

LOCUS KT781692 601 bp DNA linear PLN 11-NOV-2015
DEFINITION Allium tuberosum internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene, complete sequence; and internal transcribed spacer 2, partial sequence.
ACCESSION KT781692
VERSION KT781692.1 GI:949326507
KEYWORDS
SOURCE Allium tuberosum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 601)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 601)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (18-SEP-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT 
FEATURES Location/Qualifiers
misc_RNA <1..>601
/organism="Allium tuberosum"
/mol_type="genomic DNA"
/db_xref="taxon:4683"
/country="India: Experimental Garden, Department of Botany, University of Calcutta, Kolkata"
/altitude="9 m"
/collection_date="10-Jan-2015"
/collection_by="Maumita Bandyopadhyay and Mou Dutta"
/identified_by="Maumita Bandyopadhyay"
/note="authority: Allium tuberosum Rottl. ex Spreng."
/note="contains internal transcribed spacer 1, 5.8S ribosomal RNA, and internal transcribed spacer 2"

ORIGIN
1 ccattgacga acaagggaccta atagtctata atattgtatg gttggaggt gttttcccttt
61 gctaattcct tcgctgctca tggcagcagaa gaaggaggt aagaataaga tattggcagc
121 gctttggcag aagcactag catttatttc gactgtttgt cttatattg atgtctctgtc
gtgcagtct gttttcctct ctgcttgggc gcatttaaag taatagaaac caatgtcgtt gttttgcacgt
181 catttttaca agcgtgagc gatcagatc tggctggtct ccacctctct gctggttcggccc
241 cgattggaagat gatttcctgt cttgcttggc ggttcctttg tattgttcca agaatgttttg
catggtcagcg tctgattgtctgc gttttgcacgtct gttttgcacg
301 aggttggcagcg tttgagttgc aatgctgct caagcgcagt gttttgcacgtct gttttgcacg
361 tcatggttct gcagcagcag gcctatccac aacattctg cattcctattac atatgtgttg
taatagaaac caatgtcgtt gttttgcacgtct gttttgcacg
421 gtaattgcg acgctgctgc tgtgctgctg ctttatttc gttttgcacgtct gttttgcacg
481 agagtgggtc atggcagcag gcctatccac aacattctg cattcctattac atatgtgttg
taatagaaac caatgtcgtt gttttgcacgtct gttttgcacg
541 gttttgcacgtct gttttgcacgtct gttttgcacg
601 a

//

Allium auriculatum voucher IC 353533 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KR349330.1

FASTA Graphics

Go to:

LOCUS KR349330    730 bp DNA linear PLN 21-JUN-2015
DEFINITION Allium auriculatum voucher IC 353533 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KR349330
VERSION KR349330.1 GI:833300817
KEYWORDS .
SOURCE Allium auriculatum
ORGANISM Allium auriculatum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 730)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 730)
AUTHORS Dutta,M. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (27-APR-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly-Data-START##
Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly-Data-END##
FEATURES Location/Qualifiers
misc_RNA 1..730
/origin="Allium auriculatum"
/mol_type="genomic DNA"
/specimen_voucher="IC 353533"
/db_xref="taxon:1667389"
/country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
/altitude="1706 m."
/collection_date="10-Oct-2014"
/collection_by="M. Bandyopadhyay"

/organism="Allium auriculatum"

/mote="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN
1 gaaaatggaa ctctacgatg attcttccgt agggtgaacc tgcggaagga tcattgtagt
gttccttttc gtacagttgt gaagttgtat tcatacccat tgaaaactat gttttgttagc
tttgcgttg tttaggtggg tttcctctgc tgccatcgtc ctgcttcatt cgaagtaagg
aggatagtag aaattagaga ccggcgcggt ttgtgccaag gacagttgtt gttagagtgc
attgcccatc ttgttgatgt gctttttgtt attctacaag tgtgagcgtc tgaatgactc
ttggcaatgg atatcttggc tctcgtttcg atgaaaaacg tagcgaaatg cgacacttgg
tgtgaattgc aaaaatcccgt gaaccatcga gtctttgaat gcaagttgcg ctcgaggcca
ttaggtcgag ggcacgtctg tttgggtgtc ataccttacg tcacgttaac cacccaccca
cgctaaacat aatgcaggtg attgtgtatg tggagattga ccttccgggc tttaattgtg
cggttggttt aagtgaatgc tgccgtaagg tccacccgcg gtgaacggtg aatccaggta
acacacgata actctaaccg cgtccaggag acctaagcaa ggcgtaacat ggactttgaa
cctttttctt gtcgcaaggt cttaaaaatga cctcccatca gacggggccc acctctgata
//

Allium albidum voucher EC-328484 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KU145488.1

FASTA Graphics

Go to:

LOCUS KU145488 649 bp DNA linear PLN 09-FEB-2016
DEFINITION Allium albidum voucher EC-328484 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.

ACCESSION KU145488
VERSION KU145488.1 GI:985651432

KEYWORDS

SOURCE Allium albidum

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.

REFERENCE 1 (bases 1 to 649)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 649)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India

COMMENT "Assembly-Data-BEGIN"

Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer

"Assembly-Data-END"

FEATURES
source 1..649
/organism="Allium albidum"
/mol_type="genomic DNA"
/specimen_voucher="EC-328484"
/db_xref="taxon:165601"
/country="India: National Bureau of Plant Genetic Resources, Bhowali, Uttarakhand"
/altitude="1706 m"
/collection_date="10-Oct-2014"
/collection_by="Mou Dutta and Mou Dutta"

misc_RNA 1..649

/author="authority: Allium albidum Fisch. ex Bieb."

1..649

"contains internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN
1 agattgagac ttgtaacctat acccatcag aacaaagccg taattgctata aatattgatat
61 tgtttagaga ggttctcctt tgctaccttc ttcctggttc accttgaacga acaatagagag
121 taraaatag atatcggcgc ggcttgkgcc aaggacagct gtgtgtgagg tgcagtctcs
181 ttctttataa tggcagcggt gaatatatgc gcagttgagc gttcagtaat cctcggcaca
241 tggatatctt ggctctcgtg tcsatgaaga acgtarcagaa atgcgcacact tgtgtgaat
301 tgcagaatcc cgtgagtcag cagtttcttg aatgctgagt gcgcctgagc cctagggtc
361 gaggacagct ctgctgtggc gtctggccac acgtatccct aaacatcctc ctatcctttaa
421 atatatggtt ctgtagaaag gatcctaggta tggctacccc tgcgtttaaa gaattgcgtggt
481 gtttaagggta ggttggcttc taggttgcgc cgtgagaaat ggtgcatgca ggttaacgcc
541 gatcttcaac tgcgtacaag agtcttccagc acagtatcaca gtaatagaaag ccaatgctgt
601 tggctgacct atggccatag gaccaagtca cctcagatca taacgatc

//
Allium ampeloprasum voucher Leek 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence

GenBank: KU145494.1

FASTA  Graphics

```
LOCUS KU145494 699 bp DNA linear PLN 09-FEB-2016
DEFINITION Allium ampeloprasum voucher Leek 2 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence.
ACCESSION KU145494
VERSION KU145494.1 GI:985651438
KEYWORDS .
SOURCE Allium ampeloprasum (leek)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Liliopsida; Asparagales; Amaryllidaceae; Allioideae; Allieae; Allium.
REFERENCE 1 (bases 1 to 699)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Molecular phylogenetic study of Indian Allium using nuclear ribosomal sequences
REFERENCE 2 (bases 1 to 699)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 699)
AUTHORS Dutta,M., Haque,I. and Bandyopadhyay,M.
TITLE Direct Submission
JOURNAL Submitted (14‐NOV‐2015) Department of Botany, University of Calcutta, 35 Ballygunge Circular Road, Kolkata, West Bengal 700019, India
COMMENT ##Assembly‐Data‐START##

Assembly Method :: Cap3 Sequence Assembly Programme v. 1999
Sequencing Technology :: ABI 3500 Genetic Analyzer
##Assembly‐Data‐END##

FEATURES Location/Qualifiers
source 1..699
/organism="Allium ampeloprasum"
/mol_type="genomic DNA"
/specimen_voucher="Leek 2"
/db_xref="taxon:4681"
/country="India: Sutton and Sons, Kolkata"
/collection_date="20-Oct-2014"
/collection_by="Mou Dutta"

/misc_RNA <1..>699

/note="contains 18S ribosomal RNA, internal transcribed spacer 1, 5.8S ribosomal RNA, internal transcribed spacer 2, and 28S ribosomal RNA"

ORIGIN

1 ttggcctgt cgaagctgat tggagtttc ctttgcaga aacggggtgttaa
61 ttgcgtcat actcgagag ttaaacctg ttagctggtg aagggcaggatgtacgtctgtgtgtgtat
121 ggtttttttttttt tgggagtgg ttttttatttt tattattg gaaatggaag aggagaaaaa
181 gacagcggaca cattttgtttg gaaacggag atgccagcct ttcacacctgctctctctctcct
241 ttttggtggt ggtccttgat ggggagcttg ggtcgacctg gctgtcgtgtg cagatgacgt
tgagaagtt gggtggcgag aatccctgctg ctttgc峡谷 ttagctgtggtg tttttggttgg ttttttgcgtgtg
301 tgggtttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
XIX Annual Conference of
Indian Association for Angiosperm Taxonomy (IAAT)
& International Symposium on

"Angiosperm Systematics & Phylogeny:
Retrospects & Prospects"

November 12 - 14, 2009

National Botanical Research Institute
(Council of Scientific & Industrial Research)
Lucknow - 226 001, INDIA
present paper highlights the 3 endangered (EN), 5 vulnerable (VU), 22 rare (R) and 46 common (C) species along with their botanical name, voucher number, family, locality, local name, life form and distribution along with their conservational measures.

Key words: Deogarh, Eastern Ghats, Fabaceae

SD/P-12 Diversity of cypselar features in eleven species of the Tribe Anthemideae (Asteraceae)
Sushanta Das and Sobhan Kr. Mukherjee
Taxonomy and Biosystematics Laboratory, Department of Botany, University of Kalyani, Kalyani, Nadia-741 235. W.B., India. Email: sobhankr@gmail.com

The tribe Anthemideae is included under sub family Asteroideae of the family Asteraceae. A comparative account of morphological features of cypselas of eleven species such as Achillea atrata, Achillea ptarmica, Artemisia vallesiaca, Chamaemelum nobile, Leucanthemum vulgare, Lonas annua, Matricaria matricarioides, Matricaria recutita, Tanacetum parthenium, Tripleurospermum inodorum, and Tripleurospermum maritimum of the tribe Anthemideae have been studied to establish their role for the evaluation of taxa at the infrageneric level with the help of dissecting and light microscopes. The emphasis has been given on the detailed morphological features of cypselas including size, shape, colour, surface ornamentation, cross sectional configuration, structure of corona and carpopodium, mode of distribution of carpopodial cells in different tires and thickness of pericarp in mature cypselas. Cypselas are longer in Tripleurospermum maritimum and Achillea atrata and significantly smaller in Artemisia vallesiaca and Matricaria recutita among the studied species. Structure of stylopodium is not significant taxonomically. Carpopodia are usually asymmetric, forming complete ring. Number of rows of carpopodial cells varies from 1-8 in different species. Number of ribs varies from 3-10 in different species. An artificial key is prepared on the basis of dissimilar morphological characters of cypselas for easy identification of the studied taxa, instead of other conventional floral and vegetative features.

Key words: Anthemideae, Asteraceae, cypselar, morphology

SD/O-14 Rescue of Clematis heynei M. A. Rau through nodal bud culture; a rare endemic plant of Western Ghats
Department of Botany, Shivaji University, Kolhapur- 416 004 (MS), INDIA, jaychavansu@gmail.com

Clematis heynei is a rare, endemic and important medicinal plant of family Ranunculaceae. An efficient protocol was developed for the rapid in vitro multiplication of C. heynei, via enhanced axillary bud proliferation from nodal explants. The physiological effects of different plant growth regulators (PGRs) were tested either alone or in combinations. The highest number of shoots (7.6) and the maximum average shoot length (6.8) were recorded on MS medium fortified with BAP (3 mg/l) in combination with IAA (0.5 mg/l). Rooting was best achieved (5.1) on half-strength MS medium augmented with NAA (1.0 mg/l). The plantlets regenerated in vitro with well-developed shoot and roots were successfully established in pots containing garden soil and grown in a greenhouse with a 75% survival rate. The regenerated plants did not show any immediate detectable phenotypic variation. The described method can be successfully employed for large-scale multiplication and conservation of C. Heynei.

Key words: Clematis, endemic, tissue culture, Western Ghats

SD/O-15 A cytogenetical study of Indian Allium L.
Mou Dutta and Maumita Bandyopadhyya
Centre of Advanced Study, Department of Botany, University of Calcutta, 35, B.C. Road, Kolkata-700019, INDIA

Allium L. (Family Alliaceae) is probably the largest genus of the monocotyledons, comprising some 750 species. Allium includes some economically important species; approximately 30 species have been regularly used for edible purposes. The genus is naturally distributed only in the Northern Hemisphere, mainly in regions that are seasonally dry. The genetic resources of Allium in India are potential source of genes for widening the crop genetic base. Despite their high economic value, limited number of germplasm accessions of wild species have been collected and conserved mainly due to difficult access to areas of
occurrence. Species of Allium reported as rare/threatened and endemic to the Himalayan region are A. clarkei, A.Fedtschenkoanum, A. humile, A. loratum, A. Prattii, A. roylei and A. wallichii. Few authors accepted only 255 species; the number of Allium species is now estimated at about 700 and taxonomy is complicated, with a proliferation of synonyms and disagreement as to the subdivision of the genus. As the methods became available and more refined, systematic studies using cytological data and molecular markers were published to complement and offset the growing amount of data based on morphological, anatomical and other traditional approaches. The present study focuses on the utilization of cytological and molecular techniques to aid in the taxonomy of Allium.

Key words : Allium, cytology, wild species

SD/O-16 An assessment of cytological diversity among different members of Zingiberaceae
Sreetama Bhadra and Maumita Bandyopadhyay
Centre of Advance Study, Department of Botany, University of Calcutta, 35, B.C. Road, Kolkata-700 019, INDIA

The family Zingiberaceae contains many important spice and condiment producing species. But the plants and drugs are very similar in morphology, and also the morphological characters differ under varying environmental conditions. Moreover the plants have prolonged dormancy period and their flowering season is very short. Morphological characters without reproductive parts are not sufficient for species identification. Proper preservation of specimens in Zingiberaceae is also extremely difficult, resulting in limited amount of type specimens, leading to ambiguous name assignment. So, cytological identification of different members of Zingiberaceae can be helpful in taxonomic delimitation of the family. The immense potential of improved techniques of chromosomes analysis has now made it possible to identify minute structural differences of chromosomes including different ploidy levels in different strains and species relationships. In case where morphological characteristics are more or less similar, karyotype analysis has long been to understand species relationships. The present study focuses on the identification of some of the common plants of Zingiberaceae using cytological technique. Karyotype analyses have helped to reveal the structural changes associated with the origin of agricultural strains.

Key words : Assessment, cytology, diversity, karyotype, Zingiberaceae

SD/P-13 Phenetic studies on some members of Cucurbitaceae occurring in and around Burdwan Sadar, West Bengal
Mobina Parveen, Siuli Batabyal and Ambarish Mukherjee
UGC Centre for Advanced Study, Department of Botany, Burdwan University, Burdwan-713104, (W.B.), INDIA, ambarishmukherjee@rediffmail.com

Taxonomy, both traditional and modern, aiming towards determination of natural relationships of living organisms and improvisation of their classification. As such, the species of Cucurbitaceae occurring in and around Burdwan Sadar of West Bengal have been studied in terms of conventional phytography and phenetics studied and their form-relationships determined. As many as 14 species (one species with two varieties) belonging to 11 genera of Cucurbitaceae were selected for the present study. Of these plants, Coccinia indica, Mukia maderspatana and Trichosanthes cucumerina, were collected from wild abodes while the remaining taxa i.e. Benisciaca hispida, Citrullus lanatus var. khero, Coccinia grandis, Cucumis melo var. momordica, Cucumis melo var. ustinas, Cucumis sativus, Trichosanthes dioica, Curcurbita maxima, Lagenaria vulgaris, Luffa acutangula, Luffa aegyptica and Momordica charantia, Solena amplexicaulis were procured from cultivation in Khalasipara, Rayan and Harigram located in the Southern part of Burdwan Sadar during the post monsoon and monsoon seasons in 2008-2009. A taxonomic account of these plants was prepared which includes key to the identification of the genera and species studied, description of each species and variety, their illustrations, distribution, flowering and fruiting times etc. Ethnomedicinal uses of the concerned taxa were also recorded. Phenetic studies involved computation of values of overall similarity between the concerned 15 OTUs with the help of the software ‘Statistica’ version 6.0 using 47-two state characters to obtain a cluster diagram. The phenogram thus obtained expresses the form-relationships between species, which may prove useful in accomplishing our taxonomic concept about them.

Key words : Burdwan Sadar, Cucurbitaceae, Phenetic studies
NUMERICAL TAXONOMIC STUDIES ON INDIAN ALLIUM SPECIES

Mou Dutta and Maumita Bandyopadhyay
Centre of Advanced Studies, Department of Botany, University of Calcutta,
35, Ballygunge Circular Road, Kolkata 700 019, West Bengal, India

The taxonomy of Allium, based on nectary morphology, inflorescence structure,
vegetative anatomy, basic chromosome number, bulb or rhizome morphology and
biogeographic patterns, is complicated with a great number of synonyms and
intrageneric groupings, with disagreements about the subdivision of the genus in
the infrageneric level and also in the knowledge of the geographical and evolutionary
relationships. Classical taxonomic treatment of the Indian Allium too is plagued
by the lack of resolution of character states, especially at the infrageneric levels.

Numerical taxonomy groups taxonomic units into taxa by numerical methods based
on their character states. The application of Numerical taxonomic methods in plant
taxonomy offers a series of advantages over classical morpho-taxonomy, most im-
portantly, objectivity. In the present study, an attempt was made to carry out nu-
merical taxonomic studies on Allium collected from various parts of India. For the
numerical analysis twenty operational taxonomical units (OTU) were selected based
on the selected morphological variations. Characters were coded following accepted
norms as dichotomies or presence/absence characters where 0 codes for absence
and 1 for presence of the feature or as quantitative characters which are either two-
or multistate where the rank is of no significance. The data matrix was subjected to
the cluster analysis. The Euclidean distance measured similarity matrix and a den-
drogram was constructed by using the complete linkage method with the NTSYSpc-
2.021 software. The main groups in the dendrogram produced by the numerical
analysis were compared with the recent classification of Friesen et al (2006) and
discrepancies between the two were discussed.

Key words: Allium spp., numerical taxonomic studies, OTU, morphological varia-
tions, euclidean distance

Email: moudutta81@yahoo.com