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KARYOLOGICAL STUDIES OF PHARMACEUTICALY IMPORTANT SPECIES BELONGING TO GENUS *SOLANUM* FOR EVALUATION OF INTERSPECIFIC PHYLOGENETIC RELATIONSHIPS

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Abstract

Solanum L. is a large and varied genus of flowering plants, including high nutritional and additional medicinal benefits. However the taxonomic confusions and non-availability of phylogenetic information leads toward hurdle in breeding, conservation and sustainable utilization of these species. Phylogenetic genetic analysis was conducted using karyological studies of the evolutionary relationship of the taxa under study. Therefore present work was designed to evaluate the 55 accessions and 16 species obtained from 14 different countries of Asia and Europe. Karyotyping is one of the most efficient techniques for the production of reliable taxonomic information. Chromosomal counts revealed during this study that the chromosome number varied over a wide range i.e., 2n=24, 36, 48, 72. The base number in the *Solanum* genus is 12. From the results of present study, it is clear that inter and intra specific variations in chromosome morphology and number can be effectively utilized for the purpose of resolving taxonomic problems. The karyotype was symmetrical in all the genotypes studied.

Keywords: Cytological characters, Genotypes, Nuclear organizer, Polyploidy

Introduction

Globe has a long history of geographical isolation in each continental land masses and has a biota, reflects that isolation is providing genetic diversity into plants. *Solanum* L. is the hyper diverse genus of family Solanaceae. The *Solanum* genus consist of more than 2000 species over the world (Oyelana & Ogunwenmo, 2009), approximately one-half of the whole plant species that comprise the Solanaceae. The *Solanum* the largest genus of Solanaceae has cosmopolitan distribution (Olmstead, 2013). According to Weese and Bohn (2007), *Solanum* consists of about 12 to 15 main clades, the largest of which comprises subgenus *Leptostemonum*, the "spiny *Solanum*" (Levin *et al.*, 2006). *Solanum* is arguably the main economically important genus containing familiar crop species such as potato (*S. tuberosum* L.), and eggplant (*S. melongena* L.), as well as many minor food plants and species containing poisonous or medicinally useful secondary compounds (Weese & Bohs, 2007).

Taxonomists have examined subgroups within the genus or have treated geographically bounded groups of species in regional floras. Phylogenetic studies of *Solanum* subgroups or of the genus as an entire have been sparse. Cladistics analyses based in morphological typescript exists for *Solanum* section *Androcerus* (Nutt.) Marzell (Whalen, 1979). Section *lasiocarpa* (Dunal) D' Arcy (Whalen *et al.*, 1981; Whalen & Caruso, 1983; Bruneau *et al.*, 1995), the *S. nitidum* Ruiz &Pav.Group Section *Holophylla* (G. Don) Walp.Pro parte; (Knapp, 1989) the *S. sessile* Ruiz &Pav.Group Section *Geminata*(G. Don) Walppro.Parte; (Knapp, 1991) subgenus *Leptostemonum* (Dunal) Bitter (Whalen, 1984), subgenus *Potatoe* (G. Don) D' Arcy (Spooner *et al.*, 1993), and subgenus *Archaesolanum* Marzell (Symon, 1994).

Most of the taxonomic confusion surrounding *Solanum* is due to its large size, morphological variation, and predominantly tropical disturiburtion. The last taxonomic monograph of entire genus is over a hundred years old (Dunal, 1852). In previous work of Nee (1999), Child & Lester (2001) and Hunziker (2001) *Solanum* was divided into 2 groups on the basis of morphological characteristics but this kind of classification restricted on new world taxa as it provides the incomplete list of the sections, sub-genera and series. So the monophyly of many *Solanum* groups documented by earlier workers was examined by Bohs, (2005) using molecular data from the chloroplast ndhF gene analyzed using cladistic tactic.

The goal of producing phylogenetic classifications has accelerated greatly in recent years due to three advances: a clear framework for interpreting phylogeny (Hennig, 1966), the integration of modern and old hypothesis about the classification methods that take data about organisms. Revised classifications depicting these ideology and methods have appeared for the Lamiaceae (Cantino *et al.*, 1992) and Asteraceae (Bremer & Jansen, 1992). Molecular techniques are more expensive, laborious, time consuming. Karyology is a technique which is inexpensive and easy to handle. Therefore in the present study this technique is purposed to figure out phylogenetic relationship and estimation of the evolutionary relationship of the taxa under study.

Materials and Methods

Inter and intra specific variation among the various species of the genus *Solanum* was explored by karyological studies in Molecular Taxonomy Lab, Department of Botany, Lahore College for Women University Lahore from August 2012 to October 2013. The seeds of 5 sections of Genus *Solanum* were taken for the present study. Seeds of 16 species represented by 55 accessions were taken from the Botanic Garden Conservation International (BGCI), Botanische Garten der Universitat Bonn and International Seed Exchange Botanischer Garten der WWU MS (Table 1).

Germination of seeds: The seeds were germinated on filter paper at temperature range of 18-20°C which was maintained in an incubator.

Preparation of slides: For the preparation of slides, modified protocol of Mirzaghaderi (2010) was followed. When the emergent roots reached upto 1-2 cm long, they were excised and pretreated in 0.05% colchicine solution for 3hrs in order to capture the cells in mitotic phase. Then the pretreated roots were fixed in 3:1 ethanol: acetic acid for 1 h. After this, the roots were placed in 45% aceto carmine for 5-10 min. Slides were prepared by squashing the root tips in a drop of 45% acetic acid, covered with a cover slip and then examined under the light microscope (model: Meiji techno) for detail analysis of chromosome counts, morphology and meiotic configurations. The sizes of chromosomes were measured with an eye piece graticule at X40 objective.

Data analysis: Photographs were taken from temporary mounts and at least five metaphase cells were examined. Chromosomes were classified according to the nomenclature of (Levan *et al*. 1964) and data was analyzed by SPSS. V 13.0.

Photography of Slides: Microphotographs were taken by using CCD digital camera (model: canon Pc1200 attached with MD lens MA151/30/73opter) fitted on light microscope (model: Mejia techno). The identification of anatomical characters were made by using high power plan (40×/0.65, ∞/0.17, F=200, WD=0.5) and lower power plan (10×/0.25,∞/0.17,F=200,WD=7.3).

Statistical Analysis: The data was evaluated by co-relation matrix and cluster analysis to determine intra specific relationship. Dendrogram was constructed on the basis of unweight pair group method with arithmetic average (UPGMA).The computer software SPSS.V 13.0 was used for this purpose

Results and Discussion

In an effort to bring together the measures of the past years and to identify where present knowledge is most complete and where further work is needed, a summary of Phylogenetic relationship on the basis of karyological studies in *Solanum* was done. Karyotype helps to sort out primitive or advance features of an organism. Therefore, it can be utilized as a reliable tool for systematics. Each of the *Solanum* subgenera Leptostemonum ,show variation into their chromosomal number, structure and behavior. The species belonging to the section *Solanum* form a polyploid series with diploid (2*n*=2*x*=24) tetraploid (2*n*=4*x*=48), hexaploid (2*n*=6*x*=72) levels. In *S. nigrum* the polyploidy series ranges from diploid to hexapolid whereas ploidy levels for *S. scrabum* comprised *of* diploid and hexapolid series while *S. americanum* contained only diploid number and *S. villosum* were tetraploid. (Table 2) According to Datta *et al*. (2010) for *S. nigrum* 2n=24 and *S. americanum*2n=72. Presence of diploid and tetraploid series in *S. nigrum* were reported in earlier researches (Olatunji, 2005).The occurrence of polyploidy in the section *Solanum* is almost certainly the most competent barrier to natural hybridization between these species. Successful crosses are more difficult between taxa of differing ploidy levels than of the same chromosome numbers, with interploidy crosses leading to transitional but sterile progeny. Therefore phonetic complexity is very common in section *Solanum*; however existence of the hybrids for this section is not reported yet.

Two of our functional food species *Solanum incanum* and *Solanum melongena* belonging to section *Melongena* were tetraploid and diploid respectively. Whereas' *Solanum macrocarpon* was recorded as hexapolid (Table 3). Olatunji (2005) worked on varieties of *S. melongena*, *S. macrocarpon* and *S. torvum* and reported these three species as diploids (2n=24). Moreover they also concluded that these species were not polyploids. The karyotype of these species consisted mostly metacentric and sub-metacentric chromosomes. However, few nearly sub-telocentric chromosomes were encountered. The taxa of *S. melongena* and *S. macrocarpon* had the largest chromosomes while *S. torvum* had the smallest (Table 3).

S. torvum was characterized by symmetrical chromosomes and regular bivalents at meiosis. This was contrary to the views of Pringle and Murray (1993) who observed a significant complement between large chromosome size and symmetry of chromosome arms.

Asymmetrical chromosomes were clearly evident in the species *S. melongena* and *S. macrocarpon.* This might have been the result of shift in the position of centromere due to breaks and the subsequent rearrangement of chromosome arms. From the report of Hanson *et al*. (2003), asymmetry of chromosomes has been linked to species' evolutionary divergence. Therefore, the emergence of several chromosome types in populations of *S. melongena* and *S. macrocarpon* appear to have been accompanied by changes in chromosome sizes. It is probable that genomic evolution among the species of *Solanum* resulted from structural chromosomal changes as evident in *S. melongena* and *S. macrocarpon* as well as changes in base chromosome number or ploidy in the few aneuploid cells encountered in the study. Evidence could be seen from chromosome fragments and unequal pairing of bivalents in few species indicative of changes in chromosome structures and dissimilar chromosome complements among species in the genus. Interspecific hybridization equally may have introduced a number of foreign genes, leading to unstable genomes. Ugborogho and Oyelana (1999) and Omidiji (1983) shared the same view.

In current studies section Potato consisting of *S. cardiophyllum, S. colombianum, S. ehrenbergii, S. sotoniferum* were studied. The accessions of *S. tuberosum* L. and *Solanum stoloniferum* were found to possess 2n = 4x = 48 chromosomes or tetraploid and *Solanum cardiophyllum*, and *S. ehrenbergii* were diploid. (Table 4). In present piece of work *Solanum colombianum* was diploid while *Solanum stoloniferum* observed same results. Species of this section are metacentric, sub-metacentric and nearly sub-telocentric chromosomes. However earlier studies (Sultana & Alam, 2007) reported presence of maximum metacentric chromosomes in genus *Solanum.* The abundance of metacentric chromosomes is a characteristic of symmetric karyotype which is primitive in nature (Stebbins, 1971). Therefore, it can be predicted that species of section Potato possess advance character of karyotyping.

In section Oligenthes the meiotic chromosomes of *S. aethiopicum* and *Solanum dulcamara* were diploid. (Table 5) They were metacentric and sub- metacentric. Oyelana A. Olatunji (2005) shared same view about *S. aethiopicum.* Chromosomes were generally symmetrical. Chromosomes were very small in *S. aethiopicum.*

Table 1 Shows Geographical areas of Genus Solanum 16 species and 55 accessions

S.no	Section	Plant Species	Accessions	Location
1	Section Solanum	*Solanum nigrum* L.	381289	Japan
			381421	Japan
			0061	Germany
			0060	Germany
			0045	Germany
			3062	Germany
			3907	Pakistan
			3906	Pakistan
2		*Solanum Scabum* Mill.	Grif 14198	US, Minnesota
			PI 643126	Pakistan
			38065	Pakistan
3		*Solanum americanum* Mill.	PI 268152	United States
			PI 268153	
			3900	Pakistan
4		*Solanum Villosum* Mill.	307	India
			123	India
			3901	Pakistan
5	Section Melongena	*Solanum anguivi* Lam.	PI 319855	Thailand
			PI 194789	India
			PI 194656	Pakistan
6		*Solanum incanum* L.	PI 390211	Japan
			PI 500922	Zambia
			PI 387339	Pakistan
7		*Solanum macrocarpon* L.	PI 441915	Brazil
			PI 643126	pakistan
8		*Solanum melongena* L.	PI 173107	Turkey, Urfa
			Grif 1254	Thailand
			18477	Egypt
			20344	Pakistan
			18482	Pakistan
			18487	Pakistan
9		*Solanum torvum* Sw.	19705	Kuba
			19708	Kuba
			6225	Pakistan
10	Section Potato	*Solanum cardiophyllum*	PI 283062	Mexico
			PI 283063	Mexico
			PI 341235	Mexico
			PI 347759	Mexico, Puebla
			PI 595466	Mexico, Puebla
			PI 341232	Mexico
11		*Solanum colombianum*	PI 561633	Ecuador, Pichincha
12		*Solanum ehrenbergii* Rydberg	PI 545824	Mexico, Zacatecas
			PI 597678	Mexico, Queretaro
13		*Solanum stoloniferum* L.	PI 558453	Mexico, Jalisco
			PI 558474	Mexico, Oaxaca
14		*Solanum tuberosum* L.	PI 243382	Pakistan
			PI 214430	Pakistan
15	Section oliganthes	*Solanum aethiopicum* L.	PI 441875	Brazil, Minas Gerais
			PI 21580	Germony
			PI 441906	Brazil
16	Section Dulcamara	*Solanum dulcamara* L.	0700	Germany
			0402	Germany
			0181	Germany
			77RD564	Germany
			331104	Germany

The center of diversity of the diploid species, however, appears to survive the New World, particularly in South America. Both Central and North America also appear to have morpho-genetically distinct diploid species, while the morphologically variable taxon S. *americanum* occurs all over the Old and New Worlds. It is also probable that *S. nigrum* might have had an autoalloploid origin, with *S. americanum* contributing two sets of genomes in the form of two infraspecific variants. Evidently more experimental work, especially involving the Afro-Asian taxa, is needed to determine the accurate mode of origin of this Old World hexaploid species. It is generally thought that the polyploid members of the section *Solanum* are mostly alloploids, since most species so far investigated cytological illustrate regular bivalent formation at meiosis. However, it is promising that some of these polyploids might have arisen through the functioning of unreduced gametes, as well as by somatic chromosome doubling. Edmond recorded both such phenomena on several occasions when the hybridization of maternal diploids with paternal tetraploids resulted in tetraploid, instead of the expected triploid, progeny. It is also very likely that these polyploids have arisen from comparatively few diploid species contributing genomes in different combinations.

For different reasons it is hard to broadly contrast widely-used morphology-based taxonomic schemes of previous *Solanum* systematics with the structure proposed in present studies. D'Arcy (1972) listed only the specific species for each section and did not provide morphological definitions for his subgenera and sections, so placing other species in his classification are difficult. Nee (1999) provides an explicit list of species thought to belong to his subgenera and sections, but his treatment is restricted mostly to New World taxa. Hunziker (2001) summarizes *Solanum* classification, but his system is based primarily on previous schemes of D'Arcy and Nee.

Cluster analysis based on karyological characters i.e., Chromosomes numbers, long arm and short arm length, arm ratio, total length, difference between long arm and short arm, centromere index and chromosomal nomenclature revealed that the fifty five accessions of 15 species of genus *Solanum* were divide into two main clusters 1 and 2 at phylogenetic distance 100% (Fig. 1). At 59% genetic linkage group 1 is further divided into 1a and 1b. At 16% genetic linkage 1a further divided into 1ai and 1aii. The Germplasm included in 1ai are *Solanum aethiopicum* 21580, *S. nigrum* 45, *S. nigrum* 60, *S. nigrum* 61, *S. nigrum* 381421, and *S. nigrum* 381289. The plants included in 1aii are *S. nigrum* 3062, *S. nigrum* 3906, *S. scabum* Griff 14198, *S. vilosum 307*, 38065, *S. stoloniferum* PI 558453, *S. incanum* PI 390211 and *S. americanum* 3900, 301, *S.villosum*123.1b is further divided into At 25% group 3 is divided into the 2a and 2b and 2c. The 2a include *S. dulcamara* 402 accessions. At 25% group b is further divided into 2bi and 2bii. The accessions include in 2bi are *Sola dulcamara* 181, 71, *S. dulcamara*, 331104, *S. macrocarpon* PI 441906, PI 194789, *S. nigrum*. The accessions include into 2bii are PI 194656, 387339, PI 194789, S. anguivi PI 319855. At 23% 2c is divided into the 2ci and 2cii. The accession included in 2ci *S. incanum* PI 500922, *S. melongena* PI 173107, *S. anguivi* 194656, *S. incanum* 390211, *and S. macrocarpon* PI 441915, 18482.

The accessions included into 2cii 18487, 19075, *S. americanum*, *S. cardiophyllum* PI 283062, *S. torvum* 6225, *S. macrocarpon*PI 441915, *S. cardiophyllum* PI 283062, *S. cardiophyllum* PI 283063, *S. scabum* Grif 14198, *S. torvum* 19705, *S. cardiophyllum* PI 341232, *S. stoloniferum* PI 558474, *S. americanum* PI 268152, S. ehrenbergii PI 545824 , *S. colombianum* PI 561633 , *S. aethiopicum* PI 441875.

Bohs, (2005) projected an unconventional classification for Solanum in which about 12-13 major lineages were recognized and given informal clade names. These clades names were, Morelliod, Normania, Leptostemonum, and Arechosolanum, African non-spiny, Potato, Regmandra, Thelopodium, Brevantherum, Geminata, and Cyphomandra. In present piece of work Morelloid, potato, Leptostemonum, Dulcarmaroid clades are examined. The Section dulcarma section potato and section Solanum are connected with each other, but section Potato was not flanked by these two sections in the previous work so we have same results with (Bohs, 2005) combined analysis of gene ndhF, trnTF and waxy data. In the Weese & Bohs (2007) research section melongena and section oliganthes are closer in Leptostemonum clade II and we have same findings with reference to that section. Phylogenetic relationship analysis was conducted using data from the chloroplast gene ndhf by (Bohs & Olmstead, 1997).

From the results of present study, it is clear that inter and intra specific variations in chromosome morphology and number can be effectively utilized for the purpose of resolving taxonomic problems. However for the phylogenetical studies some other techniques also have to combine with this to figure out the true picture of phylogeny of the genus *Solanum*.

Based on present study it is concluded that karyology is very efficient and cheap tool for evaluating the phylogenetic relation, However additional karyotype studies are badly needed in more members, using not only classical but modern techniques like fluorescent banding and FISH techniques to reach an embracing view of the evolutionary tendencies in the Solanoideae clade. From the results of present study, it is clear that inter and intra specific variations in chromosome morphology and number can be effectively utilized for the purpose of resolving taxonomic problems.

Table 2: Karyological information of Section *Solanum*

S. No	Plant Species	A	n	L (µm)	S (µm)	T=S+L	R=L/S	d =(L-S)	S/T×100	Chromosome nomenclature
1	*Solanum nigrum*	381289	12	5.2	3.2	8.4	1.62	2.0	38.09	metacentric
		381421	24	7.1	3.5	10.6	2.02	3.6	33.01	Sub-metacentric
		0061	24	3.7	2.4	6.1	1.54	1.3	39.34	metacentric
		0060	48	5.2	2.7	7.9	1.92	2.5	34.17	Sub-metacentric
		0045	72	7.2	4.2	11.4	1.71	3.0	36.84	Nearly sub-metacentric
		21580	48	7.5	3.5	11	2.14	4.0	31.81	Sub-metacentric
		3062	48	6.1	4.1	10.2	1.48	2.0	40.19	metacentric
		3907	48	5.3	2.5	7.8	2.12	2.8	32.05	Sub- metacentric
		3906	48	6.0	3.9	9.9	1.54	2.1	39.33	metacentric
2	*Solanum Scrabum*	Grif 14198	24	5.4	3.2	8.6	1.68	2.2	37.20	metacentric
		PI 643126	72	6.9	4.8	11.7	1.43	2.1	41.02	metacentric
		38065	24	5.5	3.3	8.8	1.67	2.2	37.50	metacentric
3	*Solanum americanum*	PI 268152	24	4.1	3.6	7.7	1.13	0.5	46.75	metacentric
		PI 268153	12	5.3	2.3	7.6	2.30	3.0	30.26	Sub-metacentric
		3900	24	4.3	3.0	7.3	1.44	1.3	41.09	metacentric
4	*Solanum villosum*	307	48	4.5	3.4	7.9	1.32	1.1	43.03	metacentric
		123	48	4.0	3.2	7.2	1.25	0.8	44.44	metacentic
		3901	48	3.0	2.5	5.5	1.20	0.5	45.45	metacentric

Key: S = short arm length, L = long arm length, R= arm ratio, T= total length, d= Difference between short and long arm, S/T×100 centromere index, chromosomal nomenclature.

Table 3: Karyological information of Section *Melongena*

S. No	Plant Species	A	CN/cell	L(µm)	S(µm)	T=S+L	R=L/S	d =(L-S)	S/T×100	Chromosome nomenclature
5	*Solanum anguivi*	PI 319855	12	6.6	4.2	10.8	1.57	2.4	38.88	metacentric
		PI 194789	12	4.0	3.0	7.0	1.33	1.0	42.85	metacentric
		6253	12	4.5	3.2	7.7	1.40	1.3	41.55	metacentric
6	*Solanum incanum*	PI 390211	48	6.1	4	10.4	1.52	2.1	38.46	metacentric
		6230	48	5.3	3.4	7.7	1.55	1.9	44.15	metacentric
		PI 500922	48	6.4	3.2	9.6	2.00	3.2	33.3	Sub-metacentric
7	*Solanum melongena*	PI 173107	*24*	7.5	7.0	14.5	1.07	0.5	48.27	Metacentric
		Grif 1254	*24*	5.0	3.6	8.6	1.38	1.4	41.86	Metacentric
		18477	*24*	8.4	7.2	15.6	1.16	1.2	46.15	Metacentric
		20344	*24*	7.1	6.3	13.4	1.13	0.8	47.01	Metacentric
		18482	*24*	9.0	8.6	17.6	1.04	0.4	48.86	Metacentric
		18487	*24*	8.2	7.1	15.3	1.15	1.1	46.40	Metacentric
		19705	*48*	1.3	0.9	2.23	1.37	0.4	40.35	Metacentric
		19708	*48*	1.5	0.7	2.14	1.45	0.8	32.71	Metacentric
		6225	*48*	1.4	0.8	2.20	1.75	0.6	36.36	Metacentric
		PI 441915	*24*	7.1	5.2	12.3	1.36	1.9	42.27	Metacentric

Key: S = short arm length, L = long arm length, R= arm ratio, T= total length, d= Difference between short and long arm, S/T×100 centromere index, chromosomal nomenclature.

Table 4: Karyological information of Section Potato

S. No	Plant Specie	A	n	L (µm)	S (µm)	T=S+L	R=L/S	d =(L-S)	S/T×100	Chromosome nomenclature
10	*Solanum tuberosum*	PI 243382.5	48	1.57	0.52	2.09	3.01	1.0	24.88	Nearly sub-telocentric
		PI 214430.1	48	1.45	0.52	1.97	2.78	0.9	26.39	Sub-metacentric
11	*Solanum cardiophyllum*	PI 283062	24	4.5	3.1	7.6	1.45	1.4	40.78	metacentric
		PI 283063	24	5.2	2.2	7.4	2.36	3.0	29.72	Sub-metacentric
		PI 341235	24	5.5	3.2	11.9	1.71	2.3	26.89	Nearly sub-metacentric
		PI 347759	24	4.8	2.1	6.9	2.28	2.7	30.43	Sub-metacentric
		PI 595466	24	7.2	5.3	12.5	1.35	1.9	42.40	metacentric
		PI 341232	24	6.4	5.4	11.8	1.18	1.0	45.76	metacentric
12	*Solanum colombianum*	PI 561633	24	5.3	4.3	9.6	1.23	1.0	44.79	metacentric
13	*Solanum ehrenbergii*	PI 545824	24	3.0	2.4	5.4	1.25	0.6	44.44	metacentric
		PI 597678	24	5.8	3.2	8.7	1.81	2.6	36.78	Sub-metacentric
14	*Solanum stoloniferum*	PI 558453	48	2.7	1.9	4.6	1.42	0.8	41.30	metacentric
		PI 558474	48	3.3	2.1	5.4	1.57	1.2	38.88	metacentric

Key: S = short arm length, L = long arm length, R= arm ratio, T= total length, d= Difference between short and long arm, S/T×100 centromere index, chromsomal nomenclature.

Table no. 5 Karyological information of Section dulcamara and oliganthes

S. No	Plant Species	A	n	L(µm)	S (µm)	T=S+L	R=L/S	d =(L-S)	S/T×100	Chromosome nomenclature
15	*Solanum dulcamara*	0070	24	7.5	3.7	11.2	2.02	3.8	33.03	Sub-metacentric
		0402	24	8.5	3.6	12.1	2.36	4.9	29.75	Sub-metacentric
		0181	24	3.1	2.5	5.6	1.24	0.6	44.65	metacentric
		0071	24	3.9	2.0	5.9	1.95	1.9	33.89	Sub-metacentric
		77RD564	24	5.4	3.2	8.6	1.68	2.2	37.20	Sub-metacentric
		331104	24	6.8	4.2	11	1.61	2.6	38.18	metacentric
16	*Solanum aethiopicum*	PI 441875	24	1.1	0.9	2.0	1.23	0.45	49.01	metacentric
		PI 441906	24	1.3	1.1	2.4	1.21	0.23	45.80	metacentric
		21580	24	5.5	4.3	14.3	1.27	1.2	30.06	metacentric

Key: S = short arm length, L = long arm length, arm ratio, total length, Difference between short and long arm, centromere index, Chromosomal nomenclature.

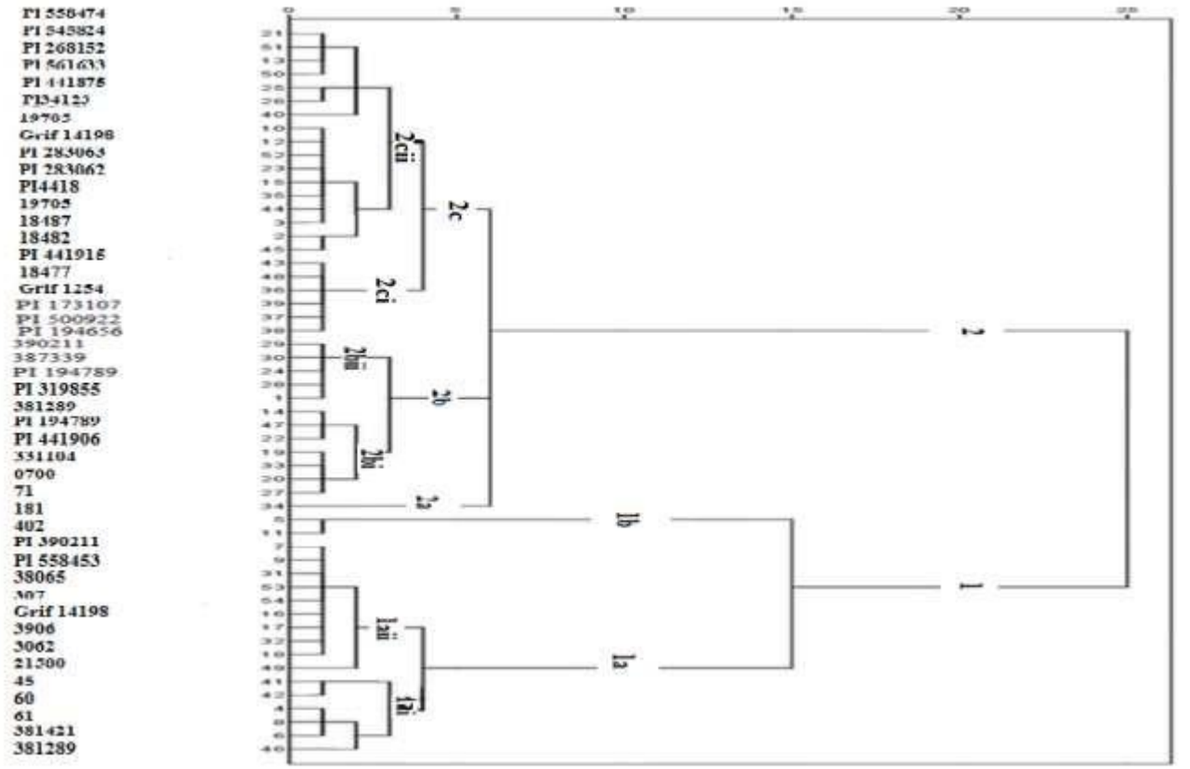

Figure 1: Cluster analysis of Genus *Solanum* containing 15 species and 55 accessions on the basis of karyological characters

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