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VARIATION IN ARRANGEMENT OF VEGETATIVE AND REPRODUCTIVE NODES ON LATERAL BRANCHES OF TWO VIRGINIA FORMS OF PEANUT GERMPLASM

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The arrangement of vegetative and reproductive nodes were examined on basal, primary and secondary branches of 75 accessions each of Virginia bunch and Virginia runner forms of cultivated peanut (Arachis hypogaea *L. ssp.* hypogaea *Krap. et. Rig. var.* hypogaea *Krap. et. Greg.). The main axis was devoid of flowers (inflorescences) on all the plants of both the forms. The node sequence, in general, started with vegetative nodes on primary branches and reproductive nodes on secondary branches in both the forms. There was predominant occurrence of one to five reproductive nodes on secondary branches of both the forms. A few accessions had a continuous sequence of three to five reproductive nodes on secondary branches. On primary branches of Virginia bunch collection, three alternate irregular pairs of node sequences starting with vegetative nodes were recorded in 43.1% plants followed by four pairs in 25.9% plants, whereas in Virginia runner, four pairs (37.%) followed by three pairs (27.7%) were frequent. On the other hand, one pair starting with reproductive nodes on secondaries was predominant in 74.8% and 68.5% plants, respectively. The regular sequence of two vegetative alternating with two reproductive nodes was found on primaries of only 17.2% and 13.1% plants of Virginia bunch and Virginia runner, respectively. The alternate irregular sequences with all possible combinations numbering 111 on primary branches and 62 on secondaries were found in both the populations and thus, sequences with predominant occurrence could not be spotted. The wide variation for this trait in the sampled population, besides overlapping variation within and between the two forms confirmed that node sequence was controlled by polygenes. This trait may not be suitable for identification of Virginia genotypes in the primary gene pool of cultivated peanuts and also in differentiation between the two forms. The role of node sequence in breeding Virginias was also discussed.*

The primary gene pool of cultivated peanuts (*Arachis hypogaea* L) was classified into two sub-species, namely, *hypogaea* Krap. *et.* Rig. and *fastigiata.* Waldron based primarily on alternate and sequential branching pattern, respectively (Gregory *et al.*, 1951; Bunting, 1955; Krapovickas and Rigoni, 1960). The central axis in sub-species *hypogaea* never bears inflorescence directly (Stockton-Petit, 1895) and lateral branches bear two vegetative branches (nodes) alternating regularly with two reproductive branches (Bigi, 1950; Gregory *et al.*, 1951 and Bunting, 1955). This sub-species was further divided into two varieties, namely, *hypogaea* Krap. *et.* Greg.

and *hirsuta* Kohler (Krapovickas, 1968, 1973 and Gregory and Gregory, 1976). In var. *hypogaea,* two forms were further recognised, namely, Virginia bunch and Virginia runner (Krapovickas, 1968), commonly referred to in India as semi-spreading and spreading forms, respectively. The number and arrangement of vegetative and reproductive branches (nodes) served as a basis for varietal classification (Gregory *et al.*, 1973) but this system was found unsatisfactory for the intermediate forms collected from South America (Krapovickas and Rigoni, 1960). Recently wide variation was observed in vegetative and reproductive node number and its sequence on the basal primary branches of 100 Virginia runner accessions and arrangement of nodes upto 3 orders were described (Bhagat *et al.,* 1987). This investigation was further extended to both Virginia bunch and Virginia runner forms and all the nodes from base to the tip of the vegetative bud on primary and secondary branches were examined to confirm variation in the arrangement of vegetative and reproductive nodes in the germplasm collection.

MATERIALS AND METHODS

The national peanut germplasm collection of Virginia bunch and Virginia runner forms (numbering 2420 accessions) was field-planted at the onset of the regular monsoon on June 19, 1986 in an augmented block design (Federer, 1956). Each entry was grown in a 3 metre long row, spaced 60cm apart, with 10cm spacing between plants within a row. The crop was raised under rainfed conditions following recommended cultural practices. For this study, 75 accessions each of Virginia bunch and Virginia runner forms were randomely selected. At the time of harvest, 14-16 random plants of each accessions were examined for all vegetative (V) and reproductive (R) nodes (branches) on the main axis (n), primary (n+1) and secondary (n+2) branches.

The entire plant population of each form was separated into two parts, based on whether the first node was vegetative or reproductive on primary and secondary branches. Each sub population was further classified on the occurrence of alternate pairs of nodes (vegetative followed by reproductive or reproductive followed by vegetative). Finally, arrangement of nodes, both alternate irregular and alternate regular, was scored on primary and secondary branches of each form. Populations of 1175 and 1057 plants of 75 accessions each of Virginia bunch and Virginia runner, respectively, were studied.

RESULTS AND DISCUSSION

It was observed that all the plants did not bear flowers on the main axis. On primary branches of both the forms, the first two nodes were predominantly vegetative in 68.8 per cent plants and in 53.7 per cent plants, respectively (Table 1). The sequence starting with one vegetative node, however, was observed in 27.8 per cent and 35.1 per cent plants in Virginia bunch and Virginia runner collections, respectively. The sequence starting with reproductive node was scored in 3.4 per cent plants of Virginia bunch and in 11.2 per cent plants of Virginia runner collections. Similar observations were earlier reported in Virginia runner collection (Bhagat *et al.,* 1987).

Table 1. Plant population starting with vegetative (V) and reproductive (R) nodes on primary and secondary branches in two Virginia peanut germplasm

First order sequence	Nodes	Virginia bunch		Virginia runner	
		Primary branch	Secondary branch	Primary branch	Secondary branch
Starting with vegetative	1V	327 (27.8)	164 (13.9)	371 (35.1)	82 (7.8)
	2V	808 (68.8)	28 (2.4)	568 (53.7)	15 (1.4)
		1135 (96.6)	192 (16.3)	939 (88.8)	97 (9.2)
Starting with reproductive	1R	–	69 (5.9)	–	77 (7.3)
	2R	24 (2.0)	477 (40.6)	54 (5.1)	442 (41.8)
	3R	13 (1.1)	350 (29.8)	41 (3.9)	330 (31.2)
	4R	3 (0.3)	70 (6.0)	14 (1.3)	99 (9.4)
	5R	–	17 (1.4)	9 (0.9)	12 (1.1)
		40 (3.4)	983 (83.7)	118 (11.2)	960 (90.8)
	Total	1175	1175	1057	1057

Figures in parentheses indicate percentage

On the other hand, the sequence starting with one to five reproductive nodes on secondary branches was observed in 83.7 per cent and 90.8 per cent plants of Virginia bunch and Virginia runner collections, respectively (Table 1). The sequence starting with vegetative nodes was, however, observed in 16.3 per cent plants of Virginia bunch and 9.2 per cent plants of Virginia runner collections. Among these, the sequence starting with two reproductive nodes was predominantly recorded in 40.6 per cent and 41.8 per cent plants in Virginia bunch and runner collections, respectively, followed by three reproductive nodes in 29.8 per cent and 31.2 per cent plants, respectively.

The sequence, in general, started with vegetative nodes on primary branches and reproductive nodes on secondary branches in both categories of the collections. In Virginia peanuts, the continuous occurrence of one to five reproductive nodes on secondary branches contribute directly towards increased number of pods and, thus, these two forms possess high productive potential than the other forms of cultivated peanuts. Higher contribution of pods formed on secondary branches in Spanish genotypes were also reported (Choudhary *et al.*, 1985; Shashidhar *et al.*, 1986). Though there was variation in number of reproductive nodes on secondary branches of both Virginia collections, a few accessions having a long sequence of three to five reproductive nodes on secondaries were available in the collection. Therefore, intensified screening of germplasm for the ideotypes having a continuous occurrence of reproductive nodes on secondaries with pods clustered around the tap root zone may be undertaken so that synchrony in pod maturity could be achieved in breeding programme, since the presently grown commercial Virginia varieties in India are devoid of this important trait and thus, the pod losses in farmers' field are high, ranging from 12 to 25 per cent.

There was variation between plants of each accessions and therefore, the entire plant population of each form was pooled for further grouping based on occurrence of alternate sequence pairs ranging from one to five (vegetative followed by reproductive or reproductive followed by vegetative nodes) from the base to the tip of primary and secondary branches, respectively. In Virginia bunch collection, three alternate pairs of sequence starting with vegetative nodes were recorded in 43.1 per cent plants followed by four pairs in 25.9 per cent plants while in Virginia runner, four pairs were observed in 37 per cent plants followed by three pairs in 27.7 per cent plants on primary branches (Table 2). One pair of node sequence was not found in both the forms on primary branches, whereas on secondary branches, it was recorded in 74.8 per cent plants of Virginia bunch and 68.5 per cent plants of Virginia runner collections. The presence of wide variation of higher order sequences ranging from 3 to 5 on primary branches and lower order 1 to 3 on secondary branches of both the forms was due to initiation of primary branches at 4-6 leaf stage followed by secondary branches on it at latter stages of the plant growth. It was further observed that the occurrence of higher order sequences in Virginia runner and lower order in Virginia bunch accessions reflected in late maturity of Virginia runner (135-150 days) as against 115-125 days in Virginia bunch accessions.

As reported, the arrangement of nodes in Virginia forms should have two vegetative alternating with two reproductive nodes uniformly on the primary and

Table 2. Number of plants with alternate (irregular and regular) sequence pairs of one to five order in Virginia bunch and Virginia runner peanut germplasm

Sequence pairs	Virginia bunch				Virginia runner			
	Primary branch		Secondary branch		Primary branch		Secondary branch	
	Number of combinations	Number of plants	Number of combinations	Number of plants	Number of combinations	Number of plants	Number of combinations	Number of plants
Alternate irregular								
(1) Starting with vegetative nodes								
1 pair	–	–	6	104 (8.8)	–	–	6	50 (4.7)
2 pairs	16	84 (7.2)	12	64 (5.5)	–	–	4	23 (2.2)
3 pairs	31	506 (43.1)	5	7 (0.6)	28	293 (27.7)	6	14 (1.3)
4 pairs	25	304 (25.9)	–	–	28	391 (37.0)	–	–
5 pairs	20	39 (3.3)	–	–	20	117 (11.1)	–	–
(2) Starting with reproductive nodes								
1 pair	–	–	16	879 (74.8)	–	–	14	724 (68.5)
2 pairs	8	11 (0.9)	20	100 (8.5)	–	–	23	205 (19.4)
3 pairs	7	25 (2.1)	3	4 (0.3)	17	76 (7.2)	11	31 (2.9)
4 pairs	4	4 (0.3)	–	–	14	38 (3.6)	–	–
5 pairs	–	–	–	–	4	4 (0.3)	–	–
	111	973 (82.8)	62	1158 (98.5)	111	919 (86.9)	64	1047 (99.0)
Alternate regular								
1 pair	–	–	1	16 (1.4)	–	–	1	8 (0.8)
2 pairs	1	15 (1.3)	1	1 (0.1)	–	–	1	2 (0.2)
3 pairs	1	126 (10.7)	–	–	1	46 (4.4)	–	–
4 pairs	1	56 (4.8)	–	–	1	62 (5.9)	–	–
5 pairs	1	5 (0.4)	–	-	1	30 (2.8)	–	–
	4	202 (17.2)	2	17 (1.5)	3	138 (13.1)	2	10 (1.0)

Figures in parntheses indicate percentage

Table 3. Number of plants showing major alternate irregular node sequence on the primary and secondary branches of two Virginia peanut germplasm

Order of sequence pairs	Virginia bunch		Virginia runner	
	Primary branch	Secondary branch	Primary branch	Secondary branch
a) *Starting with vegetative nodes*				
(1V+1R)	-	21 (1.8)	-	-
(1V+2R)	-	46 (3.9)	-	26(2.4)
(1V+3R)	-	21 (1.8)	-	-
(2V+2R) + (1V+2R) + (2V+2R)	73 (6.2)	-	34 (3.2)	-
(2V+3R) + (2V+2R) + (2V+2R)	67 (5.7)	-	37 (3.5)	-
(2V+2R) + (1V+2R) + (2V+2R) + (2V+2R)	77 (6.5)	-	57 (5.4)	-
b) *Starting with reproductive nodes*				
(3R+2V)	-	191 (16.2)	-	144 (13.6)
(2R+2V)	-	228 (19.4)	-	169 (16.0)
(3R+2V) + (2R+2V)	-	23 (1.9)	-	43 (4.1)
(2R+2V) + (2R+2V)	-	-	-	59 (5.6)

Figures in parentheses indicate percentage secondary branches (Bigi, 1950; Gregory *et al.*, 1951 and Bunting, 1955), but in the present material this regular sequence was recorded on primary branches of only 17.2 per cent plants of Virginia bunch and 13.1 per cent plants of Virginia runner and on secondary branches of only 1.5 per cent and 1 per cent plants, respectively (Table 2). On the other hand, alternate irregular sequence numbering 11 on primary branches and about 62 combinations on secondary branches with all possible combinations of vegetative (1-3) and reproductive (1-5) nodes were recorded in majority of plants of both the forms (Table 2). In these highly variable populations, sequence which occurred in more than 20 plants are listed in Table 3. Among these, only one order sequence starting with reproductive nodes, namely, 2R+2V and 3R+2V occurred often, respectively, on secondary branches of 19.4 per cent and 16.2 per cent plants of Virginia bunch and 16 per cent and 13.6 per cent plants of Virginia runner accessions.

The majority of the sampled Virginia accessions included in this study constitute from secondary (29) and tertiary (116) centres of diversity and the genetic variation in this trait might have generated either by infrequent cross pollination in nature (Stone, 1973) or inter-sub-specific hybridization attempted by the breeders followed by purposeful selection for desired intermediate forms. The arrangement of vegetative and reproductive nodes on both primary and secondary branches of two Virginia populations appeared quantitative in nature confirmed earlier (Wynne, 1975). Further, the wide variation within each accessions and overlapping variation between the two forms for this trait made differentiation of Virginia bunch and runner forms based on node sequence difficult. Thus, this trait may not be considered suitable for identification of Virginia genotypes in the primary gene pool of cultivated peanuts. However, of course, accessions of these forms were devoid of flowers (inflorescences) on the main axis and may continue to be a basic characteristics in botanical classification.

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