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Characterization and selection of superior walnut (*Juglans regia* L.) genotypes based on growth parameters in the North-Western Himalaya

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Abstract

North-Western Himalayan region of Jammu and Kashmir has significant Persian walnut (*Juglans regia* L.) trees, most of which are of seedling origin. The region have rich morphological, phenological, and carpological walnut diversity because of the large variability of native walnut, resulting from cross-pollination and seedling propagation. The present study was carried out in order to document the available genetic variability in walnut germplasm and to select elite walnut genotypes possessing superior attributes and quality traits. During the survey, data was recorded on fifty five (55) walnut trees growing in Budgam and Ganderbal areas of Kashmir valley. Remarkable variability was observed in seedling walnut trees for different morphological, nut and kernel characters. Studies on tree vigour and growth habit revealed substantial variability among the seedling raised walnuts genotypes in Kashmir valley. Tree vigour ranged from low to high. Out of 55 genotypes 21 genotypes (38.18%) possessed medium tree vigour, 34 genotypes (61.81%) were strong in tree vigour. Growth habit of 10 (18.18%) genotypes exhibited upright habit five from each district, sixteen (29.09%) genotypes had semi upright growth habit and 29 (52.76%) genotypes possessed spreading growth habit.

Keywords: Walnut, diversity, tree vigour and growth habit

1. Introduction

Walnut (*Juglans regia* L.) belongs to the family Juglandaceae with sporophytic chromosome number $2n=2x=32$. It is commonly recognized as a "Jupiter's royal acorn" and in Kashmiri language it is called 'Doan'. English or Persian walnut is a member of the genus *Juglans* comprising of over 20 species including eastern black walnut (*J. nigra*), heartnut (*J. ailantifolia* var. *cordiformis*), and butternut (*J. cinerea*). *Juglans regia* is monoecious and self-fertile but usually outcrosses because it is heterodichogamous, with some genotypes protoandrous (male shed pollen first) and others protogynous (female become receptive first). An ideal walnut cultivar must have late leafing, both terminal and lateral bearing, low incidence of pistillate flower abscission, relatively smooth shell, 50% kernel recovery, plump and light-colored kernel, high yielding nuts (6 MT/ha) with large size, and at least moderately resistant to pests and diseases (Cosmulescu *et al.*, 2010, Botu *et al.*, 2010) [46, 34]. Walnut breeding is important for developing new cultivars through hybridization, although it is both time consuming and cumbersome. Furthermore, the collection, evaluation, and identification of superior genotypes from existing populations are prerequisites in any walnut-breeding programme (Botu *et al.*, 2010) [34]. Therefore, it is convenient to exploit existing variability by making appropriate selections based on ideal characters such as tree vigour, growth habit, late leafing, lateral bearing, precocity, high productivity, nut and kernel quality, and resistance to major diseases. For the selection of superior genotypes, walnut's germplasm is commonly evaluated with morphological descriptors. This is the first step in classifying and describing germplasm (Khadivi-Khub, 2014) [37] and the selection of superior genotypes suited to specific growing conditions.

Experimental Methods

The present investigation entitled 'Characterization and selection of superior walnut (*Juglans regia* L.) in the North-Western Himalaya based on growth characteristics was carried out during the crop seasons of 2018 and 2019. The studies comprised two clusters of germplasm extending over the main geographical distribution of cultivation in the two districts of Kashmir valley (Budgam and Ganderbal).

Genetic variability studies and diversity were estimated in the natural walnut population of Kashmir valley forming two cluster populations. Two standard check cultivars (Sulaiman and Hamdan) were used for comparison. Cluster-I: In this cluster comprised 26 earmarked seedling raised genotypes were identified after detailed survey of the areas having large concentration of the crop in the district of Budgam. Cluster-II: This cluster comprised of 29 open populated seedling raised plants or genotypes that were identified. The data of both the clusters (over 2 years) was pooled together for statistical analysis. Morphological characters were recorded as per the Standard Descriptor of Walnut recommended by UPOV, 2015 and PPV&FRA, 2012 [5].

Results and Discussion

The present investigation comprised of fifty five seedling genotypes found growing in various regions of Kashmir valley together with two standard checks (Sulaiman and Hamdan). Most of the seedling trees were indigenous of Kashmir valley. Tremendous variation in configuration of land surface, vegetation aspect, and meteorology and soil type was encountered during the study. The geographical variation has resulted in sizeable genetic diversity in walnuts. The seedlings identified and catalogued in this study represent a cross section of walnut germplasm available in Kashmir. An attempt has been made to evaluate this germplasm in respect of various descriptive and quantitative characters and measures their diversity. Studies on tree vigour and growth habit was revealed substantial variability among the seedling raised walnuts genotypes in Kashmir valley. From (table 1 & Fig 1) it was revealed that out of 55 genotypes, 10 (18.18 %) genotypes had upright growth habit and another 16 genotypes (29.09%) had semi-erect/semi upright growth habit, while

remaining 29 genotypes (52.76%) had spreading growth habit. Walnut genotypes PnWS-053, KhWS-050, PWS-065, SWS-048, CWS-023, NWS-005, RWS-004, NMWS-027, KhWS-057 and KhWS-058 had upright growth habit, TWS-041, MWS-026, RWS-018, MWS-025, SWS-033, MWS-035, RWS-003, CWS-051, AWS -011, BWS-025, NWS-069, SWS-005, KWS 045, NWS 012, OWS-042, KWS-056 and Sulaiman walnut selections exhibited erect/semi upright growth habit. Whileas, SWS-068, PWS 033, BWS-028, GWS-023, KWS-025, CWS-047, SWS-007, BWS-027, BWS-024, AWS-038, PWS-016, AWS-037, BWS-043, KWS-002, AWS036, SWS-002, KhWS050 RWS-039, TWS-039, RWS-006, TWS-044, LWS-055, RWS-008, NWS-070, CWS-046, GWS-030, BWS-046, NzWS-054, PnWS-061 and Hamdan showed spreading growth habit. In the present study out of 55 genotypes 21 genotypes (38.18%) possessed medium vigour and 34 genotypes (61.81%) were strong genotypes in terms of vigour and 0 genotypes showed weak and very strong genotypes. Walnut selections KWS-025, CWS -047, SWS-007, BWS-027, BWS-024, AWS-038, KWS-045, NWS-012, OWS-042, KWS-056, SWS-068, PWS-033, BWS-028, GWS-023, TWS-041, MWS-026, RWS-018, MWS-025, SWS-033, MWS-035, RWS-003 and Sulaiman were intermediate in tree vigour and walnut selections CWS-051, AWS-011, BWS-025, NWS-069, SWS-005, AWS-037, BWS-043, PnWS-053, KhWS-050, PWS-065, SWS-048, CWS-023, NWS-005, RWS-004, NMWS-027, RWS-039, TWS-039, RWS-006, TWS-044, LWS -055, RWS-008, NWS-070, CWS-046, GWS-030, BWS-046, NzWS-054, PnWS-061, KWS-002, AWS036, SWS-002, KhWS-050, KhWS-057, KhWS-058, PWS-016 and Hamdan were strong in vigour.

Table 1: Tree characteristics of walnut (*Juglans regia* L.) genotypes.

Parameter Location	Growth habit			Total	Tree vigour				Total
	Upright (1)	semi upright (2)	Spreading (3)		Weak (5)	Medium (3)	Strong (7)	Very strong (9)	
Budgam	5	9	12	26	0	10	16	0	26
	19.2%	34.6%	46.2%	100.0%	0%	38.52%	61.51%	0%	100.0%
Ganderbal	5	7	17	29	0	11	18	0	29
	17.24%	24.13%	58.62%	100.0%	0%	37.91%	62.11%	0%	100.0%
Total	10	16	29	55	0	21	34	0	55
	18.18%	29.09%	52.76 %	100.0%	0%	38.18%	61.81%	0%	100.0%

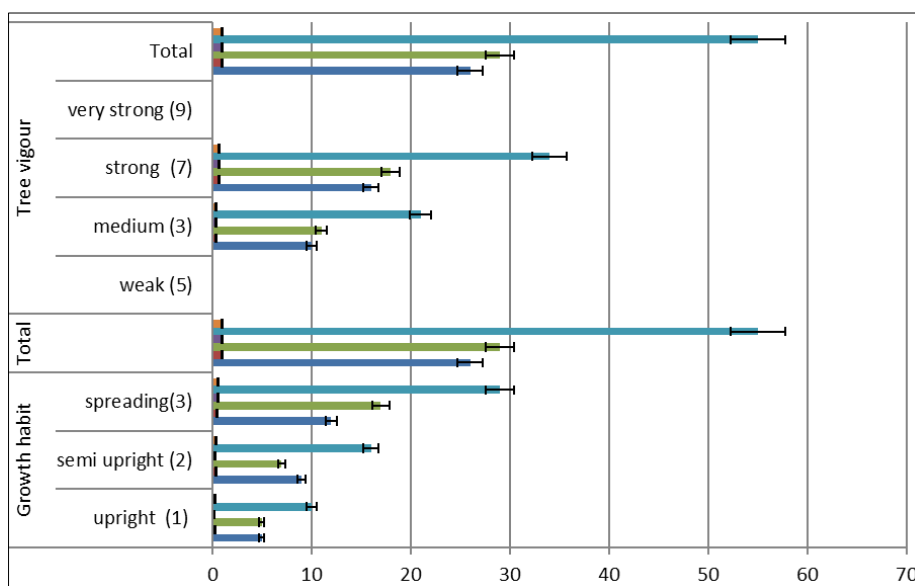


Fig 1: Frequency distribution of fifty five genotypes based on growth habit and tree vigour

This variation observed in the tree vigour and growth habit could be due to age, soil fertility and environmental conditions. Cultivars of walnut studied by other workers were found to vary tremendously in size and growth habit from erect, upright to spreading and tree vigour ranged from low to high. Similar observations were made by Godeanu and Botu (1997) [12] when they evaluated 16 walnut genotypes from Oltenia (Romania) on the basis of their agro-productive characteristics. Among these genotypes two genotypes were found to be vigorous, six genotypes had intermediate vigour and eight genotypes were found to produce high vigour trees. Solar and Stamper (2006) [30] reported that 'Ramsau' variety had most vigorous growth habit with dense branching habit and majority of genotypes studied over a period of 3 years exhibited semi-erect to semi-spreading growth habit. The exceptions were "Z-62" with markedly erect habit and "C-6/7" with spreading branches. The Northwestern Himalayan region is one of the richest and most diverse gene pool of the cultivated walnuts. China, Iran and India are extremely rich sub centers of walnut germplasm diversity (Bhat *et al.*, 1992) [3, 4]. Joolka and Sharma (2005) [39] and Sharma *et al.* (2014) [38] in their study, reported that most (70%) of the walnut of seedling origin possessed strong tree vigour. Angmo *et al.* (2014) [36] found that three of four genotypes had intermediate vigour. Khadivi-Khub (2014) [37] and Lotfi *et al.* (2019) [40] found that walnut accessions with medium-strong or strong vigour. Low-vigour walnut genotypes may be attributed to the heterozygous nature (Solar and Stampar, 2003) [43], which could provide valuable genetic material for tree-size control. Solar *et al.* (2002) [45] also found walnut cultivar's growth habit varying from erect, semi-erect to spreading types. Sharma *et al.* (2014) [38] observed the spreading growth habit in elite clones of walnut with medium tree vigour. Joolka and Sharma (2005) [39] also found that the majority (60.00%) of the autochthonous walnut plants possess spreading growth habits. Angmo *et al.* (2014) [36] found that spreading growth habits more common than semi-erect growth habits. The success of any breeding programme depends on the presence of sufficient genetic variability to pursue effective selection. It is necessary to assess the relative magnitude of the existing genetic diversity in order to use such information together with other selection parameters for the improvement of fruit yield and other quality parameters of any fruit crop through adoption of an effective breeding approach. The extent of genetic variability indicates the potential of exercising selection of a particular genotype, whereas, heritability (h^2) along with genetic advance (% of mean) are more useful in predicting the resultant effect of selection of the best genotypes. Data on lateral fruit percentage show that 80 genotypes (95.23%) predominantly bear fruit buds on terminal shoots. Joolka and Sharma (2005) [39] found most seedling walnut trees to be terminal bearers. Germain, (1990) also discovered three types of fruiting in the walnut terminal, intermediate, and lateral. A small proportion (< 5%) of lateral-bearing genotypes observed by Botu *et al.* (2010) [34]; Solar *et al.* (2002) [45] and Rouskas and Zakyntinos (2001) [44]. Lateral-bearing trees produce more yield than terminal bearers Amiri *et al.* (2010) [35] and is also associated with precocity (Serr, 1962, Forde, 1979) [41, 42]. Tree vigour and growth habit parameters are important for yield or yield efficiency. Strong vigour with spreading behaviour walnut tree increases the bearing potential by increasing the laterals or subterminal or terminal leafy shoots. Spreading type trees have weak apical dominance as a result have reduced IAA

cumulative effect (Chanda *et al.*, 2017) [48] Knowledge of the extent of genetic variation and diversity for fruit phenology, quality, maturity and yield component traits in walnut populations (seedling origin) and subsequent identification of adapted superior genotypes/cultivars as potential donors for yield, quality improvement, nut weight, kernel weight, kernel colour, kernel recovery percentage, extension of harvest period, etc. is therefore, essential. Potent variability is the result of prolonged natural and artificial selection, which is heritable and accumulation of the significant magnitude of variability for economic traits leads to the genetic diversity, which is important for creation of new genetic variability through hybridization and reorganization of new gene constellation. Being highly cross-pollinated because of unisexual flowers, each seedling raised plant is therefore, a distinct genotype due to their highly heterozygous nature of genotype. The magnitude of cross pollination together with diversity at allelic level for most of the genes results in formation of new gene groups and constellations in the resultant seed. Thus, tremendous genetic variability is created which on the outer play of environmental conditions produce some excellent genotypes (possessing many desirable traits in a single plant).

Summary and conclusion

Keeping in view the importance of diversity of walnut genotypes, it is important to survey these populations and identify superior genotypes for their use in the future breeding programme through in situ conservation and subsequent use in the hybridization. The study was accordingly taken up to characterize and catalogue the local gene pool and identify some promising genotypes for future improvement of this fruit crop species.

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Conflict of interest

The authors declare no conflict of interest.

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