# Genetic Divergence of Ashwagandha (*Withaniasomnifera* (L.) Dunal)


## ABSTRACT

Genetic divergence among 32 Ashwagandha (*Withaniasomnifera* (L.) Dunal) accessions of different geographic origins was assessed using Mahalanobis $D^2$ statistics. Observations revealed significant genotypic differences, and accordingly, genotypes were classified into six clusters. Cluster I was the largest, with twenty genotypes, followed by the II cluster, which has eight, and clusters III, IV, V, and VI contained only one most divergent genotype. The maximum divergence was observed between clusters II and III ($D^2$ = 47.90), followed by clusters V and VI ($D^2$ = 43.95), and clusters III and VI ($D^2$ = 42.29). Cluster IV had the least inter-cluster distance ($D^2$ = 22.82) with cluster VI. Clusters III, IV, V, and VI had only one genotype each, and hence, the intra-cluster distance was zero. The genotype of cluster V was unique as it had the highest values for fresh and dry root weight per plant, diameter and length of the main root, number of secondary roots per plant, number of berries per plant, and girth of stem with a high seed yield per plant. Cluster VI was desirable in respect of days to 50 per cent flowering and days to root harvest. Cluster II exhibited the highest value for height of plant and branches per plant. Cluster IV had the highest mean values for the number of seeds per berry. Thus, hybridization among these genotypes can generate desirable transgressive segregants.



**Keywords**: Mahalanobis, Withania, genetic divergence, inter-cluster and genotypes.


## INTRODUCTION

Ashwagandha [*Withaniasomnifera* (L.) Dunal] belongs to the family Solanaceae with chromosome number 2n=48. Ashwagandha is one of the most popular medicinal crops being commercially cultivated as a dryland crop in late kharif season in India. The crop has been assigned several names with distinct meanings such as "Indian winter cherry" or "Indian ginseng" in English, "Punir" or "Asgandh" in Hindi and "Hiremaddinagida" in Kannada. The species name has been ascribed as '*somnifera'*, which means "sleep-inducer" in Latin, owing to its prodigious anti-stress characteristics. As the roots possess a characteristic 'wet horse' smell, it has been named as Ashwagandha. The economic part of ashwagandha is root which is rich in alkaloids, steroidal lactones and saponins. According to the research findings, the total alkaloid content in the Indian roots range between 0.13 per cent and 0.31 per cent. Withaferin A and Withanolide D are the two main withanolides which contribute to most of the biological activity of ashwagandha Matsuda [11]. The therapeutic benefits of ashwagandha roots are immense, and they are used in many traditional Indian medical systems, including Ayurveda, Unani, and Siddha Sharma [15]. According to Bhattacharya and Muruganandam [4], it possesses anti-stress qualities. Cytotoxic, antimicrobial, antifungal, immunosuppressive, and

immunomodulatory qualities Atta-ur-Rahman [3]. As a sedative, for rheumatoid arthritis, for joint inflammation, for feminine diseases, for hiccups, against colds and coughs, for ulcers, as leprosy, etc. Al-Hindwani [1]. This plant's bruised leaves are used as an anti-inflammatory and to treat tumors and tubercular glands Jayaprakasam [9], Chopra [5].Additionally, the leaves are hypnotically used to treat alcoholism. The leaves are applied externally to treat boils, painful eyes, and hand and foot edema. They work well as a pesticide to eradicate body lice. In fact, an ointment prepared by boiling the leaves heals effectively for wounds and bed sores. Anthrax pustules are a different illness for which the fresh leaf juice is used Farooqiand Sreeramu [7].

In many situations, the evaluation of genetic diversity through the use of both quantitative and qualitative features has shown crucial, especially when it comes to identifying distinct populations. In self-pollinated crops, choosing the parents for a breeding program is essential since the outcome of the program depends on the way the hybrid derivatives are separated between the parents, especially if increasing yield or other quantitative attributes is the goal. Divergence analysis based on quantitative features has been proposed in multiple ways to meet different purposes and facilitate the breeder in identifying the superior parents. Of them, the Mahalanobis $D^2$ analysis holds a special position and is a highly effective technique for determining the degree of genetic diversity, which measures the variations in several types of quantitative and qualitative characteristics.

**Comment [A1]:** Mention research urgency here

## MATERIALS AND METHODS

The present investigation, comprising 32 genotypes of ashwagandha, evaluation was carried out during 2020-21 and 2021-22 late *kharif* at the Horticulture Research Station, Department of Horticulture, College of Agriculture, UAS, GKVK, Bengaluru, which geographically, lies at a latitude of 13°.05' N, a longitude of 77°.33' E and an altitude of 925 metres above mean sea level. The treatments included thirty-two genotypes of ashwagandha, with their sources of collection are enlisted in Table 1. The experiment was conducted using Randomized Complete Block Design (RCBD) with three replications in Bengaluru conditions following 30 cm x 20 cm spacing with the individual gross plot size was 2.6 $m^2$. The recommended doses of organic manures and fertilizers were applied at the time of field preparation. 10–12 tons of FYM, 15 kg of nitrogen and 25 kg of phosphorus per hectare were applied at the time of land preparation of experimental plots. Seeds were sown to a depth of 1 to 2 cm by line sowing method. All agronomic practices were carried out in accordance with UHS,Bagalkote, package of practises Anonymous [2], and required preventative plant protection measures were taken to protect the crop from pests and diseases. According to the accepted statistical practise, the mean data on yield and parameters that contribute to yield were treated to an analysis of variance using a randomised block design. $D^2$ statistic was employed to measure the genetic distance between genotype Mahalanobis [10] All the germplasm lines were evaluated systematically for grouping them into different clusters using Mahalanobis $D^2$ statistical analysis Using Tocher's technique, as defined by Rao [14], the genotypes of ashwagandha were categorised based on minimum generalised distance. The average inter- and intracluster distances as well as the contribution of various traits to genetic divergence were calculated using the Singh and Chaudhary [16] method.

**Comment [A2]:** Black font color

**Comment [A3]:** Black font color

## RESULTS AND DISCUSSION

The analysis of variance in 32 ashwagandha genotypes indicated a highly significant difference among the genotypes for all 13 quantitative characters studied, indicating the existence of adequate genetic diversity among the genotypes. In order to assess the genetic diversity among the 32 genotypes, a $D^2$ statistic was carried out. The procedure suggested by Tocher Rao [14] was used to group 32 ashwagandha genotypes into various clusters by treating estimated $D^2$ values as the square of the generalized distance. The pattern of distribution of 32 genotypes into various clusters is indicated in Table 2.Out of 6 clusters formed, cluster I is the largest group, comprising 20 genotypes (DWS-05, DWS-22, DWS-132, DWS-141, DWS-144, DWS-197, DWS-250, DWS-252, DWS-253, DWS-258, DWS-260, DWS-262, DWS-272, DWS-281, DWS-284, DWS-315, DWS-316, DWS-317, Arka Ashwagandha, and Poshita), followed by cluster II with 8 genotypes (DWS-09, DWS-41, DWS-259, DWS-270, DWS-280, DWS-296, DWS-309, DWS-319), whereas clusters III (DWS-40), IV (DWS-257), V (DWS-279), VI (DWS-143) were monotypic or solitary. Similarly, 37 diverse genotypes of Ashwagandha were grouped into 8 clusters by Misra [12]. Gupta [8] carried out a similar type of genetic divergence study on 75 genotypes of ashwagandha and grouped them into 14 clusters using Tocher's method.

The relative contribution of different characters to genetic divergence ($D^2$) is given in Table 3. The number of berries per plant contributed the greatest (29.64%) to the total genetic diversity among the genotypes, followed by fresh root weight per plant (23.59%), dry root weight per plant (22.22%), height of plant (8.233%), days to root harvest (4.64%), length of main root (3.21%), number of seeds per berry (3.02%), days to 50 per cent flowering (1.81%), number of branches per plant (1.61%), diameter of main root (0.81%), seed yield per plant (0.81%), and girth of stem (0.40%). The characters that predominantly contributed to divergence in this study also happen to be the main components of yield. The results of the present study point out the positive contribution of genetic divergence for yield components, and this can be of considerable help in selecting yield and other economic traits.

**Comment [A4]:** Mention some possible application with differences of yield

The mean intra and inter-cluster $D^2$ values among the various clusters are presented in Table 4. The intra-cluster distance varied from 0.0 to 19.94. Among the six clusters, cluster II with eight genotypes showed maximum intra-cluster diversity ($D^2$ = 19.94), followed by cluster I ($D^2$ = 17.88). Clusters III, IV, V, and VI had only one genotype each, hence the intra-cluster distance was zero.Based on distance between clusters, i.e., inter-cluster distances, maximum divergence was observed between clusters II and III ($D^2$ = 47.90), followed by clusters V and VI ($D^2$ = 43.95), and clusters III and VI ($D^2$ = 42.29). Cluster IV had the least inter-cluster distance ($D^2$ = 22.82) with cluster VI. The inter-cluster distance was minimum between clusters IV and VI ($D^2$ = 42.29), indicating narrow genetic diversity, whereas the inter-cluster distance was maximum between II and III ($D^2$ = 47.90), followed by clusters V and VI ($D^2$ = 43.95), and clusters III and VI ($D^2$ = 42.29), indicating wider genetic diversity between these groups. The selection of parents from these diverse clusters for hybridization would help in achieving novel recombinants. Similar types of observations were reported by Misra [12]and Gupta [8]. The clusters with a single genotype indicated their independent identity and importance due to the various unique characters they possessed.

**Comment [A5]:** Explain more about the corelation between hybridization and novel recombinant

The cluster means for each of 13 traits are presented in Table 5The genotype belonging to cluster V found the highest mean girth of stem (16.15 mm), followed by cluster III (15.67 mm) and cluster II (15.45 mm), while genotypes belonging to cluster IV recorded the lowest average girth of stem (13.18 mm). The highest cluster mean for the number of berries per plant was observed in cluster V (558.90), followed by cluster II (447.55), and cluster VI (417.00). The lowest cluster mean was observed in cluster III (316.17). Genotypes belonging to cluster V reported the highest cluster mean for length of main root (21.67 cm), followed by cluster II (16.04 cm) and cluster IV (14.95 cm). The lowest cluster mean was observed in cluster III (11.00 cm). The highest cluster mean for the diameter of the main root was observed in cluster V (2.71 cm), followed by cluster II (2.22 cm) and cluster IV (2.18 cm). The least cluster mean was observed in cluster VI (1.44 cm). Genotypes belonging to cluster V showed the highest cluster mean for secondary roots per plant (2.71), followed by cluster II (2.22) and cluster IV (2.18), while the lowest cluster mean was observed in cluster VI (1.44).The genotype belonging to cluster V reported a maximum cluster mean for seed yield per plant in cluster (11.89 g), followed by cluster II (9.77 g) and cluster IV (9.15 g), while a minimum cluster mean was observed in cluster III (3.20 g). The genotypes belonging to cluster V found the highest mean fresh root weight per plant (31.19 g), followed by cluster II (21.09 g) and cluster IV (17.66 g), while genotypes belonging to cluster III recorded the lowest average fresh root weight per plant (16.40 g).The genotypes belonging to cluster V registered the highest mean dry root weight per plant (6.80 g), followed by cluster II (5.68 g) and cluster IV (4.92 g), while genotypes belonging to cluster I recorded the least average dry root weight per plant (4.33 g). The genotypes belonging to cluster II recorded the maximum mean height of plant (66.44 cm), followed by cluster VI (62.50 cm) and cluster IV (53.44 cm), while genotypes belonging to cluster III recorded the minimum average height of plant (42.42 cm). The number of branches per plant was highest in cluster II (14.41), followed by cluster V (14.20) and cluster IV (14.00). However, the lowest cluster mean was observed in cluster I (10.83). The genotypes belonging to cluster IV exhibited the highest cluster mean for the number of seeds per berry (41.18), followed by cluster V (37.92) and cluster II (37.89), while genotypes belonging to cluster III reported the lowest average number of seeds per berry (22.46). The traits of days to 50% flowering recorded the maximum value in the genotypes of cluster IV and VI (84.00), followed by cluster III (79.00) and cluster I (72.55), while genotypes of cluster V (66 days) exhibited the minimum mean value for days to 50% flowering. Day to root harvest found the maximum value in the genotypes of cluster VI (176.00), followed by cluster III (165.00) and cluster IV (164.00), while genotypes of cluster V (148.00) exhibited the minimum mean value for days to root harvest. Genotypes belonging to clusters with maximum intra-cluster distance are genetically more divergent, and hybridization between genotypes in divergent clusters is likely to produce wide variability with desirable segregates Sharma [15].

The significant variation observed in mean values across clusters and characters studied points to extensive diversity among the examined genotypes. Therefore, in addition to opting for genotypes from clusters with high inter-cluster distances for hybridization, breeders may consider selecting parents based on their genetic divergence concerning a specific trait. For instance, if the

**Comment [A6]:** Use black font color

goal is to enhance root yield, breeders can option for parents with significant dissimilarity in this trait. The decision of parents about heterosis breeding and expression is influenced by the genetic diversity they possess. Cress [6] demonstrated that while 'genetic diversity' is crucial for significant heterosis, it alone is not sufficient to guarantee it. Inter-crossing of diverse groups would lead to broad genetic base and greater opportunities for recombination to occur which intern may unlock hidden variability by breaking undesirable linkages. Several reports suggest that hybrids from genetically diverse parents exhibit greater heterosis compared to those from more closely related parents (Ram and Panwar [13]; Singh and Sharma [17]. In future crop improvement programs, this research aids plant breeders in identifying, characterizing, and choosing verified genotypes. Consequently, these genotypes are expected to gain commercial significance due to their genetic content and medicinal value.

## CONCLUSION

$D^2$ analysis classified all genotypes into six clusters based on their morphological characteristics. It was found that the inter cluster distance is greater than the intra cluster distance, indicating that there is a high genetic diversity in ashwagandha genotypes. The genotypes of clusters II and III and clusters V and VI showed high genetic divergence between them and complimentary for the majority of traits may result in high genetic gain for selected characters and might be chosen for selection to create new varieties.

**Comment [A7]:** There should be correlation between problem statement and conclusion. Please write problem statement in the introduction section

## REFERENCES

**Comment [A8]:** Use more newest references


1. Al-Hindwani MK, Al-Khafaji S, Abdul-Nabi M. Antigranuloma activity of Iraqi *Withaniasomnifera.* J. Ethnopharmacol.1992; 3(7):113-116.
2. Anonymous. Integrated cultivation practices for horticultural crops (Kannada). University of Horticultural Sciences, Bagalkot (Karnataka), 2022:223–224.
3. Atta-Ur-Rahman A, Chaudhary MI, Qureshi S, Gul W, Yousuf M. Two new ergostane type steroidal lactones from *Withaniacoagulans*. J. Nat. Prod. 1998;61:812-814.
4. Bhattacharya SK, Muruganandam AV. Adaptogenic activity of *Withaniasomnifera*: an experimental study using a rat model of chronic stress. PharmacolBiochemBehav. 2003;75(3):547-555.
5. Chopra RN. Glossary of Indian Medicinal Plants. New Delhi. Academic Publishers India. Council of Agricultural Research Publication 1994;87-89.
6. Cress CE. Heterosis of the hybrid related to gene frequency differences between two populations. Genetics. 1966; 53:269-274.
7. Farooqi, Azhar Ali, and B. S. Sreeramu. Cultivation of medicinal and aromatic crops. Universities Press, 2004.

8. Gupta AK, Verma SR, Gupta MM, Saikia D, Verma RK, Jhang T. Genetic diversity in germplasm collections of *Withaniasomnifera* for root and leaf alkaloids. J. Trop. Med. 2011; 12:59-69.
9. Jayaprakasam B, Zhang Y, Seeram N, Nair M. Growth inhibition of tumor cell lines by withanolides from *Withaniasomnifera* leaves. Life Sci. 2003;74(1):125-132.
10. Mahalanobis, P. C. On the generalized distance in statisticsProc. Indian Natl. Sci.1936;2:49-55.
11. Matsuda H, Murakami T, Kishi A, Yoshikawa M. Structures of withanosides I, II, III, IV, V, VI and VII new withanolide glycosides from the roots of Indian *Withaniasomnifera* and inhibitory activity for tachyphylaxis to clonidine in isolated guinea pig ileum. Bioinorg. Chem. 2001;96:1499- 1507.
12. Misra HO, Sharma JR, Lal RK, Sharma S. Genetic variability and path analysis in Asgandh (*WithaniaSomniferaDunal*.). J. Med. Aromat. Sci. 1998;20(3):753-756.
13. Ram J, Panwar DVS. Intraspecific divergence in rice. Int. J. Plant Breed. 1970;30(1):1-10.
14. Rao CR. Advanced statistical methods in biometric research. John Willey and Sons, New York 1952;357-359.
15. Sharma, A., Vats, S.K. and Pati, P.K., 2014. Post-infectional dynamics of leaf spot disease in *Withaniasomnifera*. *Ann. Appl. Biol.* 165(3):429-440.
16. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. Biometrical methods in quantitative genetic analysis.1977:178–185.
17. Singh SP, Sharma JR. Genetic improvement of Pyrethrum. IV. Selective divergences, heterosis and potential hybrid clones. Theor. Appl. Genet. 1989;78:841-846.

**Table 1: List of ashwagandha genotypes**

| Treatments | Genotypes | Source of collection |
|---|---|---|
| $T_1$ | DWS-05 | DMAPR, Boriavi, Anand, Gujarat |
| $T_2$ | DWS-09 | DMAPR, Boriavi, Anand, Gujarat |
| $T_3$ | DWS-22 | DMAPR, Boriavi Anand, Gujarat |
| $T_4$ | DWS-40 | DMAPR, Boriavi, Anand, Gujarat |
| $T_5$ | DWS-41 | DMAPR, Boriavi, Anand, Gujarat |
| $T_6$ | DWS-132 | DMAPR, Boriavi, Anand, Gujarat |
| $T_7$ | DWS-141 | DMAPR, Boriavi, Anand, Gujarat |
| $T_8$ | DWS-143 | DMAPR, Boriavi, Anand, Gujarat |
| $T_9$ | DWS-144 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{10}$ | DWS-197 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{11}$ | DWS-250 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{12}$ | DWS-252 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{13}$ | DWS-253 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{14}$ | DWS-257 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{15}$ | DWS-258 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{16}$ | DWS-259 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{17}$ | DWS-260 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{18}$ | DWS-262 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{19}$ | DWS-270 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{20}$ | DWS-272 | DMAPR, Boriavi, Anand, Gujarat |

| | | |
|---|---|---|
| $T_{21}$ | DWS-279 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{22}$ | DWS-280 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{23}$ | DWS-281 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{24}$ | DWS-284 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{25}$ | DWS-296 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{26}$ | DWS-309 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{27}$ | DWS-315 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{28}$ | DWS-316 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{29}$ | DWS-317 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{30}$ | DWS-319 | DMAPR, Boriavi, Anand, Gujarat |
| $T_{31}$ | Arka Ashwagandha | IIHR, Bengaluru |
| $T_{32}$ | Poshita | CIMAP Research Station, Bengaluru |

**Table 2: Cluster-wise distribution of thirty-two genotypes of ashwagandha for growth and yield attributing traits**

| Sl. No. | Cluster | No. of genotypes | Genotypes |
|---|---|---|---|
| 1 | I | 20 | DWS-05, DWS-22, DWS-132, DWS-141,DWS-144 DWS-197, DWS-250, DWS-252, DWS-253, DWS-258, DWS-260, DWS-262, DWS-272, DWS-281, DWS-284, DWS-315, DWS-316, DWS-317, Arka Ashwagandha and Poshita |
| 2 | II | 08 | DWS-09, DWS-41, DWS-259, DWS-270, DWS-280, DWS-296, DWS-309, DWS-319 |
| 3 | III | 01 | DWS-40 |
| 4 | IV | 01 | DWS-257 |
| 5 | V | 01 | DWS-279 |
| 6 | VI | 01 | DWS-143 |

**Table 3: Per cent contribution of different characters to the divergence in different genotypes of ashwagandha**

| Sl. No. | Source | Relative contribution | |
|---|---|---|---|
| | | Times Ranked 1st | Contribution (%) |
| 1 | Height of plant (cm) | 34 | 8.23 |
| 2 | Number of branches/plant | 8 | 1.61 |
| 3 | Girth of stem (mm) | 2 | 0.4 |
| 4 | Days to 50% flowering | 9 | 1.81 |
| 5 | Days to root harvest | 23 | 4.64 |

| | | | |
|---|---|---|---|
| 6 | Number of berries/plant | 147 | 29.64 |
| 7 | Number of seeds/berry | 15 | 3.02 |
| 8 | Seed yield/plant (g) | 4 | 0.81 |
| 9 | Length of main root (cm) | 16 | 3.21 |
| 10 | Diameter of main root (cm) | 4 | 0.81 |
| 11 | Number of secondary roots/plant | 0 | 0 |
| 12 | Fresh root weight/plant (g) | 117 | 23.59 |
| 13 | Dry root weight/plant (g) | 106 | 22.22 |

**Table 4: Intra (diagonal) and inter-cluster distances for six clusters of *W. somnifera*(L.) Dunal for growth and yield attributing traits.**

| Cluster | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|
| **I** | **17.88** | 32.95 | 24.62 | 25.72 | 27.85 | 34.20 |
| **II** | | **19.94** | 47.90 | 34.12 | 30.87 | 31.54 |
| **III** | | | **0.00** | 27.57 | 37.49 | 42.29 |
| **IV** | | | | **0.00** | 33.74 | 22.82 |
| **V** | | | | | **0.00** | 43.95 |
| **VI** | | | | | | **0.00** |

**Table 5: Cluster means for various characters in 32 genotypes of *W. somnifera* (L.)**

| Sl. No. | Character | I | II | III | IV | V | VI |
|---|---|---|---|---|---|---|---|
| 1 | Height of plant (cm) | 52.95 | 66.44 | 42.42 | 53.44 | 51.26 | 62.50 |
| 2 | Number of branches/plant | 10.83 | 14.41 | 11.67 | 14.00 | 14.20 | 11.20 |
| 3 | Girth of stem (mm) | 13.44 | 15.45 | 15.67 | 13.18 | 16.15 | 15.14 |
| 4 | Days to 50% flowering | 72.55 | 71.00 | 79.00 | 84.00 | 66.00 | 84.00 |
| 5 | Days to root harvest | 160.60 | 153.87 | 165.00 | 164.00 | 148.00 | 176.00 |
| 6 | Number of berries/plant | 324.52 | 447.55 | 316.17 | 383.53 | 558.90 | 417.00 |
| 7 | Number of seeds/berry | 34.92 | 37.89 | 22.46 | 41.18 | 37.92 | 34.56 |
| 8 | Seed yield per plant (g) | 5.64 | 9.77 | 3.20 | 9.15 | 11.89 | 3.21 |
| 9 | Length of main root (cm) | 14.45 | 16.04 | 11.00 | 14.95 | 21.67 | 14.00 |
| 10 | Diameter of main root (cm) | 1.80 | 2.22 | 1.76 | 2.18 | 2.71 | 1.44 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 11 | Number of secondary roots/plant | 1.80 | 2.22 | 1.76 | 2.18 | 2.71 | 1.44 |
| 12 | Fresh root weight/plant (g) | 16.46 | 21.09 | 16.40 | 17.66 | 31.19 | 16.45 |
| 13 | Dry root weight/plant (g) | 4.33 | 5.68 | 4.60 | 4.92 | 6.80 | 4.80 |