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# Genetic Variability and Diversity Analysis in Yard Long Bean [*Vigna unguiculata* (L.) walp subsp. *sesquipedalis* (L.) verdcourt] Accessions under Coastal Saline Ecosystem

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## ABSTRACT

**Background:** Yard long bean despite being highly nutritive summer legume vegetable crop, it is not cultivated on large scale due to seasonal constraints with progressing research activities, Tamil Nadu is yet to came up with a suitable commercial variety of yard long bean with higher yield and superior pod quality. Considering this, the present study with 30 yard long bean germplasm accessions was undertaken to estimate the genetic parameters and deciphering the extent of genetic divergence for nine quantitative traits in yard long bean.

**Methods:** The genetic material comprising 30 different sources of germplasm accessions were evaluated for various quantitative traits in randomized block design (RBD) with triplicate replication at the Garden land, Department of Horticulture, Faculty of Agriculture, Annamalai University during 2022. TNAUSTAT and R Software has been used for data analysis.

**Result:** Analysis of variance exhibited significant differences among the accessions for all the nine quantitative traits indicating the presence of genetic variability. The magnitude of high phenotypic and genotypic coefficient of variation was obtained for all the traits except days to maturity and days to fifty per cent flowering. High heritability coupled with genetic advance per cent as mean was observed for pod yield per plant followed by number of pods per plant, test weight, pod girth, number of seeds per pod, plant height and pod length indicating the predominance of additive gene action. Direct selection for above indicate traits could be valuable for yield improvement programme. Further, genetic divergence analysis revealed that seven clusters could be identified from 30 genotypes. The cluster I was largest having twelve genotypes. The maximum inter cluster distance was found between cluster I and cluster VII followed by cluster I and IV and the intra cluster distance was noted in cluster III followed by cluster I. Among the yield contributing traits, maximum contribution towards genetic divergence existed for pod length followed by test weight, days to maturity and pod yield per plant. Hence, hybridization between cluster VII (IC-630381), V (IC-630379), IV (IC-630383) and I (IC-626143) could be utilized for superior recombinants with desirable traits in segregating generations of yard long bean.

**Key words:** Genetic divergence, Genetic parameters, Hybridization programme, Pod yield, Yard long bean.

## INTRODUCTION

Yard long bean [*Vigna unguiculata* (L.) walp subsp. *sesquipedalis* (L.) verdcourt] is distinct form of cowpea and is an underexploited crop with rich nutritional properties. It is a highly self pollinated crop due to cleistogamous mechanism of the flower and its chromosome number is (2n=2x=22). Yard long bean is characterized by its very long pods (0.5-1 m in length) with seeds generally 8-12 mm long. It is commonly known by several names such as asparagus bean, string bean, snake bean, chinese long bean, pea-bean, bora, juro-kusasagemae (Japanase), dowgauk (Chinese) and sitaw (Filipino). This bean was initially cultivated in West Africa and it is presently grown in Bangladesh, India, Indonesia, Philippines, Thailand and Sri Lanka (Phansak *et al.,* 2005). Extensive cultivation has reported in Kerala, Karnataka and Maharashtra. In India, yard long bean is covering an area of 18,560 to 20,160 ha$^{-1}$ annually (Sarada and Rao, 2020). It's cultivated mainly for crisp and tender pods are eaten both fresh and cooked. The tender green pods are rich in calcium (72.0 mg), phosphorous (59 mg), iron (2.5 mg), carotene (564 mg), thiamine (0.07 mg), riboflavin (0.09 mg) and vitamin C (24 mg) per 100 g of edible pods. Food legumes provide low - fat protein (24-27%) in the human diet and hence are referred to as "poor man's meat" Jayasinghe *et al.* (2015). Despite being a highly nutritious summer leguminous vegetable, Tamil Nadu is yet to release a commercial variety of yard long beans with higher yield and superior pod quality

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and no proper research effort has been given for the improvement of this vegetable. Lack of improved varieties, poor market value, incidence of pest and diseases, susceptible to abiotic stress are major constraints resulting low production of this vegetable. Thus, there is a paucity of information regarding genetic parameters and diversity of this legume vegetable crop. The vital breeding strategies is to increase pod yield by number of pods per plant and to improve other related attributing traits namely earliness, determinate and less with growth habit, resistance to biotic and abiotic stress and wider adaptation to various agro climatic conditions.

Mahalanobi's $D^2$ statistics is a powerful tool to quantify the degree of genetic divergence and develop strategies to incorporate useful diversity in their breeding programs. In any breeding programme selection of parents is prerequisite to develop a variety with desirable traits. The better knowledge on the genetic diversity and variability could help in designing suitable breeding methods. Besides study of genetic parameters and illuminated superior traits will allow plant breeders to predict the response to selection. With this background the aim of the present study was evaluated to estimate the genetic parameters and magnitude of genetic distance among the 30 yard long bean accessions.

## MATERIALS AND METHODS

### Genetic material and experimental site

The present study was conducted at the Garden Land (Plot No.7), Department of Horticulture, Faculty of Agriculture, Annamalai University, Tamil Nadu during February-April 2022. The experimental material comprising of 30 germplasm accessions were procured from National Bureau of Plant Genetic Resources (NBPGR), New Delhi (Fig 1). The experiment was laid out in a randomized block design with three replications. Spacing adopted was 1.50 m x 1 m. The size of each experimental plot is 8.75 m. The seeds were directly sown in field on 02nd February. The recommended packages of practices were applied to raise a healthy crop.

### Phenotyping of quantitative traits

Data was recorded on ten plants in each genotype in each replication for nine phenological, growth and yield attributing traits such as days to first flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod, pod length, pod girth, test weight and pod yield per plant. The data on quantitative traits were recorded as per minimal descriptors of NBPGR (Srivastava *et al.,* 2001).

### Data analyses

Analysis of variance and summary statistics was calculated as per Panse and Sukatame (1967). A standard statistical procedure was followed to measure the variability and to estimate genetic parameters for individual traits. The phenotypic and genotypic coefficient of variation (PCV and GCV) were determined as per the procedure of Burton and Devane (1953), broad sense heritability ($h^2b$), genetic gain over percent of mean (GAM) were computed as per Johnson *et al.* (1955). The analysis of variance (ANOVA), adjusted means, descriptive statistics and genetic variability were computed using the R-Studio. 3.6.1 (Variability R-Package). Multivariate analysis was done utilizing Mahlanobis (1936) $D^2$ statistics and genotypes were grouped into different clusters following Toucher method as described by Rao (1952).

## RESULTS AND DISCUSSION

### Analysis of variance (ANOVA)

The analysis of variance (ANOVA) revealed a wide range of variation and significant (P=0.001) differences among the 30 yard long bean accessions for all the characters studied (Table 1). It indicated that elucidating the presence of genetic variation for the respective traits exists in the yard long bean accessions under study. Hence, there is an opportunity for plant breeder to evaluate further breeding pursuit like yard long bean hybridization programme. Substantial variability in yard long bean accessions were previously reported by Zakia Sultana *et al.* (2020) and Mithun Kumar *et al.* (2021).

**Table 1:** Analysis of variance (ANOVA) for yield and yield contributing traits among diverse 30 yard long bean accessions.

| Source of variations | Mean sum of squares (MSS) | | |
|---|---|---|---|
| | Replication | Genotypes | Error |
| Degree of freedom | 2 | 29 | 58 |
| Days to fifty per cent flowering | 62.547 | 24.025** | 0.983 |
| Days to maturity | 351.23 | 172.58** | 5.150 |
| Plant height | 1151.3 | 6113.7** | 115.9 |
| Number of pods per plant | 40.31 | 466.07** | 0.80 |
| Number of seeds per pod | 8.641 | 31.144** | 0.129 |
| Pod length | 64.070 | 204.274** | 1.054 |
| Pod girth | 0.188 | 0.740** | 0.003 |
| Test weight | 5.572 | 46.889** | 0.095 |
| Pod yield per plant | 64.544 | 269.326** | 3.727 |

### Estimates of mean and range

The descriptive statistics, including maximum and minimum quantitative traits mean value, standard error of the means and critical differences (1% and 5%) for all nine pod yield and yield contributing traits are summarized in (Table 2). The widest range was recorded for pod yield per plant (259.06-1361.05) followed by plant height (164.71-377.70), days to maturity (84.56-125.33), number of pods per plant (22.87-76.55), days to first flowering (37.74-52.16), pod length (24.38-59.31), number of seeds per pod (9.26-22.55), test weight (8.19-20.44) and pod girth (1.43-3.72) indicating the presence of considerable variation among the genotypes used in the present study. This would help in selecting the best genotypes from existing selection. The existence of high variability for different traits among yard long bean accessions had been earlier reported by Rambabu *et al.* (2016).


IC-622569 (G1) IC-622579 (G2) IC-622590 (G3) IC-622597(G4) IC-622598 (G5)
IC-622599 (G6) IC-622600 (G7) IC-622601 (G8) IC-6222602 (G9) IC-630376 (G10)
IC-626137 (G11) IC-626138 (G12) IC-626139 (G13) IC-626140 (G14) IC-630377 (G15)
IC-630378 (G16) IC-626142 (G17) IC-626143 (G18) IC-626145 (G19) IC-630379 (G20)
IC-630380 (G21) IC-630381 (G22) IC-626146 (G23) IC-626147 (G24) IC-626148 (G25)
IC-626149 (G26) IC-626152 (G27) IC-626153 (G28) IC-626154 (G29) IC-630383 (G30)

**Fig 1:** Diverse 30 genotypes of yard long bean selected for genetic divergence analysis.

### Phenotypic and genotypic coefficient of variation

Genotypic and phenotypic coefficient of variation for pod yield and yield components are presented in (Table 2). The components used to measure the variability present in a population are GCV and PCV. The GCV provides a valid basis for appraising and comparing the range of genetic variability for quantitative traits. PCV estimates the augment of total variation. Expectedly phenotypic coefficient of variation (PCV) was higher than the genotypic coefficient of variation (GCV) in all the characters studied. Result from the present study in this context, records highest PCV and GCV ((45.07, 44.15) for pod yield per plant followed by number of pods per plant (34.85, 34.77), test weight (29.37, 29.28), pod girth (21.11, 20.96), number of seeds per pod (20.33, 20.20) and plant height (20.84, 20.26). PCV generally ranged between 7.44 for days to maturity to 45.07 for pod yield per plant, indicating that the presence of inherent variability among the accessions. Similarly, GCV range varied from 7.12 for days to maturity to 44.15 for pod yield per plant. The slight edge of PCV over GCV indicated good scope for making selection for the improvement of these characters. Similar findings of higher PCV than GCV were also reported by Sivakumar *et al.* (2014).

Moderate estimates of PCV and GCV were recorded in present study for pod length. Similar findings were also obtained by Haque *et al.* (2021).

Relatively least difference between the magnitude of PCV and GCV were observed for days to fifty per cent flowering and days to maturity indicating a lack of variability and limited scope for improvement through selection for these traits among the genotypes. Similar findings were earlier studied by Yadea *et al.* (2011) for days to fifty per cent flowering and days to maturity.

### Heritability and genetic advance

The heritability estimates assist in identifying genotypes from a broad genetic pool. Heritability values helps in predicting the expected progeny to be achieved through the selection process. In the present study, the estimates of broad sense heritability ranged from 88.65% for days to fifty percent flowering to 99.49% for number of pods per plant (Table 2). In present study tested genotypes showed high heritability for all the characters. Highest heritability estimates were observed for number of pods per plant (99.49%), test weight (99.39%), number of seeds per pod (98.76%), pod yield per plant (95.96%), pod girth (98.59%), pod length (98.47%), plant height (94.52%), days to maturity (91.55%) and days to fifty percent flowering ( 88.65%), which indicated that characters are least influenced by environmental factors and potency of these characters for transmission to next generation. In addition phenotypic selection would also be effective.

The heritability alone does not given the idea about expected gain in the subsequent generation. But still, it should be considered in connection with the genetic advance. The characters exhibiting highest value of genetic advance over per cent as mean (GAM) was obtained for pod yield per plant (89.11%) followed by number of pods per plant (71.44%), test weight (60.14%), pod girth (42.89%), number of seeds per pod (41.36%), plant height (40.58%) and pod length (37.60%) while other traits such as days to maturity (14.03%) and days to fifty percent flowering (12.25%), showed less than 20% of genetic advance mean (Table 3).

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was recorded for the traits, pod yield per plant, number of pods per plant, test weight, pod girth, number of seeds per pod, plant height and pod length which indicated lesser environmental influence on these traits and predominance of additive gene action. Hence, simple selection may be practiced to improve these traits. This is in conformity with findings of Manju Devi and Jayamani (2018) for plant height and test weight and single plant yield.

**Table 2:** Summary statistics and genetic parameters for flowering and yield attributing traits in diverse 30 yard long bean accessions.

| Traits | Range | | Grand | SE (m) | CD | CD | Co-efficient of variation | | $h^2$(b) | GAM |
|---|---|---|---|---|---|---|---|---|---|---|
| | Max | Min | mean | | (5%) | (1%) | PCV (%) | GCV (%) | (%) | (%) |
| DTFF | 52.16 | 37.74 | 43.86 | 0.572 | 1.62 | 2.15 | 8.66 | 7.68 | 88.65 | 12.25 |
| DM | 125.33 | 84.56 | 104.91 | 1.310 | 3.71 | 4.93 | 7.44 | 7.12 | 91.55 | 14.03 |
| PH | 377.70 | 164.71 | 220.66 | 6.216 | 17.59 | 23.41 | 20.84 | 20.26 | 94.52 | 40.58 |
| NPPP | 76.55 | 22.87 | 35.81 | 0.515 | 1.45 | 1.94 | 34.85 | 34.77 | 99.49 | 71.44 |
| NSPP | 22.55 | 9.26 | 15.91 | 0.208 | 0.58 | 0.78 | 20.33 | 20.20 | 98.76 | 41.36 |
| PL | 59.31 | 24.38 | 44.73 | 0.592 | 1.62 | 2.23 | 18.53 | 18.39 | 98.47 | 37.60 |
| PG | 3.72 | 1.43 | 2.36 | 0.031 | 0.09 | 0.12 | 21.11 | 20.96 | 98.59 | 42.89 |
| TW | 20.44 | 8.19 | 13.48 | 0.177 | 0.50 | 0.67 | 29.37 | 29.28 | 99.39 | 60.14 |
| PYPP | 1361.05 | 259.06 | 259.06 | 35.24 | 99.77 | 132.75 | 45.07 | 44.15 | 95.96 | 89.11 |

Max- Maximum, Min- Minimum, SE(m)- Standard error mean, CD- Critical difference @ 5 and 1% level, PCV- Phenotypic coefficient of variation, GCV- Genotypic coefficient of variation, $h^2$(b)- heritability ($h^2$-customary symbol, not for its square), GAM- Genetic advance per cent as mean, DTFF- Days to fifty percent flowering, DM- Days to maturity, PH- Plant height, NPPP- Number of pods per plant, NSPP- Number of seeds per pod, PL- Pod length, PG- Pod girth, TW- Test weight and PYPP- Pod yield per plant.

High heritability accompanied with moderate genetic advance per cent as mean recorded for days to fifty per cent flowering and days to maturity suggests that these traits are controlled by both additive and non-additive gene action. Similar kind of high heritability and moderate genetic advance was exerted for days to fifty per cent flowering and days to maturity by Rambabu *et al.* (2016).

### Clustering pattern

On the basis of relative magnitude of $D^2$ values, the 30 yard ling bean genotypes were grouped into seven clusters following Tocher's method (Table 3). Cluster size varied from 1 to 12 genotypes. Cluster I was having maximum number of genotypes (12), followed by cluster II had 11 genotypes and cluster III consisted 3 genotypes. The remaining four clusters namely cluster IV, V, VI and VII comprised only one genotype each, as these could not be clubbed with any other genotypes, respectively. The group of clustering constellation in the present study culled out that eco- geographical diversity was not related to the genetic diversity. The clustering pattern reflected the presence of substantial amount of genetic divergence in the genetic accessions. The existence of genetic divergence in the yard long bean accessions were earlier reported by Widyawan *et al.* (2020).

### Cluster-distances

Based on the procedure given by Singh and Choudhary (1979), the average intra and inter cluster distance values were computed and presented in (Table 4). The values of average intra cluster $D^2$ values ranged from 0.0 (cluster IV to VII) to 98.10 (cluster III) respectively. The highest value of intra cluster distance III ($D^2$ = 98.10) possessing 3 genotypes, followed by I (($D^2$ = 94.59) consisted 12 genotypes and minimum distance was observed by cluster II ($D^2$ = 83.58). Data further revealed that there is good scope for selection for many traits of economic and agricultural importance within a cluster as indicated by the high magnitude of intra cluster distance among clusters. Hence, selection of divergent genotypes from the clusters I and III indicated that these cluster consisted genotypes which are highly diverse.

The minimum distance was noted between cluster IV and VII ($D^2$ = 113.23), indicating close relatedness among the genotypes included. The maximum inter cluster distance was found between cluster I and cluster VII ($D^2$ = 550.41) followed by the cluster I and IV ($D^2$ = 458.96) indicating wider genetic diversity among the genotypes between these clusters. To exploit genetic diversity through hybridization program inter-cluster distance must be taken into consideration. Hence, hybridization between the genotypes from these clusters would result in maximum hybrid vigour and high number of useful heterotic hybrids. Similar findings were reported by Valarmathi *et al.* (2007).

### Cluster means performance

Considerable differences in cluster mean values were evident for all the characters studied (Table 5). In the present

**Table 3:** Distribution of 30 accessions of yard long bean into seven clusters.

| Cluster | Number of genotypes | Name of the genotypes |
|---|---|---|
| I | 12 | G18 (IC- 626143), G21 (IC- 630380), G15 (IC- 630377)G26 (IC- 626149), G14 (IC- 626140), G13 (IC- 626139) G8 (IC- 622601), G9 (IC- 622602), G19 (IC- 622145) G27 (IC- 626152), G1 (IC- 622569), G23 (IC- 626146) |
| II | 11 | G4 (IC- 622597), G11 (IC- 626137), G12 (IC- 626138) G28 (IC- 626153), G10 (IC- 630376), G17 (IC- 626142) G16 (IC- 630378), G3 (IC- 622590) G25 (IC- 626148) G5 (IC- 622598), G24 (IC- 626147) |
| III | 3 | G6 (IC- 622599), G7 (IC- 622600), G29 (IC- 626154) |
| IV | 1 | G30 (IC- 630383) |
| V | 1 | G20 (IC- 630379) |
| VI | 1 | G2 (IC- 622579) |
| VII | 1 | G22 (IC-630381) |

**Table 4:** Average intra and inter cluster distance.

| Cluster | Cluster I | Cluster II | Cluster III | Cluster IV | Cluster V | Cluster VI | Cluster VII |
|---|---|---|---|---|---|---|---|
| Cluster I | 8948.97 | 29099.19 | 1471171.05 | 210646.33 | 46954.45 | 104476.38 | 302954.95 |
| Cluster II | | 6987.28 | 58756.57 | 99456.28 | 16288.68 | 16779.07 | 164020.57 |
| Cluster III | | | 9624.67 | 13725.10 | 48202.08 | 14424.63 | 35093.73 |
| Cluster IV | | | | 0.00 | 76728.46 | 35657.09 | 12822.44 |
| Cluster V | | | | | 0.00 | 32873.06 | 142656.18 |
| Cluster VI | | | | | | 0.00 | 70501.71 |
| Cluster VII | | | | | | | 0.00 |

**Table 5:** Cluster mean for nine characters in 30 diverse accessions of yard long bean.

| Cluster | DTFF | DM | PH | NPPP | NSPP | PL | PG | TW | SYPP |
|---|---|---|---|---|---|---|---|---|---|
| Cluster I | 43.75 | 104.35 | 225.98 | 36.32 | 15.06 | 18.10 | 2.24 | 7.49 | 274.98 |
| Cluster II | 43.77 | 103.27 | 210.19 | 31.10 | 16.28 | 26.97 | 2.51 | 11.92 | 418.67 |
| Cluster III | 43.15 | 111.00 | 229.57 | 36.50 | 14.18 | 41.15 | 2.73 | 17.39 | 675.92 |
| Cluster IV | 49.13 | 101.55 | 215.29 | 49.20 | 21.89 | 46.41 | 2.90 | 19.50 | 747.48 |
| Cluster V | 45.92 | 103.51 | 309.51 | 75.05 | 17.44 | 30.13 | 2.70 | 12.82 | 459.97 |
| Cluster VI | 41.44 | 118.15 | 183.02 | 36.47 | 17.33 | 40.25 | 2.26 | 12.30 | 478.80 |
| Cluster VII | 43.51 | 102.88 | 199.51 | 26.26 | 18.24 | 51.03 | 3.01 | 21.10 | 962.15 |
| Grand mean | 43.86 | 104.91 | 220.66 | 35.81 | 15.91 | 44.73 | 2.36 | 13.48 | 673.79 |

**Table 6:** Superior genotypes of yard long bean based on cluster mean performance and genetic divergence.

| Cluster number | Genotype | Desirable traits |
|---|---|---|
| I | IC-626143 | Days to first flowering and plant height |
| IV | IC-630383 | Days to maturity and number of seeds per pod |
| V | IC-630379 | Number of pods per plant |
| VII | IC-630381 | Pod yield per plant, test weight, pod length and pod girth |

**Table 7:** Relative contribution of nine characters towards genetic divergence in 30 yard long bean accessions.

| Characters | Per cent of contribution | Time rank |
|---|---|---|
| Days to fifty per cent flowering | 0.00 | 0 |
| Days to maturity | 7.81 | 34 |
| Plant height | 0.00 | 0 |
| Number of pods per plan | 6.66 | 29 |
| Number of seeds per pod | 0.22 | 1 |
| Pod length | 68.27 | 297 |
| Pod girth | 0.00 | 0 |
| Test weight | 13.10 | 57 |
| Pod yield per plant | 3.94 | 17 |
| Total | 100 | 435 |

study, dwarf plant (183.02) earliest flowering (41.44) and earlier maturity (101.55), number of seeds per pod (21.89) were observed in cluster IV and VI respectively. Cluster VI ranked first and recorded highest pod yield per plant (962.15), test weight (21.11), pod length (51.03) while this also produced minimum pod girth (3.01). Cluster V exhibited maximum number of pods per plant (75.05).

The genotypes suggested for use as parents for hybridization based on their mean value and genetic divergence for traits are listed in (Table 6). The genotypes with maximum mean value are used as parental material in progressive breeding. Based on the genetic distance values, cluster constellation, the most divergent genotypes were from clusters I, IV, V and VII which could be involved in a crop improvement programme. Genotype IC- 630381 present in clusterVII has highest pod yield per plant and can be used in future breeding programmes for developing variety with high pod yield content. Genotype IC-626143 Cluster (I), IC-630379 (cluster V) and IC-630383 (Cluster IV) might be used in breeding for improved early varieties of yard long beans. These findings were supported by the results of Ullah *et al.* (2011).

### Character's contribution to diversity

The ranking technique was adopted to rank the characters in the order of the contribution to total genetic divergence. The contribution towards the total genetic divergence was represented in (Table 7). The relative contribution of individual character towards the expression of genetic diversity studied, revealed maximum contributions of 68.27 per cent by pod length followed by test weight (13.10 per cent), days to maturity (7.81 per cent) and pod yield per plant (3.94 per cent). Remaining characters had very less contribution to genetic divergence. Similar studies were conducted by Sulanthi *et al.* (2007); Hossain *et al.* (2013).

## CONCLUSION

The study has provided crucial information on variability in yard long bean accessions in terms of respective traits. From the results it could be concluded that selection would be rewarded for the characters *viz.,* pod yield per plant, number of pods per plant, test weight, pod girth, number of seeds per pods, plant height and pod length was most dominant traits. The results indicated high heritability and genetic gain for these traits, predominantly due to additive genetic control. Direct section for above traits would be reliable and relevant yardsticks for selection in yard long bean crop improvement program. $D^2$ statistics revealed that thirty genotypes fall into seven clusters. The genotypes in cluster VII (IC-630381), V (IC-630379), IV (IC-630383) and I (IC-626143) had highest inter cluster distance as wells as cluster mean for most of the yield contributing traits. This suggests that identified genotypes were most diverse among 30 yard long bean germplasm accessions, which could be utilized as potential donor parents in future hybridization programme of yard long bean breeding and varietal development.

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### Conflict of interest

The authors declared that there is no conflict of interest.

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