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Branching Pattern and Harvest Index as Important Selection Criteria for Improvement of Mungbean [*Vigna radiata* (L.) Wilczek]

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Thirty-six mungbean genotypes were evaluated for twenty-six agro-morphological traits to assess the genetic variability and genetic relationship. The maximum genotypic coefficient of variation and phenotypic coefficient of variation was exhibited by number of secondary branches per plant followed by number of primary branches per plant, stem pubescence density, leaf pubescence density and leaf area. Among the agro-morphological traits, primary branch angle, biological yield per plant and harvest index exhibited high heritability coupled with high genetic advance, strong positive association and high positive direct effect on seed yield, suggested that cautious approach of optimizing these traits can be utilized for yield improvement of mungbean. The negative association of primary branch angle with main stem and biological yield per plant with harvest index reflected that relation of branch angle, which helps in the making of the canopy of the plant and biological yield per plant, need to be critically analyzed for reflecting seed yield per plant due to optimized harvest index.

Key words: Genetic Parameters, Mungbean, Pubescence traits.

Mungbean is one of the important grain legumes of India. It is widely used in human diet, animal feed and green manuring. It also improves the soil health by fixing the atmospheric nitrogen into the soil (Hoorman *et al.,* 2009). Mungbean yield is constrained by several diseases and insect pests. Pubescence trait is a good criterion to develop insect resistant/ tolerant varieties of crops (Aliyu *et al*., 2000, Mohammad *et al*., 2010). The MYMV disease is a major disease of mungbean spreaded by the vector white fly. The pubescence traits may help to manage/ reduce the infestation of white fly, resulting in the low infection of MYMV and indirectly increases the yield. To achieve this goal, the information on the nature and magnitude of genetic variability for different traits present in the available stocks is required. The adequate information on extent of variability parameters may be helpful to design the breeding strategies and improve the selection response. Estimates on genetic parameters are environment specific. These estimates should be incorporated and specifically applied only to the population and environment sampled (Singh *et al.,* 2014a). Thus, it is necessary to determine the variance components and h^2 under target production environment. The knowledge on trait association along with their h^2 estimates helps the breeder to make an improvement in a complex character. Keeping the above facts under consideration the present experiment was conducted to estimate the genetic parameters and association analysis to identify the major yield determinants. Results of this study may assist in strategic breeding and manipulation of trait(s) for mungbean improvement.

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Materials and Methods

The present investigation consisted of 36 mungbean genotypes to assess the genetic parameters and genetic relationship. The experiment was conducted at Crop Research Farm, TCA, Dholi (25.5^0N, 35.4^0E, 52.12 m MSL) in RBD with three replications during summer 2012. Each genotype was sown in six rows in plot of 4 m length with 30 x 10 cm plant geometry. Five random plants were tagged from each plot to record the data on 26 traits except days to first flower opening (DFFO) and days to maturity (DM). These agro-morphological traits were plant height (PH), number of primary branches per plant (NPBP), number of secondary branches per plant (NSBP), primary branch angle with main stem (NSBP), leaf area (LA), petiole length (PetL), number of clusters per plant (NCP), number of pods per cluster (NPC), node of first productive peduncle (NFPP), number of nodes on main stem (NMS), average inter-nodal length (AIL), pod angle with peduncle (PAP), pod length (PL), beak length (BL), leaf pubescence density (LPD), stem pubescence density (SPD), pod pubescence density (PPD), petiole pubescence density (PetPD), number of seeds per pod (NSP), seed index (SI), biological yield per plant (BYP), harvest index (HI) and seed yield per plant (SYP). Leaf area was calculated by formula as per Yoshida *et al.* (1972). The data on yield and its other related traits were subjected to analysis of variance, genetic parameters, correlation and path analysis by using statistical package WINDOSTAT 9.1 version.

Results and Discussion

The success of any breeding programme is almost dependent on genetic variation present in breeding materials. The magnitude and extent of genetic variability existing in genotypes is very important. More variability gives the more chances to incorporate the traits/ genes from one genotype to other. The coefficient of variation studies indicated that the magnitude of PCV were higher (slightly to more) than the corresponding GCV for all the characters studied, which indicated that these traits

Table 1. Variance components and genetic parameters on various pubescence and agro-morphological traits in mungbean

GP Traits	DFFO (Days)	PH (cm)	NPBP (Number)	NSBP (Number)	PetL (cm)	LA (cm_2)	NNMS (Number)	AIL (cm)	PBAMS (Degree)	NFPP (Number)	PedL (cm)	PAP (Degree)	LPD (cm_2)
$\sigma_2 g$	34.17	19.03	1.11	3.67	1.78	97.80	1.91	0.28	179.58	0.31	3.15	166.23	965.40
$\sigma_2 p$	39.95	28.23	1.42	4.09	2.46	145.51	2.52	0.50	209.94	0.59	4.16	204.88	988.17
GCV	12.43	13.44	39.79	61.60	15.89	34.64	17.26	12.75	18.91	13.15	20.33	15.85	36.90
PCV	13.44	16.37	44.92	65.02	18.69	42.25	19.83	17.20	20.45	18.19	23.36	17.60	37.33
h^2 (bs)	0.86	0.67	0.78	0.90	0.72	0.67	0.76	0.55	0.86	0.52	0.76	0.81	0.98
GAM at 5%	23.68	22.74	72.61	120.23	27.83	58.50	30.95	19.45	36.04	19.58	36.44	29.41	75.13

Contd...

GP Traits	SPD (cm_2)	PPD (cm_2)	PetPD (cm_2)	NCP (Number)	NPC (Number)	PL (cm)	BL (cm)	NSP (Number)	PFI (%)	SI (g)	BYP (g)	SYP (g)	HI (%)
$\sigma_2 g$	2571.65	391.13	438.07	5.13	0.23	0.47	1.48	1.64	56.01	0.28	20.41	38.65	4.63
$\sigma_2 p$	2636.10	415.95	466.57	7.48	0.63	0.69	1.76	2.45	81.81	0.47	26.58	69.70	6.01
GCV	38.12	13.56	34.26	28.48	9.82	10.28	29.34	13.35	10.83	12.04	21.46	15.04	25.11
PCV	38.60	13.98	35.36	34.39	16.30	12.45	31.99	16.30	13.09	15.65	24.49	20.20	28.60
h^2 (Broad Sense)	0.98	0.94	0.94	0.69	0.36	0.68	0.84	0.67	0.68	0.59	0.77	0.55	0.77
GAM at 5%	77.57	27.08	68.40	48.59	12.18	17.49	55.44	22.53	18.46	19.09	38.74	23.07	45.41

GP= Genetic parameters, $\lceil_2 g$= Genotypic variance, $\sigma_2 p$= Phenotypic variance, GCV= Genetic coefficient of variation, PCV= Phenotypic coefficient of variation, $h_2 bs$= Heritability in broad sense, GAM= Genetic advance as % of mean, Abbreviations are given in materials and methods

Table 2. Phenotypic correlation among seed yield, pubescence traits and agro-morphological traits in mungbean

Traits	DFFO	PH	NPBP	NSBP	PetL	LA	NMS	AIL	PBAMS	NFPP	PedL	PAP	LPD
DFFO	1.000	-0.361**	0.634**	0.649**	-0.259**	-0.402**	0.201*	-0.433**	0.042	-0.013	-0.277**	0.102	0.206*
PH		1.000	-0.316**	-0.335**	0.150	-0.073	0.338**	0.543**	-0.181	0.235*	0.152	0.079	-0.040
NPBP			1.000	0.790**	-0.425**	-0.269**	0.327**	-0.511**	0.197*	-0.123	-0.086	0.098	0.062
NSBP				1.000	-0.409**	-0.365**	0.262**	-0.420**	0.259**	-0.250**	-0.166	0.199*	0.095
PetL					1.000	0.564**	-0.315**	0.365**	-0.246*	0.130	0.074	-0.117	0.091
LA						1.000	-0.250**	0.109	-0.005	0.028	0.145	-0.301**	-0.067
NMS							1.000	-0.554**	0.074	0.327**	-0.148	-0.099	0.024
AIL								1.000	-0.188	-0.079	0.160	0.211*	-0.053
PBAMS									1.000	-0.207*	0.070	-0.086	-0.069
NFPP										1.000	-0.290**	-0.190*	0.137
PedL											1.000	0.126	0.043
PAP												1.000	0.170
LPD													1.000

Contd...

Traits	SPD	PPD	PetPD	NCP	NPC	PL	BL	NSP	PFI	SI	BYP	HI	SYP
DFFO	-0.201*	0.036	0.029	0.085	0.059	0.096	-0.163	0.108	-0.246*	0.007	0.198*	-0.253**	-0.004
PH	0.240*	-0.178	0.069	-0.227*	-0.051	-0.101	-0.135	-0.020	-0.058	-0.271**	-0.364**	-0.033	-0.345**
NPBP	-0.126	-0.140	-0.071	0.381**	0.083	0.133	0.127	-0.136	0.029	0.035	0.256**	-0.160	0.139
NSBP	-0.125	-0.119	-0.056	0.395**	0.134	0.182	0.044	-0.143	0.026	-0.043	0.342**	-0.115	0.259**
PetL	0.355**	0.273**	0.365**	-0.102	-0.221*	-0.102	-0.172	0.237*	-0.216*	0.054	-0.022	-0.024	-0.063
LA	0.239*	0.008	0.282**	0.201*	-0.220*	-0.173	0.117	-0.025	-0.009	0.044	0.099	0.226*	0.248**
NMS	-0.016	-0.211*	0.064	-0.016	0.017	-0.170	0.009	-0.492**	0.096	-0.374**	-0.350**	-0.023	-0.288**
AIL	0.197*	0.024	0.018	-0.163	-0.084	0.022	-0.185	0.316**	-0.139	0.013	-0.004	-0.056	-0.075
PBAMS	0.019	-0.085	-0.068	0.298**	0.125	0.115	0.101	-0.158	0.211*	0.081	0.372**	-0.241*	0.196*
NFPP	-0.001	0.236*	0.357**	-0.305**	-0.141	-0.304**	-0.221*	-0.161	-0.167	-0.262**	-0.402**	-0.059	-0.414**
PedL	0.272**	-0.185	0.011	0.333**	-0.056	-0.044	0.305**	0.131	0.004	0.062	0.179	0.033	0.170
PAP	-0.063	-0.130	-0.121	0.175	0.079	-0.068	-0.222*	0.073	-0.170	-0.036	0.078	-0.159	-0.021
LPD	-0.175	0.204*	0.279**	0.028	-0.065	-0.187	-0.184	0.107	-0.308**	-0.172	-0.080	0.140	0.021
SPD	1.000	-0.010	0.192*	0.159	-0.073	-0.146	0.134	-0.031	-0.069	-0.076	0.156	-0.113	0.088
PPD		1.000	0.163	-0.161	-0.112	0.062	-0.086	0.117	0.004	0.142	0.056	-0.202*	-0.093
PetPD			1.000	0.027	0.071	-0.475**	-0.228*	-0.079	-0.404**	-0.213*	0.135	-0.211*	-0.025
NCP				1.000	0.048	0.001	0.328**	-0.066	0.029	0.028	0.384**	0.145	0.468**
NPC					1.000	0.072	-0.113	0.218*	-0.150	0.120	0.217*	-0.192*	0.087
PL						1.000	0.123	0.442**	0.483**	0.570**	0.359**	0.045	0.352**
BL							1.000	-0.072	0.218*	-0.021	0.026	0.269**	0.227*
NSP								1.000	-0.456**	0.368**	0.286**	-0.055	0.200*
PFI									1.000	0.321**	0.073	0.133	0.162
SI										1.000	0.480**	-0.071	0.381**
BYP											1.000	-0.281**	0.717**
HI												1.000	0.446**
SYP													1.000

were less influenced by environment (except NPC) (Table 1). NPC showed more genotypic and phenotypic differences, indicated that NPC was highly influenced by the environment. Study on flower formation, pod development and number of harvested pod may give the information about effect of environment on NPC. The high estimates of GCV and PCV (>20%) was exhibited by NSBP followed by NPBP, SPD, LPD, LA, PetPD, BL, NCP, SYP, BYP and PedL, whereas rest of the traits showed moderate values (except NPC). NPC showed low estimates of GCV, whereas an estimates of PCV was moderate. The high estimates of GCV and PCV for SYP has earlier been observed by Yimram *et al.* (2009).

High h_2 (>70%) was recorded for fifteen agro-morphological traits studied *viz.*, DFFO, NPBP, NSBP, PetL, NNMS, PBAMS, PedL, PAP, LPD, SPD, PPD, PetPD, BL, BYP and SYP, whereas ten agro-morphological traits *viz.*, PH, LA, AIL, NFP, NCP, PL, NSP, PFI, SI and HI showed moderate estimates of h_2 (50-70%) . However, the estimates of variance components and h_2 of traits are environment specific and selection was done on the basis of variance components and h_2 estimates alone may mislead. Preponderance of additive gene action was reflected by LPD, SPD and PetPD, indicated that these traits may be included in breeding programme after study of association and cause-effect relationship to identify their contribution towards seed yield. The pubescence density, studied in the present investigation, clearly depicted least influence of environment in its manifestation and could be utilized as important genetic trait/ descriptor. Singh *et al.* (2012) reported positive association between pod pubescence and water imbibitions percentage by pods, which may be due to retention of water on the pod surface for longer period and higher imbibitions of water by pods. If the wall of pod is thin, then it may imbibe the seeds in pod during the maturity and may promote the sprouting of seeds in pod on mungbean plants. Thus, selection of genotypes having high pod pubescence density along with some other traits *viz.,* high pod pubescence length and thick pod wall may give better response to develop the insect tolerance lines. Yimram *et al.* (2009) suggested the consideration of variance components, heritability estimates and genetic advance together to give better chance of selection of appropriate trait(s) for mungbean improvement. Thus, the pubescence traits showed high h_2 coupled with high genetic advance as well as low GCV and PCV differences, which indicated the involvement of additive gene action in governing these traits due to high h_2. Besides this, other the agro-morphological traits viz., NSBP, NPBP, PBAMS, NMS may be taken for consideration to develop suitable plant type by simple plant selection. PH and AIL also help to evolve suitable plant type for lodging resistant or tolerant, but it showed moderate h_2 coupled with high GAM, which indicated the non additive type of gene action and hence, may be improved by recombination breeding.

The SYP exhibited positive and highly significant association with BYP, HI, NCP, SI, PL, NSBP and LA, whereas positive significant association with BL, NSP and PBAMS indicated that these traits (directly and/or indirectly) may be included for yield improvement of mungbean (Table 2). Similar findings have earlier been reported by Khan *et al.,* 2001 (NBP and BYP), Venkateswarlu, 2001 (SI, NSP, PL). The negative and highly significant association was observed for NFP, PH and NMS. But, Lavanya and Toms (2009) reported the results in contradiction to the present findings. Singh and Singh (1973) had also reported that the genotypes with taller plants may not always demonstrate higher yield. However, plant with medium stature, erect growth habit, short internodes and more effective flowering nodes may in fact utilize solar energy more effectively compared to the taller genotypes. Pubescence traits, which are important for developing the insect tolerant varieties, were not inherently associated with SYP. BYP showed negative significant association with HI and positive significant association with DFFO, indicated that the reproductive growth was highly influenced by vegetative growth. Biomass depends on time taken by plants before starting the reproductive growth. This may be due to the fact that late flowering varieties are provided with more time for growth. The positive and highly significant association of BYP with SI, NCP, PL, NSP and SYP, indicated that biomass might have improved these pod and seed traits and finally the yield by accumulation of food material from source to sink.

The maximum direct effect was exhibited by BYP followed by HI, PH and NSP, which indicated that high yielding mungbean genotypes could be obtained by selecting the genotypes with high biomass along with high HI, short plant structure and more NSP (Table 3). Some of the traits *viz*., SI, PL, NCP and LA showed negative direct effect on SYP but it showed positive association with SYP, which was built up due to the contribution of indirect effect of these traits via other agro-morphological traits. The positive association of SYP independent BYP and HI; negative association between BYP and HI clearly reflected optimization of BYP as it helps in manifestation of HI. Singh *et al.* (2014b) also optimized the HI in mungbean for high seed yield.

The present investigation indicated the importance of pubescence traits, which could be utilized as descriptive traits. This study also suggested that optimization of these traits is necessary. The trait PBAMS was positively associated with BYP and SYP but, exhibited negative association with HI. This findings clearly reflected the relation of branch angle, which helps in making the canopy erect, semi-erect or spreading.

Table 3. Direct (diagonal) and indirect contribution (non-diagonal) of various pubescence and agro-morphological traits to seed yield in mungbean

Traits	DFFO	PH	NPBP	NSBP	PetL	LA	NMS	AIL	PBAMS	NFPP	PedL	PAP	LPD
DFFO	**-0.043**	0.015	-0.027	-0.028	0.011	0.017	-0.009	0.018	-0.002	0.001	0.012	-0.004	-0.009
PH	-0.010	**0.028**	-0.009	-0.009	0.004	-0.002	0.009	0.015	-0.005	0.007	0.004	0.002	-0.001
NPBP	-0.008	0.004	**-0.012**	-0.010	0.005	0.003	-0.004	0.006	-0.002	0.001	0.001	-0.001	-0.001
NSBP	0.032	-0.017	0.039	**0.050**	-0.020	-0.018	0.013	-0.021	0.013	-0.012	-0.008	0.010	0.005
PetL	0.012	-0.007	0.019	0.018	**-0.045**	-0.025	0.014	-0.016	0.011	-0.006	-0.003	0.005	-0.004
LA	-0.019	-0.003	-0.012	-0.017	0.026	**0.046**	-0.012	0.005	0.000	0.001	0.007	-0.014	-0.003
NMS	0.009	0.016	0.015	0.012	-0.014	-0.011	**0.046**	-0.025	0.003	0.015	-0.007	-0.005	0.001
AIL	0.016	-0.020	0.019	0.015	-0.013	-0.004	0.020	**-0.037**	0.007	0.003	-0.006	-0.008	0.002
PBAMS	0.001	-0.004	0.005	0.006	-0.006	0.000	0.002	-0.005	**0.024**	-0.005	0.002	-0.002	-0.002
NFPP	0.000	-0.006	0.003	0.007	-0.003	-0.001	-0.009	0.002	0.005	**-0.027**	0.008	0.005	-0.004
PedL	0.011	-0.006	0.003	0.007	-0.003	-0.006	0.006	-0.006	-0.003	0.012	**-0.040**	-0.005	-0.002
PAP	0.005	0.004	0.005	0.010	-0.006	-0.015	-0.005	0.010	-0.004	-0.009	0.006	**0.049**	0.008
LPD	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**-0.001**
SPD	-0.009	0.010	-0.005	-0.005	0.015	0.010	-0.001	0.008	0.001	0.000	0.012	-0.003	-0.007
PPD	0.001	-0.006	-0.005	-0.004	0.009	0.000	-0.007	0.001	-0.003	0.008	-0.006	-0.004	0.007
PetPD	0.000	0.001	-0.001	-0.001	0.004	0.003	0.001	0.000	-0.001	0.004	0.000	-0.001	0.003
NCP	-0.002	0.005	-0.008	-0.008	0.002	-0.004	0.000	0.003	-0.006	0.006	-0.007	-0.004	-0.001
NPC	0.001	0.000	0.001	0.001	-0.002	-0.002	0.000	-0.001	0.001	-0.001	-0.001	0.001	-0.001
PL	-0.002	0.002	-0.003	-0.004	0.002	0.004	0.004	-0.001	-0.003	0.007	0.001	0.002	0.005
BL	-0.003	-0.002	0.002	0.001	-0.003	0.002	0.000	-0.003	0.002	-0.004	0.005	-0.004	-0.003
NSP	0.004	-0.001	-0.005	-0.005	0.009	-0.001	-0.019	0.012	-0.006	-0.006	0.005	0.003	0.004
PFI	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SI	0.000	-0.007	0.001	-0.001	0.001	0.001	-0.009	0.000	0.002	-0.007	0.002	-0.001	-0.004
BYP	0.178	-0.326	0.229	0.307	-0.020	0.089	-0.314	-0.003	0.334	-0.361	0.161	0.070	-0.072
HI	-0.181	-0.024	-0.114	-0.082	-0.017	0.161	-0.016	-0.040	-0.172	-0.042	0.024	-0.113	0.100
SYP	**-0.004**	**-0.345****	**0.139**	**0.259****	**-0.063**	**0.248****	**-0.288****	**-0.075**	**0.196***	**-0.414****	**0.170**	**-0.021**	**0.021**

Cont……..

Traits	SPD	PPD	PetPD	NCP	NPC	PL	BL	NSP	PFI	SI	BYP	HI
DFFO	0.009	-0.002	-0.001	-0.004	-0.003	-0.004	0.007	-0.005	0.011	0.000	-0.008	0.011
PH	0.007	-0.005	0.002	-0.006	-0.001	-0.003	-0.004	-0.001	-0.002	-0.008	-0.010	-0.001
NPBP	0.002	0.002	0.001	-0.005	-0.001	-0.002	-0.002	0.002	0.000	0.000	-0.003	0.002
NSBP	-0.006	-0.006	-0.003	0.020	0.007	0.009	0.002	-0.007	0.001	-0.002	0.017	-0.006
PetL	-0.016	-0.012	-0.016	0.005	0.010	0.005	0.008	-0.011	0.010	-0.002	0.001	0.001
LA	0.011	0.000	0.013	0.009	-0.010	-0.008	0.005	-0.001	0.000	0.002	0.005	0.010
NMS	-0.001	-0.010	0.003	-0.001	0.001	-0.008	0.000	-0.023	0.004	-0.017	-0.016	-0.001
AIL	-0.007	-0.001	-0.001	0.006	0.003	-0.001	0.007	-0.012	0.005	0.000	0.000	0.002
PBAMS	0.000	-0.002	-0.002	0.007	0.003	0.003	0.002	-0.004	0.005	0.002	0.009	-0.006
NFPP	0.000	-0.006	-0.009	0.008	0.004	0.008	0.006	0.004	0.004	0.007	0.011	0.002
PedL	-0.011	0.007	0.000	-0.013	0.002	0.002	-0.012	-0.005	0.000	-0.003	-0.007	-0.001
PAP	-0.003	-0.006	-0.006	0.009	0.004	-0.003	-0.011	0.004	-0.008	-0.002	0.004	-0.008
LPD	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SPD	**0.043**	0.000	0.008	0.007	-0.003	-0.006	0.006	-0.001	-0.003	-0.003	0.007	-0.005
PPD	0.000	**0.032**	0.005	-0.005	-0.004	0.002	-0.003	0.004	0.000	0.005	0.002	-0.007
PetPD	0.002	0.002	**0.012**	0.000	0.001	-0.006	-0.003	-0.001	-0.005	-0.003	0.002	-0.002
NCP	-0.003	0.003	-0.001	**-0.021**	-0.001	0.000	-0.007	0.001	-0.001	-0.001	-0.008	-0.003
NPC	-0.001	-0.001	0.001	0.000	**0.009**	0.001	-0.001	0.002	-0.001	0.001	0.002	-0.002
PL	0.004	-0.001	0.011	0.000	-0.002	**-0.024**	-0.003	-0.011	-0.012	-0.014	-0.009	-0.001
BL	0.002	-0.001	-0.004	0.005	-0.002	0.002	**0.016**	-0.001	0.004	0.000	0.000	0.004
NSP	-0.001	0.005	-0.003	-0.003	0.008	0.017	-0.003	**0.038**	-0.017	0.014	0.011	-0.002
PFI	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**-0.001**	0.000	0.000	0.000
SI	-0.002	0.004	-0.005	0.001	0.003	0.014	-0.001	0.009	0.008	**0.025**	0.012	-0.002
BYP	0.140	0.051	0.121	0.344	0.195	0.322	0.023	0.256	0.065	0.431	**0.897**	-0.252
HI	-0.080	-0.144	-0.151	0.104	-0.137	0.032	0.192	-0.040	0.095	-0.050	-0.201	**0.713**
SYP	**0.088***	**-0.093**	**-0.025**	**0.468***	**0.087**	**0.352****	**0.227****	**0.200****	**0.162**	**0.381****	**0.717****	**0.446****

Abbreviations are given in materials and methods

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