



**Genetic analysis of common bean
(*Phaseolus vulgaris* L.) for yield and
yield components under managed
drought stress conditions**

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Rationale and Justification

- Drought stress – has become common problem in common beans
- Yield losses (>66%) due to drought stress (Bates et al., 2008).
- Expected to increase with global warming
- Over 50% of food emergencies are due to droughts (FAO, 2004)

Rationale and Justification cont!

- Breeders have used plant breeding to develop adaptable varieties to drought prone areas
- However, its Important that breeding value for drought tolerance in all genetic materials meant to be used for drought is understood
- Drought tolerance is a physiologically complex trait

Rationale and Justification cont!

- Its inheritance is considered to be a quantitative ([Schneider et al., 1997](#), Blair et al., 2010).
- Drought tolerance traits can also be expressed at different stages during crop development ([Rao, 2001](#)).
- Two different types of drought are known, intermittent and terminal drought (study looked at terminal drought)

Rationale and Justification cont!

- The traits associated with tolerance to drought in common bean have been studied and identified by many scientists (White and Castillo, 1985; Acosta-Gallegos and Shibata, 1989; Schneider et al., 1997; Ramirez-Vallejo and Kelly, 1998; Frahm et al., 2004; Rosales-Serna et al., 2004; Beebe et al., 2008).

Rationale and Justification cont!

- However, the underlying genetic basis of most of these traits remains to be understood.
- traits reported to be valuable in drought tolerance are earliness and yield components (Acosta-Gallegos and Shibata, 1989).
- Making significant genetic gain for adaptation to drought stress in breeding requires a better understanding of the nature and level of drought tolerance in genotypes used

Research objectives

- This study therefore focused on determining the nature and levels of drought tolerance of selected Zambian bean genotypes.
- The specific objective was to estimate the genetic parameters for yield and yield components under managed drought stress conditions.

MATERIALS AND METHODS

- Eight female and six male parents were used
- Female genotypes used were all well adapted genotypes to bean production regions with preferred grain types by the farmers and consumers
- male parents were selected from landraces through a comprehensive screening experiment (conducted under this study) other materials were obtained from (CIAT).

MATERIALS AND METHODS cont!

- Parental genotypes were inter-mated using the
- North Carolina Design II scheme as described by (Comstock and Robinson, 1948) to generate 48 F_1 crosses.
- F_1 plants were advanced to the F_2 generation (Used for evaluation)

MATERIALS AND METHODS

- Evaluation sites-Mt. Makulu (at latitude $15^{\circ}13.10'$, longitude $28^{\circ}14.93'$, altitude of 1200 m), and Nanga ($15^{\circ}32.87'$ longitude $27^{\circ}32.93'$, altitude of 1190 m above sea level).
- Two sites are similar in soil type and climate
- Evaluation plots were planted off season (to manage drought-towards end of February)

Trial layout and management

- 64 entries (48F1, 2 checks (CIAT) and 14 parental lines)
- alpha-lattice design
- Planted 5 m rows at a spacing of 75 cm by 30 cm

Trial layout and management cont!

- Recommended good trial management practices followed
- Fertilizer-NPK (200kg N /ha)
- Supplementary irrigation was applied to until 50% flowering (Water withdrawing)

Data collection and data analysis

- Data was collected from the whole plot (30 plants-segregating popln)
 - **Days to flower (DAF)** – number of days from 50% seedling emergence to 50% flowering.
 - **Days to physiological maturity (PM)** – number of days from 50% seedling emergence to 50% physiological maturity and plant senescence.
 - **Hundred seed mass (HSM)** – It was recorded in grams after harvesting dry pods and was taken as the mass of 100 seeds drawn at random.
 - **Yield** – was estimated by harvesting mature plants by hand from both rows in each plot and the sample was allowed to dry in the open air. Dry pods were threshed and seeds were weighed on individual plant basis.
 - **Flower abortion (FA)** – was taken as the difference between the number of flowers counted at 50% flowering and the number of mature pods.
 - **Number of seeds per pod (NSP)** – It was recorded as the average number of mature seeds in a pod.
 - **Number of pods per plant (NPP)**– This was recorded by counting on average the total number of pods on one plant

Data collection and data analysis cont!

- general linear models as random model for all terms were used for the analysis of variance (ANOVA) using PROC MIXED procedure of SAS (SAS Institute, 2002).
- SAS programme for the line x tester analysis was used to compute the GCA and SCA effects following the procedure presented by (Singh and Chaudhary, 1977).

Results

Analysis of Variance

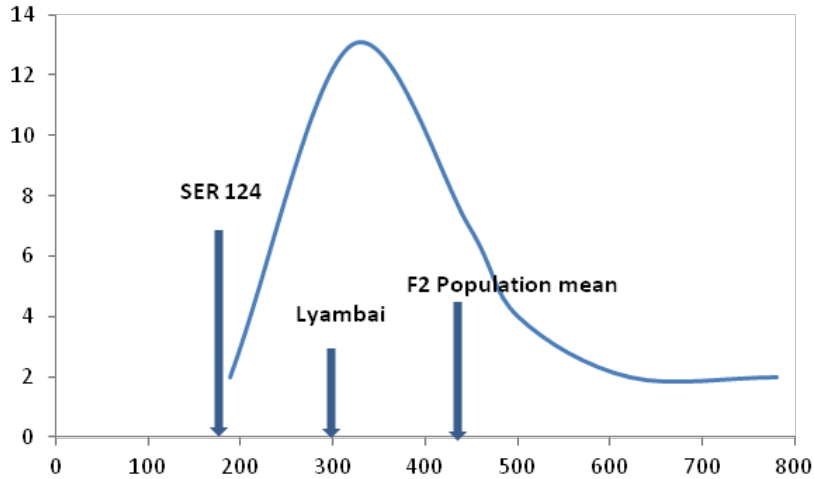
Source	DF	Yield	NSP	DAF	FA	NPP	HSM
Site	1	15561228.97 ***	253.28	1442.4 1**	1167.2 1**	16213.6 6**	27726.7 5**
GCA _F	7	247051.83**	2982.86 **	19.32	261.86 *	1686.84	7410.92
GCA _M	5	312450.36**	219.66*	21.77	193.43 **	2474.58 **	2403.21
SCA _{F*M}	35	135446.23**	428.89*	24.88*	195.87 *	4691.81	6076.62
Error	70	623.44	101.21	29.00	88.10	548.99	911.70
Bakers ratio		0.81	0.88	0.62	0.70	0.47	0.62
Narrow Sense Heritability		0.60	0.33	0.42	0.49	0.38	0.42

General Combining Ability-Yield

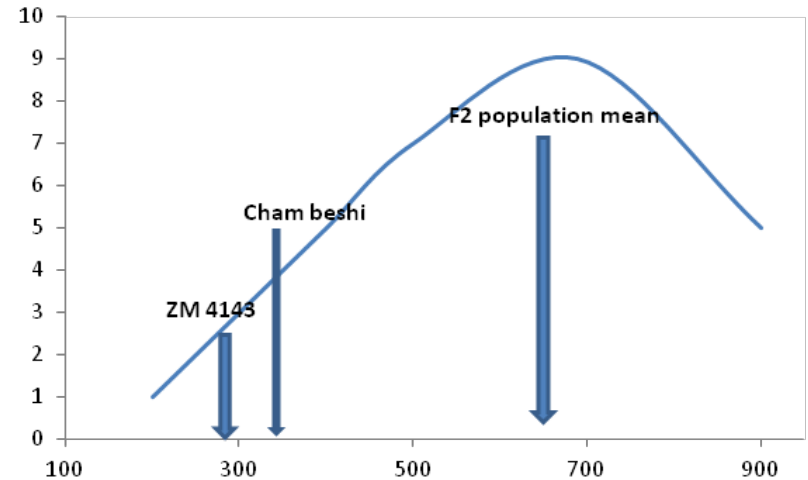
Genotype	Nanga	Mt. Makulu	Across drought sites
GCA effects – Female			
ZM 05	51.29*	-52.07**	135.43**
Chambeshi	108.04**	-3.16	94.25*
Pan 148	125.38**	49.34**	-33.92*
Kabulangeti	-60.71*	-78.82	-56.94*
Kalungu	-107.13**	-32.41**	-103.64**
Lyambai	69.38	35.01	29.43*
Kapisha	-37.88	-36.57**	-95.95*
SCCI-2	-148.38**	118.68*	31.33*
GCA effects – Male			
ZM 4143	1.23	-91.51	-146.56*
ZM 4497	314.88**	345.06*	591.41*
SER 124	357.88**	329.19*	526.03*
Ly4-4-4-B	228.25	332.75*	487.20*
ZM 3831	171.25*	363.19*	459.31*
SEN 39	265.06**	277.94*	506.13*
*Significant at P≤0.05, **Significant at at P≤0.01			

Frequency distribution for yield- Selected crosses

Lyambai X SER 124

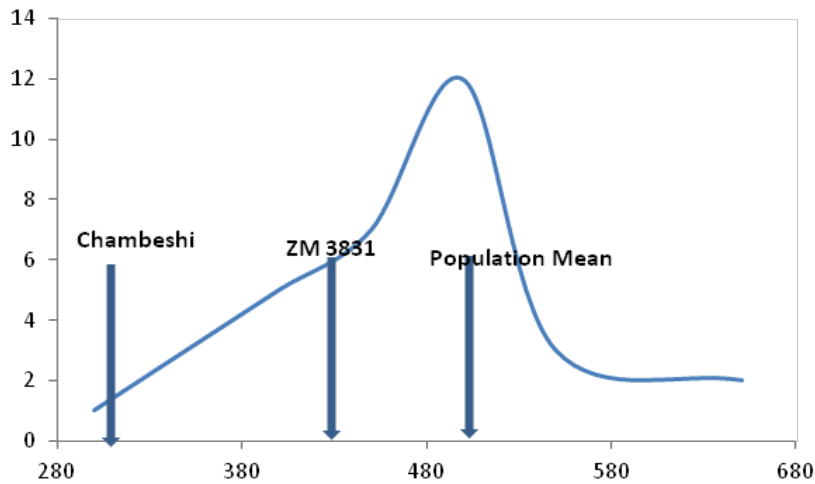


Chambeshi X ZM 4143

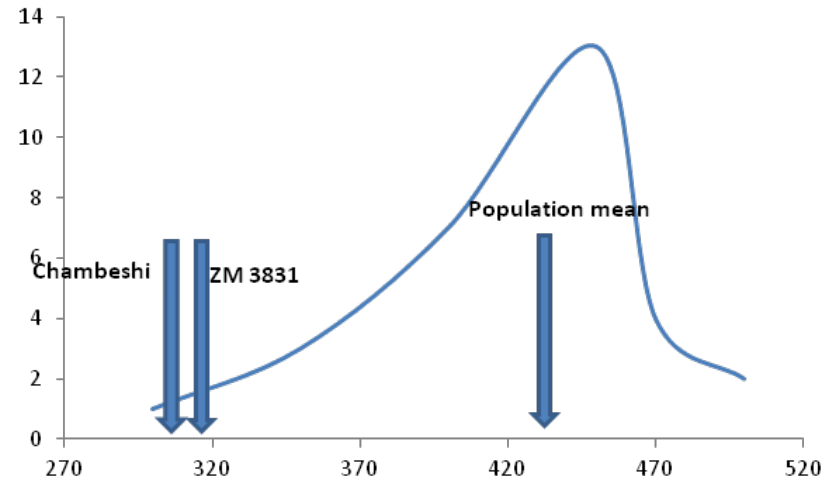


Frequency distribution for yield- Selected crosses

Pan 148 X ZM 4143



Chambeshi X ZM 3831



Correlation with measured traits and yield components

DAF	1					
HSW	-0.65**	1				
FA	-0.61**	0.54*	1			
NPP	0.43*	0.16	0.79**	1		
NSP	0.46*	-0.048	0.13	0.16	1	
Yield	0.27	0.18	0.29*	0.61**	0.15	1
	DAF	HSM	FA	NPP	NSP	Yield

Discussion and conclusion

- mean squares due to GCA were significant for yield and number of seeds per pod
- similar results were exhibited for SCA mean squares
- Significant GCA and SCA effects for yield implies both additive and non additive gene actions were important
- However, additive gene effects were more important going by the high bakers ratio
- Greatest positive GCA exhibited suggests that best progenies can be derived from the crosses of such parents as suggested by Arunga et al. (2010)

Discussion and conclusion cont!

- ZM 4497, SER 124, Ly4-4-4-B, ZM 3831 SEN 39 had high and positive GCA effects for yield
- Lyambai and SCCI-2 also exhibited high GCA effects (Female parents)
- it would imply therefore that selection for yield would be achieved easily and fast from segregating early generations of such parents in right combinations

Discussion and conclusion cont!

- Significant GCA effects for NSP and Flower abortion indicates that the two traits can be used as indirect traits to select for drought tolerance
- Significant mean squares for SCA effects for FA indicates that both additive and non-additive gene action may be controlling the inheritance for flower abortion

Discussion and conclusion cont!

- Positive and significant correlation between Yield and number of pods per plant/flower abortion further confirms the usefulness of the two traits for selection for drought selection
- Significant and positive GCA effects and high Baker's ratio for NSP across the environments imply that the additive gene action was important in its inheritance.

Discussion and conclusion cont!

- The 60% heritability estimate for grain yield is adequate to make progress in breeding for drought tolerance in common bean
- However, the magnitudes of heritability estimates are products of the population being tested, and environments within which the testing is done and traits being measured
- Low heritability estimate for other traits may be attributed to the large environmental variations in F2 population

Discussion and conclusion cont!

- Low heritability estimates for these traits (NSP, DAF, FA, NPP and HSM) are expected since inheritance for drought tolerance is considered as polygenic
- The transgressive segregation observed with the measured traits such as yield (results shown), number of pods per plant and number of seeds per pod (results not presented) provides an opportunity for further selection

- **In conclusion,**
 - this study focused on the genetics of inheritance to drought tolerance for selected traits in common bean.
 - Significant GCA and SCA mean squares for yield showed the importance of both additive and non-additive gene effects.
 - The Baker's ratio results showed that additive gene effects were more important than non-additive gene effects for all traits (can make progress in breeding)
 - The high heritability of 60% for yield further confirms the importance of additive gene effects for drought tolerance in common beans.
 - Local germplasm is available for use in breeding for drought
 - Transgressive segregation was also found among the F_2 populations for drought tolerance indicating the possibility of making appropriate choices from segregating populations

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