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TITLE OF THESIS . GENETIC ANALYSIS OF CREENCRAM (Vigna

radiata (L.) Wilczek) SUITABLE FOR LATE RICE FALLOWS IN PENNAR DELTA.

ANDHRA PRADESH

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## **ABSTRACT**

Studies were conducted on "Genetic analysis of greengram (Vigna radiata (L.) Wilczek) suitable for late rice fallows in Pennar delta, Andhra Pradesh" at Agricultural Research Station, Podalakur, Nellore district, Andhra Pradesh from 1999 to 2001 during rabi season in black soils. Rice yields in South India are stagnating in recent years due to continuous monocropping. This is more particular in Nellore district of Andhra Pradesh. Rice is being cultivated round the year in three continuous monocroppings, overlapping seasons in pennar delta of Andhra Pradesh. More dependency on chemical fertilizers, more depletion of organic matter and other nutrients from the soil has led to the stagnation of rice yields in this region. In addition to meet the growing demand for pulses, legumes have to be introduced in rice fallows in rice monocropping areas to sustain and improve rice production. Keeping this in view an attempt has been made to identify the suitable parameters and their inheritance in greengram to develop varieties for late rice fallows of Pennar delta. A study has been undertaken through combining ability and

triple test cross analysis, and variability studies were carriedout by utilizing cross combinations derived from a line x tester programme to understand the genetics of shoot dry weight, along with yield and yield components through combining ability analysis and to estimate the variability, heritability, genetic advance of yield and component traits.

Data were recorded on days to 50% flowering, days to maturity, plant height, pods / plant, seeds / pod, 100 seed weight (g), shoot nitrogen (%), seed protein (%), shoot dry matter and seed yield / plant.

Variability studies indicated existence of wider variability for plant height, pods / plant, shoot dry weight and seed yield / plant. These characters also recorded high heritability coupled with high genetic advance, suggesting the importance of additive gene action for these traits.

High heritability along with low genetic advance was found to be important for days to maturity, seeds per pod, shoot nitrogen and seed protein.

Combining ability analysis revealed that plant height, seeds / pod, seed protein and shoot dry weight are under the influence of additive gene action while, days to flowering, days to maturity, pods / plant, 100 seed weight, shoot nitrogen and seed yield are under the control of both additive and non-additive gene action. Pusa 9672 among lines and LGG 407 among testers were found to be good general combiners for most of the characters studied. Positive and significant heterosis over better parent was noticed for pods/plant, shoot dry weight, seed yield in LGG 410 x LGG 407, MGG 341 x LGG 407, Pusa 9672 x WGG 2, Pusa 9672 x TARM 21 and Pusa 9672 x LGG 440. All these cross combinations also recorded high mean values

coupled with high *sca* effects for seed yield. It is suggested that these cross combinations can be handled through cyclic hybridization followed by selection so as to capitalize both additive and non-additive genes and for isolation of transgenic segregants.

Triple test cross analysis indicated the existence of epistatic gene actions in the inheritance of all the seven characters studied. Both additive and non-additive gene actions were found to be important with predominant role of additive genetic variations in the governance of the characters.

Days to flower, Days to Maturity, 100 seed weight, Plant height, Pods/plant, Seeds / pod and shoot dry weight had showed positive and significance with seed yield both at phenotypic and genotypic level. Associations among these components were also positive and significant. Shoot dry weight had maximum positive direct effect on seed yield followed by pods / plant, 100 seed weight and seeds / pod. Shoot dry weight, pods / plant, 100 seed weight and seeds / pod also had considerable positive indirect effects on seed yield through other yield components.

An overall view of the results obtained from the present study indicate that both additive and non-additive gene actions are involved in the inheritance of major yield contributing characters viz., pods / plant, shoot dry weight, seeds / pod and 100 seed weight. Hence, breeding programs may be modified in such a way so as to accumulate both additive and non-additive genes. Pods / plant, shoot dry weight, seeds / pod and 100 seed weight should be given due consideration in the selection process while constructing selection indices as they have significant associations with seed yield and maximum direct and indirect effects on seed yield. Shoot dry weight has close association and direct positive effect on seed yield / plant. This is the

clear indication for a genotypic suitability under rice fallow condition. A genotype with more biomass has the capacity to grow fast and occupies the gaps in rice fallows. This leads to suppress the weed growth and conserve the soil moisture, which ultimately results with high seed yield. Selection based on this character will definitely result with high yielding genotypes suitable for rice fallow. Parents, Pusa 9672 and LGG 407 may be exploited extensively in breeding programmes aimed at development of high yielding varieties. The most productive cross combinations may be exploited by isolating desirable segregants in the subsequent generations.