**Development of diverse parental lines in castor through single seed descent method**

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**Introduction**

Commercial exploitation of heterosis in castor led to a rise in production and productivity from 2.1 to 10.03 lakh tonnes and 220 to 1334 kg/ha during the last seventy years. More than 90 percent castor growing areas, especially under irrigated conditions is occupied by castor hybrids. However, a gradual decrease in genetic diversity of the parental base led to a plateau in the experimental hybrids (Lavanya and Solanki, 2010). Continuous selection pressure for wilt resistance in the early generations led to genetic erosion of several yield contributing genes. Many wilt resistant parents failed to generate a breakthrough in the yield plateau. The conventional breeding methods like pedigree and pure line selection relied on selection for low heritable traits like seed yield in wilt resistance background. An attempt is made, for the first time in castor, to conserve the diversity generated in F2 for further selection in later generations (F6 onwards) through single seed descent (SSD) method.

**Methodology**

VP-1, the most popular, wilt susceptible, pistillate line in castor, with distinct morphological characters like green stem, condensed nodes, cup shaped leaves, spiny capsules, is crossed with a wilt resistant, male or monoecious line, 48-1, of contrasting morphological characters. Fifty plants of F1 raised in *rabi* 2009 were selfed to generate nearly 200 F2 seeds. 200 single plant selections of F2 of VP-1and 48-1, along with parental lines are sown in *rabi* 2010-11. Data on morphological characters, yield components, seed yield of every single plant are recorded and each plant is selfed to advance the population through single seed descent (SSD) method.

One selfed seed from each F2 plant is raised to generate F3. Selfed seed from each F3 plant is grown in a progeny row and single seed of a single plant is represented in each generation up to F6. Among the eighty three inbreds in F6, 40 inbreds were found stable and homozygous for morphological characters. 37 inbreds were grown in *kharif*, 2017-18, in a RBD along with four male or monoecious checks, DCS-107, 48-1, GC-3 and DCS-78 in two replications. The same set of inbreds was also screened in wilt sick plot at IIOR, Hyderabad.

**Results and Discussion**

Single seed descent method, was proposed as an alternative to pedigree selection to quicken the pace of generation advancement in soya bean (Brim, 1966). Lack of selection pressure and pedigree records followed by multiple generations hastened the generation of diversity through single seed descent method. Recombinant inbreds generated in F2 were intact even up to F6 and provided the scope for genetically diverse wilt resistant inbreds in a high yielding back ground. Among the 37 inbreds, 14 inbreds were found promising for yield contributing traits like effective spike length (60-70 cm), early (85-90 DAS) to medium (100-110 DAS) maturity to first picking. Among the 37 inbreds screened for wilt resistance in wilt sick plot at IIOR, Hyderabad, 3 lines *viz*., Kh-4-3-44, Kh-3-5-21, Kh-3-5-49 with <20% wilt incidence were wilt resistant while, five lines were moderately resistant (<25% wilt incidence) compared to the susceptible check, JI-35 (93%) and resistant check, 48-1 (10.5%).

**Conclusion**

Single seed descent method is an efficient breeding technique to conserve the genetic diversity. In a long duration crop like castor with extensive vegetative growth, single seed descent method is more effective as it requires less space and record keeping compared to pedigree selection. The method is suitable for traits with low heritability like plant height, maturity and seed yield.

**References**

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