PERFORMANCE OF NEW CYTOPLASMIC MALE STERILE SORGHUM LINES DEVELOPED FOR TOLERANCE TO TOXIC LEVELS OF ALUMINUM IN ACID SOILS.

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The fertility non-restoring line from the Texas A&M/USDA Sorghum Conversion Program, IS 7173c(SC 283), a genetic source for tolerance to Al toxicity in acid soils was used to incorporate this trait into various sources of non-restoring lines with the objective of developing commercial male sterile lines tolerant to Al toxicity. The susceptible male sterile B-lines, BR 007, Redlan, Wheatland, Dwarf Redlan, and SC 566 were crossed with SC 283. Several hundred head to row F4 families visually selected for desirable agronomic traits were selected for Al tolerance under acid soil conditions (45% Al saturation) at the National Maize and Sorghum Research Center (CNPMS) of the Brazilian Agriculture Research Corporation (EMBRAPA). Progenies were selected for root development based on their reaction to moisture stress during prolonged periods without rain. Turgid plants were assumed to have a better developed root system than moisture stressed plants and were classified as having Al tolerance. Selected F7 progenies were backcrossed to a source of cytoplasmic male sterility to develop respective A lines for each selected B line progeny. The B lines of 55 selected A and B pairs were evaluated for tolerance to Al toxicity using relative seminal root growth (RSRG) of seedlings in nutrient solution with 4ppm of Al for seven days as the indicator. The average RSRG of the tolerant (SC283) and susceptible (BR 007B) checks were 50.6% and 6.6% respectively. The RSRG of the 55 selected progenies from 16 family groups ranged from 2.8% to 75.5%. Eleven progenies from four family groups were susceptible. Tolerant progenies selected from families derived from Redlan and Dwarf Redlan crosses had lower RSRG than tolerant progenies from families derived from BR 007 and Wheatland. Head to row progenies from three groups segregated for tolerance and susceptible reaction, confirming three near isogenic (96.9%) pairs for this trait. The relative high frequency of segregation after the S5 generation suggests that one or a few major genes control this characteristic.