

Analysis of recurrent parent genome recovery in marker-assisted backcross breeding program in watermelon

ABSTRACT

Marker-assisted backcross (MABC) is a breeding technique used to develop improved varieties by transferring a gene or QTL into the genome background of an elite variety after 2-3 generations. It is an advanced way of overcoming challenges facing conventional backcross methods as it speeds up the recurrent parent genome recovery (RPG). In order to develop a Fusarium wilt resistant watermelon variety, MABC was used to incorporate wilt resistant gene from the resistant inbred line CS-19 into the genome of the high yielding but wilt susceptible inbred line BL-14. There was estimation of RPG recovery in earlier generations with the use of polymorphic simple sequence repeat (SSR) markers. A total of 380 SSR markers were tested to identify polymorphism between the parents and 78 of them were found to be polymorphic. Background analysis revealed 74.7 – 94.4 and 86.6 – 96.8 % recovery in BC1F1 and BC2F1 generations, respectively. In the BC2F2 generation, RPG recovery ranged from 95.1 and 96.9 and the average in the selected lines was 96.14 %. This study led to the selection of plants that are similar to the recurrent parent and it showed the usefulness of MABC for the quick recovery of a parental genome in a backcrossing population.

Keyword: Fusarium wilt; Marker-assisted backcross; Marker-assisted selection; Polymorphism; Recurrent parent genome recovery; Watermelon