Introduction

The transgenic RHBV resistant rice was generated by splicing in genes from the RHBV virus into Cica 8 variety (Lentini et al., 1996), selected by the breeders as potential parent donor of the transgene for future conversion of modern varieties because of its good grain quality, high productivity, and broad adaptation including low soil humidity, and acceptance to large and small resource farmers. Thus this transgenic resistance could be used to complement the breeding resistance that has been deployed so far and does not protect plants when younger than 5 to 20 day-old. In addition to selection for RHBV resistance and yield potential, the advanced lines were evaluated for tolerance to Rhizoctonia, resistance to Pyricularia, and grain quality traits. Progress in previous years led to a shift from the testing of concepts towards the final steps for its potential release to farmers’ fields.

The main goal for this project is to provide new source(s) of resistance to complement the single source of resistance present in most of the commercial varieties currently grown in Latin America.

Materials and Methods

RHBV resistance and agronomic performance in the field of selected families derived from crosses (total 14) derived from self cross.

Results and Discussion

Five F6 generation lines derived from crosses with Oryzica 1, and five T7 and T10 self progeny advanced transgenic lines were clustered jointly with Fedearroz 2000 showing the highest level of RHBV resistance (score ≤ 3). Based on this RHBV resistance profile, the agronomic performance including yield potential, sheath blight and blast resistance as well as for grain quality traits, three F6 generation lines from the cross with Oryzica 1, one T7 and four T10 from the original Cica 8 transgenic lines were included in the field final selection.

Future Activities

The selected lines are currently being processed through anther culture to generate doubled haploid (complete homozygous) lines, convenient material for gene multiplication, replicated multi-location field trials and molecular genotyping.

References
