

Validation of some disease-resistance molecular markers associated with multiple diseases in tomato for marker-assisted selection program

ABSTRACT

Marker-assisted selection (MAS) is a tool that is widely applied in tomato resistance breeding. To determine the robustness of some molecular markers commonly used in MAS, extensive screening of 964 tomato lines was performed under a controlled experimental condition. Initially, the application of 36 molecular markers targeting 26 resistance genes (R genes) and 14 major diseases was evaluated. Here, we employed basic molecular biology and bioinformatics techniques for analysis where polymorphism, accuracy and clearness of amplicons constituted the selection criteria of markers. Upon initial analysis, 20 of these markers designated as efficient markers, among which 8 were considered gene-based markers and referred to as perfect markers were selected for detail evaluation. Information extrapolated from PCR result revealed 18 R genes that control 12 diseases were grouped under efficient markers. On the other hand, grouping of breeding lines based on the number of R gene harbored comprehensively revealed 62% of the lines to be void of R gene, while 38% carry different types of R genes. This provides us with an avenue to better understand new sources of resistance in the breeding lines. Conclusively, these efficient markers and their limited PCR condition can be suggested as basis of a diagnostic kit for MAS applications against 12 major tomato diseases and the identified resistant breeding lines could be conserved in order to be propagated as different sources of resistance for the development of new resistant varieties. Therefore, in areas with high vulnerability to diseases, high efficiency combination of the relevant R genes and their pyramiding into commercial tomato varieties are proposed to be implemented as a pragmatic approach.