

عنوان مقاله:

Genealogy and Molecular Diversity of Iranian Grapevine Progenies

محل انتشار:

مجله علوم و فناوری کشاورزی, دوره 13, شماره 7 (سال: 1390)

تعداد صفحات اصل مقاله: 15

نویسندگان:

M. Hadadinejad - Department of Horticulture, College of Agriculture and Natural Resources, University of Tehran, .Karaj, Islamic Republic of Iran

A. Ebadi - Department of Horticulture, College of Agriculture and Natural Resources, University of Tehran, Karaj, Islamic Republic of Iran.

M. R. Naghavi - Department of Agronomy and Plant Breeding, College of Agriculture, University of Tehran, Karaj, Islamic Republic of Iran.

R. Nikkhah - Department of Horticultural Science, College of Agriculture, Persian Gulf University, Boushehr, Islamic .Republic of Iran

خلاصه مقاله:

Grapes are among the world most planted horticultural crops. Since the last century, attempts have been made to improve the quality of grapes in the world. Meanwhile, the necessity of having knowledge about the history of progenies families led to the link between genealogy and breeding. Considering some previous mislabeling, in order to find out the accuracy of the controlled crosses as well as determining the possible parents and genealogy of the hybrid progenies, Ym grapevine genotypes were studied by using IF SSRs loci. These progenies included IY promising lines selected from YY crosses as well as their parents that included four seedless and seven seeded cultivars from Iranian Grape Breeding Program, The highest similarity between a female parent and its progenies, which was progenies (S&F, S&A, SF.). Results rejected any cross-selfing in female parents and also discriminated progenies from parents. Due to possible common genetic backgrounds in the parents, assigning progenies to their parents by cluster analysis or allele counting was impossible. Therefore, parentage analyses were done within likelihood based assignment approach using CERVUS ".. software. By this approach, true parents could be identified from candidate parents based on calculated positive and negative LOD scores. Also, by using this approach, genotyping errors, which were previously derived from low number of SSR loci or similarity in the parents' backgrounds, decreased in the final results. In addition, full sib and half sib relationships between Saa and SaF with SFo were obvious. Furthermore, wherever prevention of inbreeding depression is required, the results could be used to select convenient parents for .backcrossing

كلمات كليدى:

Grapevine, Breeding, Likelihood based assignment, Microsatellite

لینک ثابت مقاله در پایگاه سیویلیکا:

https://civilica.com/doc/1827087

