Absence of concordance between polyembryony and apomixis in maize confirmed through DNA sequencing [

2019

text (article)

Analítica

ABSTRACT Maize (Zea mays L.) polyembryony is a useful feature for genetic improvement of this specie, not only by its potential to generate multiple plants per seed, but also by its influence on increasing of fatty acids and amino acids content in the grain. It has been considered a possible association between apomixis and polyembryony in maize. With the objective to evidence the relation between apomixes and polyembryony, were used sequences of internal transcribed spacers (ITS), and intergenic spacers (IGS) and amplification of simple repeated sequences (SSR). The analyses were performed in 5 families derived from the IMM-UAAAN-BAP ("D") maize population. Within each of the families were analysed the female parent plant, and two types of progenies (individual and polyembryonic). Nucleotide sequences and genotypic class were compared and also a molecular variation analysis was performed. In these analyses only a close but not identical relationship between polyembryonic plants was found. With the use of these techniques, it was demonstrated that reproduction of the maize plants is of a sexual type, and that based on the molecular markers used, no evidence was obtained about the probable relationship of a common genetic basis between polyembryony and apomixis. Sequencing of the ITS and IGS regions, and use of SSR microsatellites of different chromosomes, was a practical and economical tool for the assessment of similarity between genotypes
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Editorial: 2019

Tipo Audiovisual: Genetic variation IGS ITS molecular markers polyembryony Zea mays IGS ITS marcadores moleculares poliembrionia variación genética Zea mays

Documento fuente: Ecosistemas y Recursos Agropecuarios, ISSN 2007-901X, Vol. 6, Nº. 18, 2019, pags. 451-461

Nota general: application/pdf

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Lengua: English

Enlace a fuente de información: Ecosistemas y Recursos Agropecuarios, ISSN 2007-901X, Vol. 6, Nº. 18, 2019, pags. 451-461