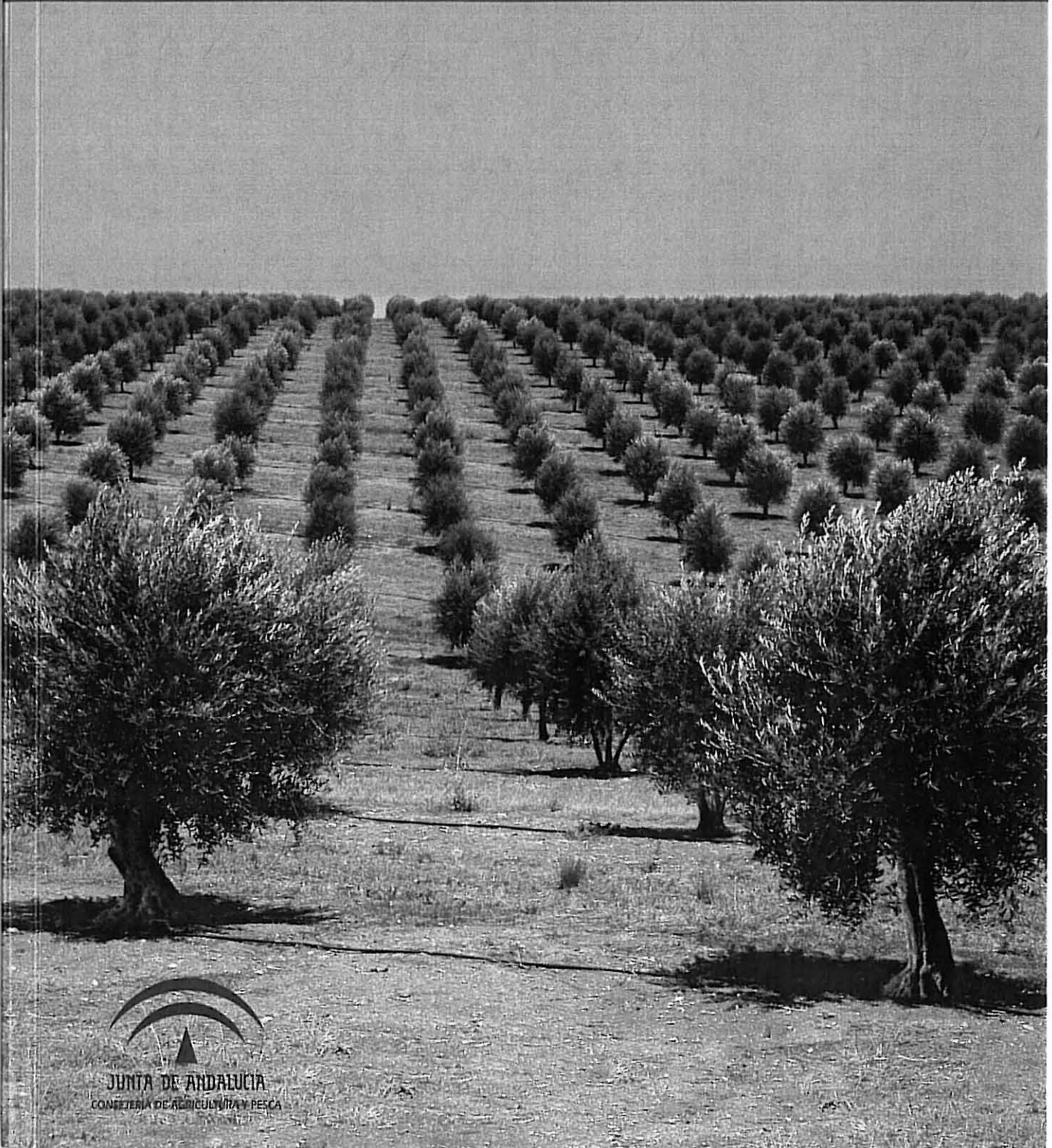


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**O 42. INTRASPECIFIC VARIATION OF THE ENTOMOPHATOGENIC FUNGI *BEAVERIA BASSIANA* COLLECTED IN OLIVE GROVES FROM DIFFERENT GEOGRAPHIC ORIGIN**

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The fungus *Beauveria bassiana* is a well-recognised entomopathogen known to infect hundreds of host species from most of the insect orders. Therefore, the use of this fungus as a biological control agent against insect pests is very promising and several commercial products have already been developed. The natural occurrence of *B. bassiana* has been reported throughout Spain. Recently, its presence has been also verified in Portugal, specifically in the Trás-os-Montes region. In the present study, we have investigated the intraspecific variation of 21 *B. bassiana* isolates, 9 of which sampled in olive trees located in Portugal (Trás-os-Montes region) and the remaining 12 in Spain (Córdoba). After the identification of fungal isolates by sequencing of the amplified internal transcribed spacer (ITS) region of rDNA, the isolates were compared by random amplified polymorphic DNA (RAPD). The average sequence lengths of ITS1, 5.8S rDNA, and ITS2 of *B. bassiana* were 215, 170, and 214 pb, respectively. When compared with the ITS region from other fungal species, all the ITS sequences from the fungal isolates showed 99.0% of identity with *B. bassiana*. Among a total of 40 arbitrary 10-mer primers, 10 primers produced polymorphic RAPD profiles. The RAPD patterns showed considerable genetic variation between isolates from different geographic origin. The significance of the findings for the genetic variability of *B. bassiana* is discussed.

**KEYWORDS:** *BEAVERIA BASSIANA*, ENTOMOPHATOGENIC FUNGI, RAPD, INTRASPECIFIC VARIATION