terior position of the excretory pore and a low value of ratio c´; males had slightly curved spicules with oblongate manubrium and mucronless tail (Fig. 1A, B, E). Isolate 20F possessed moderately curved lamina of spicule, presence of rostrum and oblongate manubrium in the males, IJs with short hyaline layer (<40%) and thus resembling *S. kraussei* (Fig. 1F).

Phylogenetic analysis

For isolates 15G and 59F, sequences from the 28S rDNA D2D3 domain were not obtained, so phylogenetic analysis of this region included just isolates 20F and 2B. The identification at species level for *Steinernema* sp. *glaseri*-group requires additional research, such as more detailed morphological and morphometric data, because not all nucleotide differences corresponded to either to *S. glaseri* or *S. arenarium* (Artyukhovsky) Wouts, Mráček, Gerdin *et* Bedding. The total evidence dataset in phylogenetic trees ranks our isolate 2B in the *affine/intermedium*-group and isolate 20F in the *kraussei/feltiae*-group because, in the nucleotide analysis of *Steinernema* species, it is difficult to determine homologous character states for many morphological characters (Nadler *et al.*, 2006). However, morphology and morphometry support identification of these isolates as *S. intermedium* and *S. kraussei*.

ITS rDNA region. Maximum parsimony (MP) analysis of ITS rDNA datasets were constructed based on 930 positions, involving 21 nucleotide sequences (Fig. 2). MP analysis groups our isolates within the *Steinernema* species and is supported by strong bootstrap values

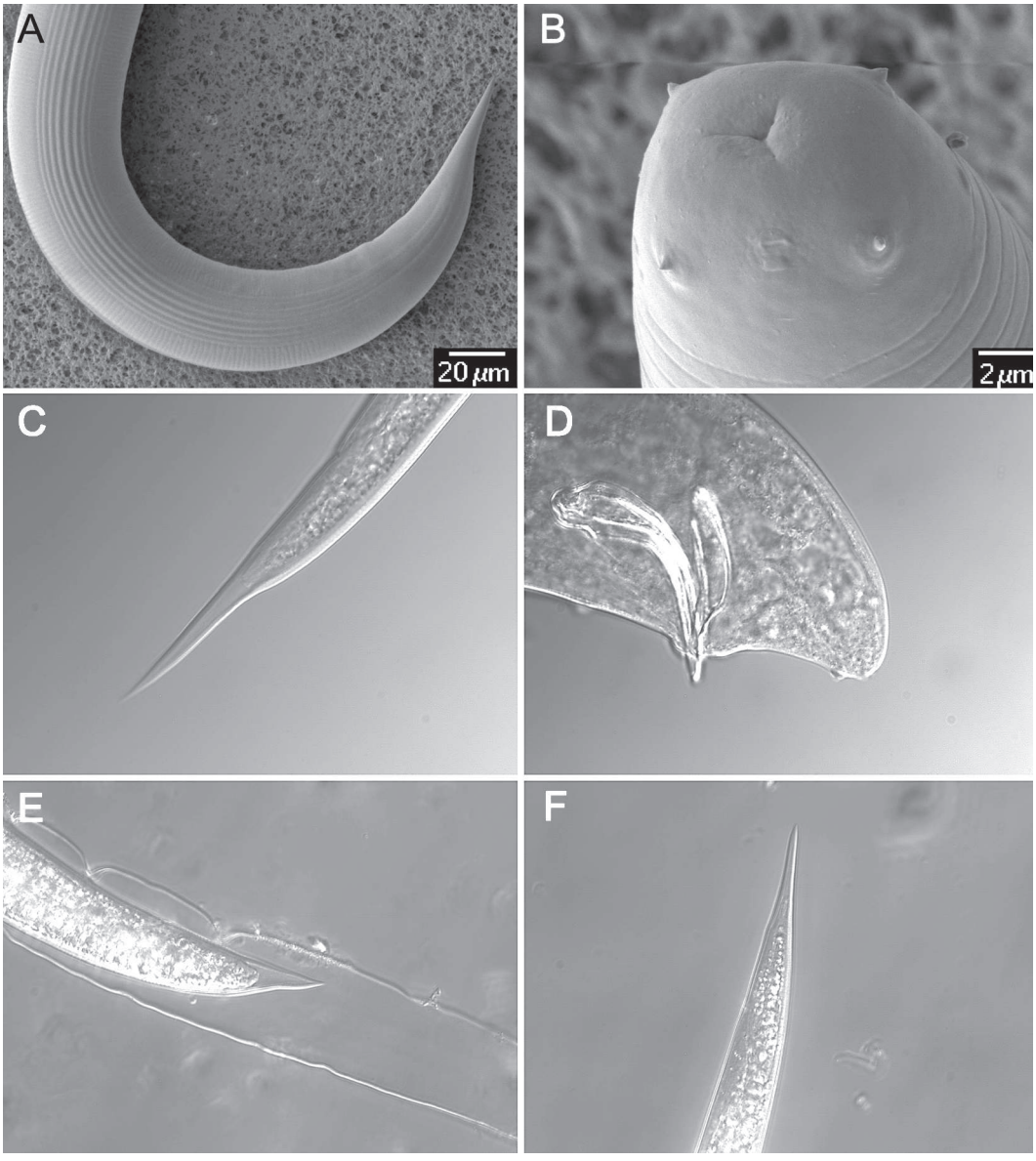

Fig. 1. Steinernematid species from continental Portugal. A,B,E *Steinernema* sp. "*glaseri* group" infective juvenile: A, lateral field with eight ridges; B, head with four cephalic papillae; E, tail with hyaline layer in sheath of the second stage juvenile. C,D, *S. intermedium*: C, IJ tail with a dorsal constriction; D, male tail with spicules. F, *S. kraussei*, IJ tail with short hyaline layer.