

FIRST REPORT OF A COLD-ACTIVE EPN *STEINERNEMA KRAUSSEI* (RHABDITIDA, STEINERNEMATIDAE) FROM IRAN

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Summary. During a survey of entomopathogenic nematodes conducted throughout the Arasbaran area, in the north-west of Iran, an entomopathogenic nematode was isolated by *Galleria* baiting method from soil samples collected from rangelands, near Chichakloo, Varzeghan. It was identified as *Steinernema kraussei* based on morphological, morphometrical, molecular and cross-breeding studies. This is the first record of *S. kraussei* from Iran.

Keywords: Entomopathogenic nematode, Iran, molecular characterization, new record.

Entomopathogenic nematodes (EPNs) of the genus *Steinernema* are frequently used as biological control agents of several insect pests (Gaugler and Kaya, 1990). They are obligate pathogens of insects. *Steinernema* harbours a bacterial symbiont, *Xenorhabdus* (Thomas and Poinar, 1979), that kills the insect host and digests tissues, providing suitable conditions for growth and development of the nematode within the cadaver (Forst and Clarke, 2002). Some 67 valid species of the genus *Steinernema* have been described worldwide and these are divided into five groups according to their morphology and molecular characteristics (Nguyen and Hunt, 2007). *Steinernema kraussei* (Steiner) Travassos was the first entomopathogenic nematode described and was isolated from infected sawflies in Germany by Steiner in 1923 (Stock *et al.*, 2001).

A survey of entomopathogenic nematodes was conducted in the Arasbaran forests and rangelands, in the north-west of Iran, during 2008. From this survey, a number of species of *Steinernema* were identified. One isolate of the genus was identified as *S. kraussei* based on morphological and molecular studies and is reported for the first time from Iran.

Steinernema sp. IRAZ20 was recovered from soil samples collected from rangelands, near Chichakloo, Varzeghan, in the north-west of Iran (from the rhizosphere of a forest habitat dominated by oak tree, *Quercus macranthera* Fish *et* Meyer, longitude E46°45,45, latitude N38°55,20, altitude 2121 m a.s.l., annual average temperature 12 °C, precipitation 415 mm/year) using the *Galleria mellonella* L. baiting method described by Bedding and Akhurst (1975). Infective juveniles (IJ) were collected from *Galleria* cadavers, using the method of White (1927) and stored in aerated water at 7 °C. All nematodes used in this study were reared on *G. mel-*

lonella larvae. Twenty *G. mellonella* larvae were exposed to a suspension of infective juveniles (about 1000 IJ/ml) in a Petri dish lined with two moistened filter papers at laboratory temperature (23 ± 3 °C). First generation males and females were collected from *Galleria* cadavers (dissected out in Ringer's solution) 4-5 days after inoculation. Infective juveniles (IJs) and second generation adults were collected during the week after their first emergence from *Galleria* cadavers and killed using hot (50-60 °C) Ringer's solution (Nguyen and Smart, 1990). Dead nematodes were fixed in triethanolamine formalin (TAF) and processed to anhydrous glycerin by a slow evaporation method (Woodring and Kaya, 1988) and mounted on microscope slides.

Morphological and morphometrical studies were made using an Olympus BX41 microscope equipped with interference contrast optics and a digital camera. Image tool software (Vilcox *et al.*, 2002) was used to obtain quantitative measurements.

Scanning electron microscopy (SEM) observations were made using Nguyen and Smart's (1995) method. First generation adults and infective juveniles were rinsed for 5 minutes in three changes of Ringer's solution. They were fixed in 3% glutaraldehyde buffered with 0.1 M sodium cacodylate at pH 7.2 for 24 hours at 8 °C. They were post-fixed with 2% osmium tetroxide (OsO₄) solution for 12 hours at 25 °C, dehydrated in a graded ethanol series, mounted on aluminium SEM stubs, coated with gold powder and studied using a LEO 440i scanning electron microscope.

Total genomic DNA was extracted from single IJs as described by Phan *et al.* (2001), with some modification. Extracted DNA was used in polymerase chain reaction. The forward and reverse primers for amplification of the complete ITS-rDNA region were used in the PCR reaction (Vrain *et al.*, 1992). Amplifications were carried out in a 50 µl volume, containing 50 mM KCl, 10 mM Tris (pH 8.4), 1.5 mM MgCl₂, 0.1% Triton×100, 0.2 mM of each dNTP, 0.4 mM of each primer, 10 µl of

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nematode lysate and 0.25 µl of Taq DNA polymerase (1.25 units). Amplifications were carried out using a Biometra thermocycler with heated lid pre-set at 95 °C and subjected to the following cycling profile: one cycle of 94 °C for 5 min followed by 35 cycles of 94 °C for 1 min, 55 °C for 1 min and 72 °C for 1.5 min. A final step of 5 min at 72 °C was also included to ensure that all of the final amplification products were full length. Amplification products were purified with a QIAGEN PCR purification kit. Purified DNA was sequenced in IBMP-CNRS, France. The ITS sequence of the studied isolate IRAZ20 (FJ860038) was aligned using the default option of Clustal X (Thompson *et al.*, 1997) with ITS sequences of 22 species of *Steinernema* that have been deposited in GenBank and *Caenorhabditis elegans* (Maupas, 1899) as the outgroup taxon (X03680). Molecular phylogenetic relationships were obtained by equally weighted maximum parsimony (MP) and maximum likelihood (ML) using PAUP 4.0b8 (Swofford, 1998).

The Iranian isolate of *S. kraussei* is characterized by the medium body length of infective juveniles (averaging less than 1000 µm); lateral field with eight ridges of which the central pair is less prominent; head smooth, lacking horn-like structures; secretory-excretory pore

located at the level of middle of pharynx. The secretory-excretory pore of adults is situated far in front of the nerve ring. In general, morphological features as observed by optical and scanning electron microscopes (not reported) agree with those reported in the literature for this species. However, the Iranian isolate can be separated from other isolates of *S. kraussei* by having longer (projected) cephalic papillae.

Phylogenetic analysis of rDNA ITS regions showed that the Iranian isolate (FJ860038) is closely related to the *S. kraussei* isolate C46 (EU914856) from Slovenia (Fig. 1). The species in the *S. feltiae* group (*S. cholashanense*, *S. feltiae*, *S. texanum*, *S. kraussei*, *S. kushidai*, *S. monticolum* and *S. oregonense*) form a monophyletic group with high bootstrap support (95%), and the Iranian isolate of *S. kraussei* does cluster with this group. Based on the available literature, this is the first record of *S. kraussei* from Iran.

Data on the intraspecific morphological variations of *S. kraussei* are very rare but some molecular studies have recently become available. Yoshida (2003) showed differences in the populations of *S. feltiae* and *S. kraussei* from Japan. He reported that a Japanese isolate of *S. kraussei* had a longer mucron and clear differences in RFLP pat-

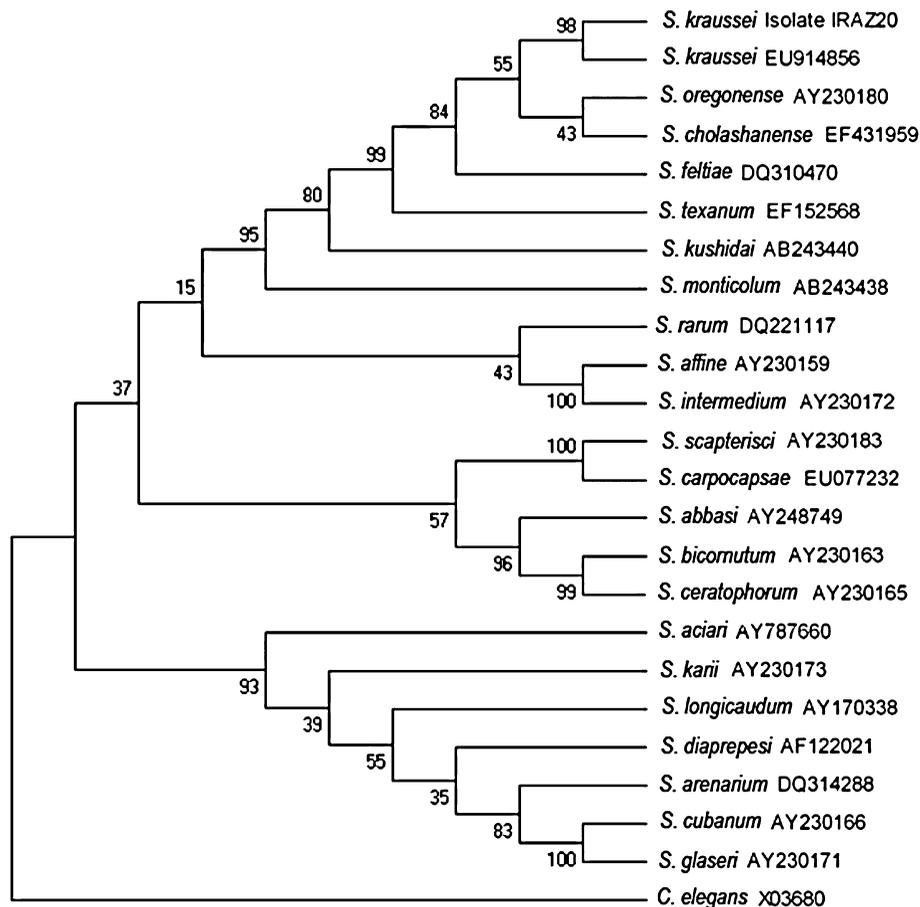


Fig. 1. Phylogenetic relationships of *Steinernema kraussei* IRAZ20 (Iranian isolate) with 22 other species of *Steinernema* based on analysis of ITS rDNA regions. The species in the *feltiae* group form a monophyletic group with high bootstrap support (95%) and *S. kraussei* IRAZ20 does cluster within that group. Numbers at the nodes represent bootstrap values.

terns of ITS rDNA compared with a UK isolate. The Iranian isolate also has a long mucron in the second generation males. Spiridonov *et al.* (2004) indicated that sequence differences between 13 *S. kraussei* isolates from Germany, Russia, UK, Belgium, Iceland, Scotland and Switzerland usually varied between 1 and 11 bp (up to 1%) but reached 21 bp (2.8%) between UK (B2) and Moscow isolates. The sequence divergence of *S. affine* ranged from 0.2-0.6% (2-5 bp) but the difference between sequences of *S. carpocapsae* strains from Europe and the USA was only 3 bp (0.4%). Therefore, the range of the intra-specific variability of *S. kraussei* ITS sequences is more than that of other studied species.

The Iranian isolate of *S. kraussei* was mainly obtained from the rangelands of Arasbaran region. Similarly, and has been reported from alpine grasslands in Switzerland (Steiner, 1996), Scotland (Gwynn and Richardson, 1996), and from alpine meadows in Bulgaria (Shishinova *et al.*, 2000). The Iceland isolate of *S. kraussei* was obtained from a swampy, treeless area in a volcanic valley. The distribution of *S. kraussei* is, almost without exception, in woodland habitats in lowland parts of Europe, although this species can also be commonly found outside woodlands at high altitudes and latitudes, where the habitat preference patterns of the species are variable.

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