CORRECTION

Correction to: Sequence variation in ribosomal DNA and in the nuclear *hsp90* gene of *Pratylenchus penetrans* (Nematoda: Pratylenchidae) populations and phylogenetic analysis

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Results

Paragraph: Ribosomal sequence characterization.

Fig. 1 This figure is missing and the legend of Fig. 1 is erroneously labeled as Fig. 2, and associated to the phylogenetic tree which corresponds to Fig. 2

-Legend of Fig. 2: The correct legend for Fig. 2 reported in the paper is erroneously labeled as Fig. 3. The correct legend should be read:

Fig. 2 Phylogenetic tree of ITS containing region describing the evolutionary relationships among different

geographical populations of *Pratylenchus penetrans* and other *Pratylenchus* species, using Maximum Likelihood (ML) method. Branch lengths are proportional to the distances as derived from the distance matrix obtained using the GTR method with the invariant site plus gamma options. Numbers at nodes indicate bootstrap values

-Legend of Fig. 3: The correct legend for Fig. 3 reported in the paper is erroneously labeled as Fig. 4. The correct legend should be read:

Fig. 3 Phylogenetic tree of D2-D3 expansion domains describing the evolutionary relationships among different geographical populations of *Pratylenchus penetrans* and other *Pratylenchus* species, using Maximum Likelihood (ML) method. Branch lengths are proportional to the distances as derived from the distance matrix obtained using the GTR method with the invariant site plus gamma options. Numbers at nodes indicate bootstrap values

Legend of Fig. 4: This legend is missing in Fig. 4. The correct legend should be read:

Fig. 4 Phylogenetic tree of the *hsp90* gene sequence dataset describing the evolutionary relationships within populations of *Pratylenchus penetrans* and other *Pratylenchus* species using Maximum Likelihood (ML) method. Branch lengths are proportional to the distances as derived from the distance matrix obtained using the GTR method with the invariant site plus gamma options. Numbers at nodes indicate bootstrap values

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[illegible]

Fig. 1