

NEW DISEASE REPORT OPEN ACCESS

First Report of *Pratylenchus hippeastri* Infecting Apple and Grapevine in Brazil

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FIGURE 1 | Grapevine exhibiting yellowing, leaf senescence (A), and root lesions caused by *Pratylenchus hippeastri* (B) in a field in the municipality of Pinto Bandeira, Rio Grande do Sul State, Brazil.

Root and soil samples were collected to identify the cause of stunting observed in apple trees (*Malus domestica*) cv. Gala, from a commercial orchard located in the municipality of Palmas, Paraná state, Brazil (26°30'38.84" S; 52°00'58.54" W) and in grapevine (*Vitis vinifera*) cv. Viognier grafted onto the Paulsen rootstock (Figure 1) in the municipality of Pinto Bandeira, Rio

Grande do Sul State (29°02'43.1" S; 51°28'10.8" W). Nematodes were extracted using the centrifugal flotation method, and a root-lesion nematode species was detected in root and soil samples from both hosts.

Ten adult females of the genus *Pratylenchus* from each host plant were recovered and temporarily mounted in water for morphological examination. The specimens exhibited two lip annuli (Figure 2A), lateral fields with four incisures (Figure 2B) and a conoid tail with a bluntly pointed terminus (Figure 2C). The mean morphometric values were for the apple population: stylet length (St) = 15.3 ± 0.5 µm, body length (L) = 502.0 ± 34.2 µm, and vulva position (V%) = 76.6 ± 2.1, and for the grapevine population: St = 14.7 ± 0.4 µm, L = 541.7 ± 47.2 µm, and V% = 78.7 ± 2.3. Males were not observed in either population. The morphological and morphometric characters were consistent with those described for *Pratylenchus hippeastri* (Inserra et al. 2007).

Molecular identification was performed by sequencing the D2/D3 expansion segments of the 28S rDNA and applying DNA barcoding techniques. The resulting sequence were deposited in GenBank under Accession Nos. PX899475 (apple) and PX933208 (grapevine). BLAST analysis revealed 100% sequence identity with *P. hippeastri* isolate xs01 (KC796703.1). The Brazilian populations from apple (PX899475, Palmas PR) and grapevine (PX933208, Pinto Bandeira, RS) consistently clustered with other *P. hippeastri* sequences (Figure 3), showing 100% bootstrap support and confirming the species identification.

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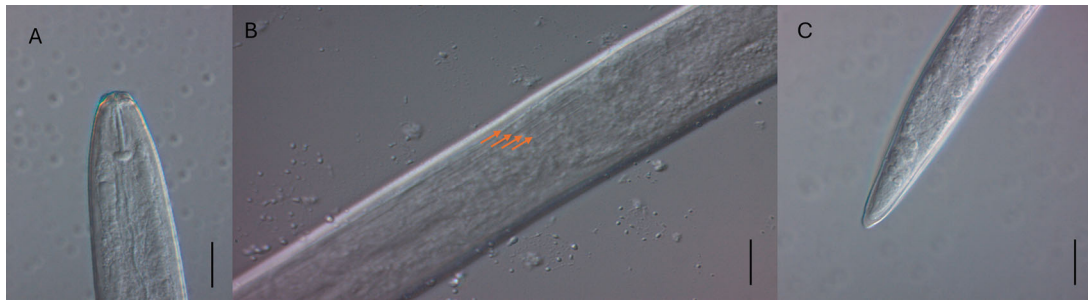


FIGURE 2 | Morphological characters of *Pratylenchus hippeastri*: anterior region with two lip annuli (A); lateral fields with four incisures (B); conoid tail with a bluntly pointed terminus (C). Bars = 10 µm.

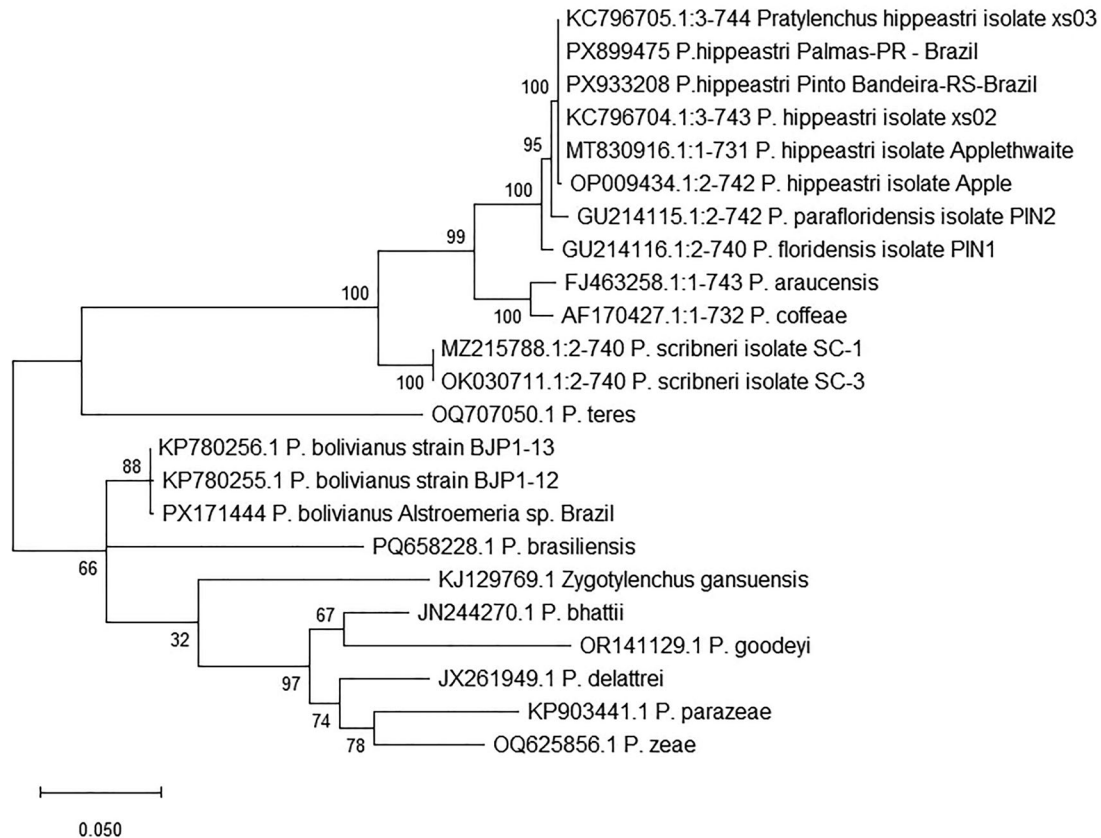


FIGURE 3 | Evolutionary analysis by the Maximum Likelihood method conducted in MEGA12. Tree showing relationships between *Pratylenchus* spp., based on the D2/D3 28S rDNA sequence.

Pratylenchus hippeastri has been described from amaryllis (*Hippeastrum* sp.), bromeliads (*Neoregelia* spp.) and *Vitis rotundifolia* in the USA (Inserra et al. 2007; De Luca et al. 2010, Habteweld et al. 2021), apple in China and Africa (Wang et al. 2016; Knoetze et al. 2019), *Acer palmatum* in Japan (Chen et al. 2014), *Salix mucronata* in Africa (Shokoohi et al. 2019). More recently, a population of *P. hippeastri* was characterised morphologically and molecularly from strawberry in Costa Rica (Brenes-Campos et al. 2021). To our knowledge, this is the first report of *Pratylenchus hippeastri* in Brazil. Following this detection, the Brazilian Ministry of Agriculture, Livestock and Food Supply was notified in order to support the implementation of phytosanitary measures aimed at mitigating the potential risks associated with this nematode species.

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