



First report of Rice stripe necrosis virus infecting rice in Sierra Leone

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While Rice stripe necrosis virus (RSNV, *Benyvirus*, *Benyviridae*) has been reported on rice plants on two continents, little is known about the diversity of this multipartite virus which is transmitted by the plasmodiophorid protist *Polymyxa graminis*. First identified in 1983 in the Côte d'Ivoire (Fauquet & Thouvenel, 1983), the disease had previously been observed in Sierra Leone without formal identification of the causal agent (Buddenhagen, pers. comm.). Later, the virus was reported in South and Central America (Colombia, Ecuador, Panama and Brazil) causing up to 40% yield losses (Morales *et al.*, 1999). Recently, RSNV was identified for the first time in several African countries including Burkina Faso (Séréme *et al.*, 2014), Benin (Oludare *et al.*, 2015) and Mali (Decroës *et al.*, 2017) suggesting a re-emergence of the virus in Africa.

In 2019, symptoms of leaf-criinkling and stripe necrosis were observed on a rice plant from the Bo District in Sierra Leone (Fig. 1). Leaf samples were analysed by serological and molecular methods to confirm the presence of RSNV in Sierra Leone. RSNV was detected by plate-trapped antibody (PTA)-ELISA using a polyclonal antiserum against RSNV (Fauquet & Thouvenel, 1983).

The presence of the virus was confirmed after total RNA extraction using 0.05 g of leaves and the RNeasy Plant Mini Kit (Qiagen) and RT-PCR amplification (10 U/µl M-MLV-reverse transcriptase, Promega; 10 U/µl Dynazyme, Finnzyme) as described previously (Séréme *et al.*, 2014, Oludare *et al.*, 2015) with primers RSNV1-2901F 5'-TGAATTGGTCTCTCTTG-3' / RSNV1-3827R 5'-TGTGGCGTTTCCAGACCTAAA-3' and RSNV2-5' 5'-TATCACTACTGACGAATTCACCTAC-3' / RSNV2-1223R 5'-AATCTGCGCGCTGTTTGTGA-3'. Specific amplicons, 926 and 1241 nt in length, were generated corresponding to sequences in the helicase domain and the coat protein (CP) genes on RSNV RNA 1 and RNA 2, respectively. The amplicons were sequenced directly and the sequences deposited in GenBank (Accession Nos. MN750254 and MN750255, respectively).

The helicase sequence obtained from the Sierra Leone RSNV isolate showed 1.8-7.3% genetic distance with those from South America (EU099844.3, MG792544, MG792545, MG792546) and only 1.4-2.2% with those from Africa (KP099623, MF115599, MF115600, MF115601, MF115602, MF115603, MK170452, MK170453). The phylogenetic analysis based on the helicase domain included the sequence obtained from the Sierra Leone within a cluster represented by RSNV from South America and West Africa (Fig. 2a). In contrast, the CP sequence from the Sierra Leone RSNV isolate revealed an unexpected genetic differentiation as compared to all the other sequences from South America (5.6%; NC_038774) or Africa (5.2-6.5%; LK023710, MF115604, MF115605,

MF115606, MF115607, MF115608, MK170454, MK170455). Interestingly, the CP sequence from Sierra Leone is located at a basal position in the phylogeny (Fig. 2b).

To our knowledge, this is the first confirmed report of RSNV in Sierra Leone. Further studies are needed to assess the molecular and biological diversity of RSNV, the spatial distribution and the incidence of this re-emerging rice disease in Africa.

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Figure 1

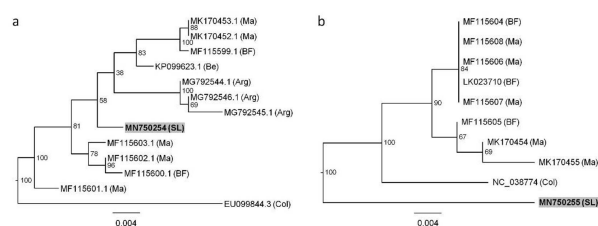


Figure 2

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