New Disease Reports

# Jute (*Corchorus capsularis*): a new host of *Peanut bud necrosis virus*

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***Received:*** *05 Nov 2010.* ***Published:*** *29 Jun 2011.* ***Keywords:*** *DAC-ELISA, RT-PCR, India*

*Peanut ud ecrosis virus* (PBNV) is a member of the genus *Tospovirus,* family *Bunyaviridae*. Tospoviruses are among the most damaging and economically important group of plant viruses causing significant crop losses in a wide range of ornamental and food crops in many regions of the world (Mumford *et al.,* 1996). PBNV has a wide host range including groundnut, tomato, chilli pepper, potato, peas, sunflower, cotton, many pulses, carrot, brinjal, various ornamentals and weeds (Reddy, 1991; Hemalatha Venkat *et al.*, 2008) and is transmitted mechanically or by thrips (*Thrips palmi*) in the field.

Jute (*Corchorus capsularis*), a member of the family Malvaceae, is the world's second most cultivated fibre crop, next to cotton. India is the world's largest jute producer, growing an area of 0.81 million ha, producing 1.84 million tones per annum (Faostat, 2009). Over a four-year period, surveys for both PBNV and *Tobacco streak virus* (TSV) were carried out across a range of crops. In August 2010, two commercial jute fields in the Chittoor district of Andhra Pradesh, India, were identified where 15-20% of plants wereshowing viral symptoms.These included mosaic, chlorotic and necrotic lesions, which occurred on young leaves and stems, and ultimately resulted in plant death (Fig. 1). Based on these symptoms, PBNV or TSV infection was suspected. Leaves with symptoms were tested for viruses by Direct Antigen Coating (DAC)-ELISA (Clark & Joseph, 1984) using polyclonal antibodies for PBNV and TSV (a kind gift from P. Lava Kumar, International Institute of Tropical Agriculture (IITA), Ibadan). Only PBNV was detected.This was confirmed by RT-PCR with total RNA extracted (RNeasy Plant Mini Kit, Qiagen, USA) from jute plants testing PBNV-positive with ELISA, using PBNV coat protein gene-specific primers (Satyanarayana *et al*., 1996).These tests resulted in an amplicon of the expected size (~800bp) (Fig. 2). This was cloned into pTZ57R/T vector (Fermentas, USA) and sequenced (GenBank Accession No. HQ324115).Sequence analysis (using BioEdit v7.0.5) showed 93-99% and 95-100% identity at nucleotide and amino acid levels respectively with other PBNV isolates (EF179100, EF179099, EF532937, FJ447355, FJ447359, HM131489, HM770020, HM770021, HM770022, DQ375811, AF467289, AY512650, AY512648, AY882003, AY529713, AY882000, AY512651, AY512647, AF515821, AY426317, AF515820, FJ355951, FJ355952, AY184354, AY472081, AY463968, DQ058078, HM195249). To the best of our knowledge this is the first report of the natural occurrence of PBNV infecting jute.

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Figure 1

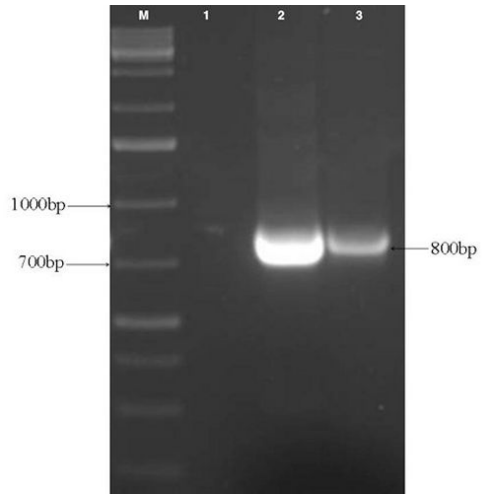


Figure 2

**To cite this report**: Sivaprasad Y, Bhaskara Reddy BV, Naresh Kumar CVM, Raja Reddy K, Sai Gopal DVR, 2011. Jute (*Corchorus capsularis*): a new host of *Peanut bud necrosis virus*. *New Disease Reports* **23**, 33. [doi:10.5197/j.2044-0588.2011.023.033]



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