



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	2008.029P	<small>(to be completed by ICTV officers)</small>
Short title: 1 new species in the genus Babuvirus <small>(e.g. 6 new species in the genus <i>Zetavirus</i>; re-classification of the family <i>Zetaviridae</i> etc.)</small>		
Modules attached <small>(please check all that apply):</small>	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input type="checkbox"/>
	5 <input checked="" type="checkbox"/>	6 <input type="checkbox"/>
	7 <input type="checkbox"/>	

Author(s) with e-mail address(es) of the proposer:

Joe Vetten (heinrich-josef.vetten@jki.bund.de) on behalf of the Nanoviridae SG
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ICTV-EC or Study Group comments and response of the proposer:

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MODULE 5: **NEW SPECIES**

Code	2008.029P	<small>(assigned by ICTV officers)</small>
To create 1 new species assigned as follows:		
Genus:	<i>Babuvirus</i>	<small>Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)</small>
Subfamily:		
Family:	<i>Nanoviridae</i>	
Order:		

Name(s) of proposed new species:

<i>Cardamom bushy dwarf virus</i>

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

<p>Species demarcation criteria published in the 8th report are:</p> <p>Since the genus <i>Babuvirus</i> has been monotypic, species demarcation criteria have not yet been defined for this genus. We propose that the criteria used for species demarcation in the genus <i>Nanovirus</i> (family <i>Nanoviridae</i>) are provisionally used also for babuviruses, as follows:</p> <ul style="list-style-type: none"> - Overall nt sequence identity of <75% is generally indicative of a distinct species, - Different reactions to antibodies to individual species, - Differences in CP aa sequences of >15%, - Differences in natural host range, and - Differences in the number and types of vector aphid species.
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Argument to justify the creation of the new species:

Cardamom bushy dwarf virus (CBDV; syn. Cardamom clump virus) has recently been found associated with a serious disease ('foorkey') of large cardamom (*Amomum subulatum* Roxb.) in India (Mandal et al., 2004). The causal agent of foorkey is not sap transmissible but persistently transmitted by the aphid species *Micromyzus kalimpingensis* Basu and *Pentalonia nigronervosa* [the vector of *Banana bunchy top virus* (BBTV)]. Using *P. nigronervosa* the virus was transmitted to small cardamom (*Elettaria cardamomum*) and wild cardamom (*Amomum* sp.), but not banana (Varma & Capoor, 1964).

Electron microscopy of negatively stained, partially purified preparations from field-infected large cardamom plants showed the presence of isometric particles measuring 17 to 20 nm. Using PCR primers derived from BBTV DNA-R, a DNA fragment (~ 860 nt) was identified, which potentially encodes an M-Rep protein and shares ca. 80% nt sequence identity with DNA-R of BBTV. The DNA fragment identified from diseased cardamom is clearly distinct from satellite-like Rep DNAs (which are frequently associated with nanovirids) and from DNA-R of viruses of the genus *Nanovirus*. Therefore, it is undoubtedly from a hitherto unknown DNA-R component (CBDV; Fig. 1). A full-length DNA-R clone of CBDV has very recently been obtained by PCR and sequenced (Mandal et al., 2008). This DNA-R had 1102 nts, contained two major ORFs encoding a 33.6-kDa protein in +3 reading frame and a 14.1-kDa protein in the -1 reading frame, and shared 74–79% sequence identity with DNA-R components of BBTV. The 33.6-kDa proteins (286 amino acids) potentially encoded by CBDV DNA-R shared 87–89% sequence identity with the master Rep protein of BBTV. Since the DNA-R of CBDV differs from BBTV DNA-Rs by 21–26% in nt sequence (whereas the nt sequence variation between the DNA-Rs of BBTV does not exceed 8%), the virus associated with foorkey disease of large cardamom appears to be a new babuvirus. This is consistent with the virion morphology observed for CBDV, type of CBDV vector (and aphid species), the restricted host range of CBDV (not infecting banana), the notion that babuviruses only infect monocots and the observation that another babuvirus (*Abaca bunchy top virus* isolates) also differs from BBTV in DNA-R nt sequences by 24%. For the aforementioned reasons, CBDV is proposed to be a new member of the genus *Babuvirus*, although no sequence information is available for the other (non-Rep) components of the CBDV genome.

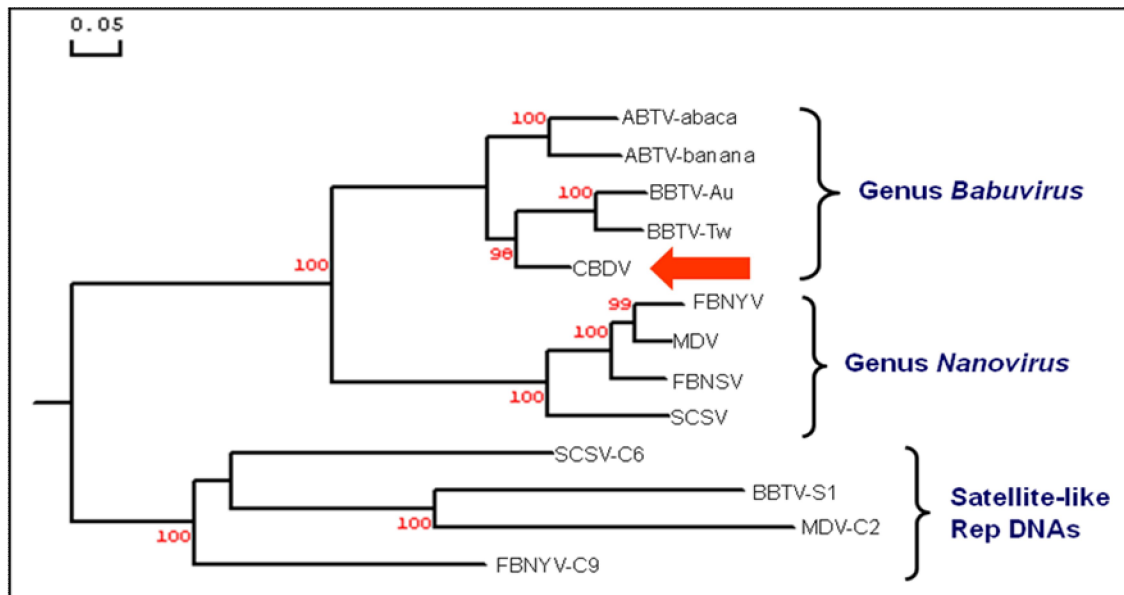


Fig. 1 Neighbour-joining dendrogram illustrating nt sequence relationships in the DNA-R of cardamom bushy dwarf virus (CBDV), abaca bunchy top virus (ABTV) isolates from abaca and banana, banana bunchy top virus isolates from Australia (BBTV-Au) and Taiwan (BBTV-Tw), faba bean necrotic yellows virus (FBNYV), faba bean necrotic stunt virus (FBNSV; not yet classified), milk vetch dwarf virus (MDV), and subterranean clover stunt virus (SCSV). For comparison, some representative members of the satellite-like Rep DNAs frequently found associated with nanovirids were included in the analysis. Horizontal distances are proportional to substitutions per site and dendrograms were bootstrapped 1000 times with values greater than 50% given at nodes.

References:

Mandal B, Mandal S, Pun KB, Varma A (2004). First report of the association of a nanovirus with foorkey disease of large cardamom in India. *Plant Disease* 88: 428.

Mandal B, Mandal S, Tripathi NK, Barman AR, Pun KB, Varma A (2008). Sequence analysis of DNAs encoding putative replicase gene of nanovirus from large cardamom affected by foorkey disease. *Indian Journal of Virology* 19 (issue 1): abstract no. S-37

Varma PM, Capoor SP (1964). 'Foorkey' disease of large cardamom. *Indian Journal of Agricultural Science* 34: 56-62.