【別紙2】

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論文名: Etiological analyses on yellow mosaic disease of jute in Bangladesh
(バングラデシュにおける黄麻黄斑モザイク病に関する疫学的解析)(要約)
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## (以下要約を記入する)

Yellow mosaic disease is a major limiting factor for jute (*Corchorus capsularis* L.) cultivation in Bangladesh. As the causal pathogen responsible for the jute yellow mosaic disease, eleven isolates of *Corchorus golden mosaic virus* (CoGMV) were collected from different regions in Bangladesh, and their genomic DNAs were cloned and fully sequenced. DNA A sequences of CoGMV Bangladeshi (BD) isolates shared highest identity 97.3–99.1% with the Indian isolates and 93.9–94.3% with the Vietnamese isolate of CoGMV, whereas DNA B shared sequence identity 93.9–94.3% with the CoGMV isolates reported from Vietnam and India. The fact that the examined DNA A components of eleven isolates of CoGMV lack the AV2 open reading frame, together with the presence of N-terminal PWRTNAGT motif in the predicted coat protein amino acid sequences indicated that BD1–11 share genetic features of New World begomoviruses. Genetic analysis revealed that CoGMV isolates originating from Bangladesh possessed greater genetic variability than the Indian and Vietnamese isolates. This is the first report of CoGMV associated with yellow mosaic disease of jute from Bangladesh.