

Abstract

Phenotypic and Genotypic Diversity of Bunyamwera Virus

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Introduction: Bunyamwera virus belongs to the genus *Orthobunyavirus* of the family Bunyaviridae, segmented RNA viruses whose members have the potential for genetic reassortment and/or drift. Although arbovirus mutant spectra have been observed in nature, the diversity within the spectra is not well described, and the phenotypic roles of minority RNAs are unknown. Moreover, traditional sequencing methods generally detect the master sequences as consensus sequences. Understanding the mutation distribution in a heterogeneous arbovirus population is thus important, given that any variant can be favoured by selection and ultimately affects fitness.

Objective: To evaluate phenotypic and genotypic diversity of Bunyamwera virus isolates obtained from diverse geographic space, time and vector species in Kenya

Methods: Seven Bunyamwera viral strains isolated from previous GEIS surveillance exercises in Ijara, Garissa and Magadi from diverse mosquito species and sites at different times were cultured in *Vero* cells to prepare viral stocks for experimentation. Plaque assay was used to identify and purify clonal population of the virus based on plaque sizes. Bunyamwera-specific primers were used to amplify the S, M and L segments of the virus phenotypes.

Results: The wild type of 6/7 viruses was composed of two major phenotypes; small plaque (SP) (0.468–0.656 mm) and large plaque (LP) (0.875–1.210 mm). One isolate consisted of a homogeneous SP size (0.305–0.372 mm). The plaque sizes were significantly different. Five isolates had plaque variants with similar S genotype as the wild type (Wt) using degenerate S primer. However, using Bunyamwera S segment-specific primers, only two samples constituted variants similar to the Wt. Three SP and two LP variants of four isolates failed to amplify with M segment-specific primer indicating possible co-circulation with another virus.

Conclusions: There is need to improve arboviral surveillance methods to include detection of circulating minority variants. There is need for complete genome sequencing of the plaque variants and comparison to the consensus sequence of the parental wild type to identify mutations that could be responsible for the observed phenotypic differences.

Key words: Bunyamwera, plaque, variant, phenotype

Received: November, 2012

Published: December, 2012