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Co-infection: Molecular evidence of dengue and chikungunya virus co-infection in Odisha and Maharashtra, India

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Dengue virus (DENV) and Chikungunya virus (CHIKV) are epidemic in different places of the world and because of similar primary symptoms, is mostly undiagnosed. Hence, we examined 204 suspected Dengue cases in a hospital based cross-sectional study in 2013 Odisha, India. It was observed that 50 samples were positive for DENV only, 28 were positive for CHIKV only and surprisingly, 28 patients were co-infected with both DENV and CHIKV. Additionally, a total of 18 confirmed Dengue samples from Maharashtra, India were screened for CHIKV and out of those, 15 were co-infected. All CHIKV strains were of East Central South African (ECSA) genotype and serotype 2 (genotype IV) was predominant in the DENV samples. Additionally, Dengue serotype 1 and 3 were also detected during this time. Further, sequence analysis of E1 gene of CHIKV strains revealed that two substitution mutations (M269V and D284E) were observed in almost 50% strains and they were from co-infected patients. Similarly, sequence analysis of *CprM* gene showed the presence of five substitution mutations, in all serotype 1 and two consistent mutations in serotype 2. Together, it appears that a significant number of Dengue patients (43, 44.8%) were co-infected with DENV and CHIKV. This emphasize the need of a continuous surveillance system for DENV and CHIKV for early and proper recognition of infecting pathogen and correlation of clinical symptoms with single or co-infection patient, this may be helpful in proper patient care in future.