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**MOLECULAR EPIDEMIOLOGY OF DENGUE VÍRUS IN THE BAHIA STATE.**MELO, P.R.S.<sup>1,5</sup>; DOMINGO, C.<sup>4</sup>; CIUFFO, I.A.<sup>2</sup>; BLANTON, R.E.<sup>3</sup>; TENÓRIO, A.; REIS, M.G.<sup>1</sup><sup>1</sup> Centro de Pesquisas Gonçalo Moniz - FIOCRUZ/Salvador-BA; <sup>2</sup> Laboratório Central do Estado da Bahia - SESAB; <sup>3</sup> Case Western Reserve University/OHIO/USA; <sup>4</sup> Instituto de Salud Carlos III/Madrid/Espanha; <sup>5</sup> Universidade Estadual de Santa Cruz/Ilhéus/Bahia

**Introduction:** Dengue fever, dengue haemorrhagic fever and dengue shock syndrome are considered to be the most important arthropod-borne viral diseases due to the high morbidity and mortality. By 2002, DENV-1 and DENV-2 had circulated for more than a decade in Brazil. In 2002, the introduction of DENV-3 into Bahia produced the first cases of dengue hemorrhagic fever transforming Bahia into an area of high endemicity. Here we report the analysis of the interval spanning the E/NS1 junction of the dengue genome for the molecular surveillance of flaviviruses. **Objective:** To determine which strains of dengue virus are circulating in Bahia. **Materials e Methods:** Viremic samples were obtained from patients with a clinical diagnosis of dengue infection from epidemiology surveillance service. Using 5 µl of viral RNA solution was added to 45 µl of a medium compatible with both the reverse transcription and PCR amplification steps. The MEGA package were used to produce phylogenetic trees using NJ as the method to reconstruct the phylogeny and Kimura-2p as nucleotide substitution calculation method. **Results:** The samples of DENV-3 were grouped with isolated of the Asian continent as DEN3-SRILANKA1989 and 1991, at the same time that it kept high similarity with Brazil's isolated as 68784-Brazil 2000 and BR74886-02-Brasil2002. The values most significant of bootstrap had been observed considering the Asian genotype for the DENV-3. The most likely genotype of DENV-1 samples is the American, demonstrating a grouping with American and African samples as for example CNM612VI05-NICARAGUA2005, 125236-VENEZUELA1994 and RIOH36589-ANGOLA1988. With regard to DENV-2, not enough strains have been analyzed. **Conclusions:** Molecular surveillance is fundamental for infectious diseases as dengue where the introduction of new genotypes can lead to important public health problems. The similarity between the isolated ones from Bahia and the Asian genotype agrees to data of other parts of the country, this circulating genotype possess a great epidemic potential that justifies its capacity of dissemination in the whole world compared with other strains. Currently we observe in Bahia what occurs in the Asian continent with the hiperendemicity where we find some circulating sorotypes and a high index of infestation for *Aedes aegypti*. Molecular monitoring is basic for the potential risk of new epidemics, for introduction of new sorotypes and even though substitution of less virulent genotypes for the other most aggressive ones with bigger epidemic capacity as we observed in 2002 in Bahia.