

Identification of dengue virus strains circulating in Panama

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Dengue is a widespread disease caused by a virus mainly transmitted to humans by mosquitos of the *Aedes aegypti* species. Every year nearly 294 million people get sick from this virus and this comes with a high cost, both economic and in loss of quality life. The disease can give flu-like symptoms or develop into more severe forms (severe dengue) that, eventually, can lead to death. Whether a patient does or does not develop severe dengue depends on many factors, including age, overall health and even ancestral origins.

Dengue virus is diverse and has many variants classified regarding how it is identified by the immune system (serotypes) and how similar their genetic code is to each other (genotypes). Knowing and watching this diversity is important when we it comes to develop an effective vaccine or when we want to be ready for future outbreaks.

Our study focused on the diversity of the virus in Panama. We wanted to find out which strains (or genetic variants) were circulating in the country during 2010 and determine how they were related to other strains present in other countries from the Americas and beyond. This process is called “genotypification” and allows you to give a “phylogenetic” name to your virus so you can perform further analysis with them. This is similar to doing a pedigree but on a bigger scale, so we can know how the viruses we found in our patients are related with each other. In order to do this, we need to get samples of sera or blood of patients diagnosed with dengue (our patients from Panama 2010), isolate the viruses and compare them with large amounts of previously sequenced viruses isolated from other patients in the past. Once we have the samples, we will analyse them so we obtain their genetic code (sequencing). When we have all the sequences we can sort and align them to build phylogenetic trees that allow us to visualize the evolutionary relationships of our strains.

From our work, we concluded that many variants of dengue were circulating at the same time. The viruses of our study were very similar to those present in nearby countries from central and south America, but also from the Caribbean islands. We also found that our viruses came from different sources but we could not confirm exactly from where.

This study is just the first step towards more complex but complete analysis that can answer important questions such as: where did the viruses we isolated come from? Are they more dangerous that others found in the past? Are those viruses present in other parts of the world?

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