Viruses and more particularly phages (viruses that infect bacteria) represent the most abundant form of “life” in aquatic and terrestrial environments. Biogeography, the study of species biodiversity and distribution across time and space, has only recently been investigated for viruses mainly due to the lack of powerful tools. With the advent of new sequencing technologies, it is now possible to analyze the genetic differences among viral genotypes and communities and to map their geographic distributions. So far, most of the studies have revealed that viruses were widely dispersed on Earth and different environments shared almost the same genotypes at different level of evenness. If this “cosmopolitan distribution” of viruses true for all ecosystems is the question we wanted to address through the analysis of viral communities in modern stromatolites, the living representative of one of the most ancient form of life on Earth. Today, these unique ecosystems are found in few places such in Hamelin Pool (Australia), in the Cuatro Cienegas Basin (Mexico) or in the Exuma Cays (Bahamas). All these places are characterized by high fauna and flora endemism. Based on comparative metagenomic analysis of viral communities associated with stromatolites from Mexico and the Bahamas, we show that viral populations can genetically diverge from a global gene pool and that endemism does also exist for viral communities.