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8th World Congress on

Virology

November 28-30, 2016 San Antonio, USA

Evaluation and characterization of the antiviral activity of *Sargassum fluitans* against some echovirus 9, poliovirus 1, coxsackievirus 5 and 24

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Nature is a prominent source of broad amount of compounds derived seaweeds and plants with vary antimicrobial and antiviral activities. Seaweeds exhibit a number of medicinal properties, playing a fundamental role by curing many diseases. Their medicinal use by population makes them an interesting target to be evaluated as antivirals, taking into account the variety of chemical metabolites they own. It has been documented that Sargassum genera are an interesting target for treating many viral diseases cause by herpesvirus. However, the antiviral activity of Sargassum fluitans against these viruses is not very well documented in bibliography. The aim of this work was to evaluate the antiviral activity of extracts from Sargassum fluitans, against enteroviruses like poliovirus 1, coxsackievirus B5 and A24 and echovirus 9. The calculation of antiviral activity (EC50) was evaluated by means of cytopathic effect inhibition in Vero cells and with viral load using quantitative RT-PCR. Preliminarily, assays with hydroethanolic extracts showed that Sargassum species were non-cytotoxic at the evaluated concentrations and showed an inhibitory activity by diminishing the viral titer more than three log in relation to the virus control. The preliminary characterization of the extracts showed several active compounds such as sulfated polysaccharides.

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Highly pathogenic porcine reproductive and respiratory syndrome virus (HP-PRRSV) strain GXBB-11 with a new deletion 20 amino acid in the NSP2 gene

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Porcine reproductive and respiratory syndrome (PRRS) is the main cause of the reproductive disorders in gilts and sows. PRRS is considered one of the most economically important swine infectious diseases around the world. PRRSV is an enveloped positive-stranded RNA virus which belongs to the family Arteriviridae. PRRSV has two distinct genotypes European type (type 1) and North American type (type 2). HP-PRRSV was classified into North American type; it has become the predominant circulating field strain in China from 2006 to till date. HP-PRRSV has a discontinuous 1+29 amino acid (aa) deletion in the NSP2 gene. The NSP2 gene is the one of most variable regions in the whole gene, although this discontinuous deletion has been proved not to the high virulence of HP-PRRSV, which reminds us that PRRSV is always mutations. ORF5 contains a neutralizing epitope, playing important roles in pathogenesis, including host cell entry and apoptosis and it is also a hypervariable region. The GXBB-11 strain was isolated from lung tissue in Guangxi, two pairs of primers amplifying NSP2 and ORF5. The PCR products were purified and cloned into pEASY-T1 vector (TransGen Biotech). Comparison of the GXBB-11 with the HP-PRRSV JXA1 by multiple alignment showed that 20 amino acid (aa) deletions (2566nt-2625nt) in the NSP2 region. Furthermore, the GXBB-11 showed 84.20% nucleotide homology with the ORF5 genome of the JXA1. The GXBB-11 genome sequence data could help us understand the evolutionary characteristics of HP-PRRSV in China.

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