Evolution of a relationship: how *Ostreococcus tauri* viruses circumvent host resistance

**SUMMARY:** The two new *Ostreococcus* viruses OtV6 and OtV15 show a high syntenic distance to OtV5. The possession of an ammonium transporter makes OtV6 very unique among the phycodnaviruses and shows the potential of viral involvement in nutrient transfer.

**BACKGROUND**

Marine microeukaryotes battle every day with environmental pressures, predators and viruses to survive. To escape and survive certain threats they often have to change their life cycle stage for the cost of a lower growth rate. Although marine viruses are ubiquitous, they cannot replicate without infecting host cells. Therefore they have to evolve as quickly as their host, adapting their infection strategy along the way.

Cultures of the green microalgae *Ostreococcus tauri* demonstrate spontaneous resistance when infected with the virus OtV5. OtV5-resistance cells infected with two recently sequenced OtV viruses revealed a complex pattern of resistance and susceptibility. While one virus could only lyse OtV5-resistant cells, the second was able to lyse both OtV5-susceptible and – resistant cells (Fig. 1).

**1. Comparing the genomes of OtV6 and OtV15 to that of OtV5**

- Similar genome size, ~200 kb (Fig. 2, Tab. 1)
- High synteny (Fig. 3); ~70% of their genes are orthologs (Fig. 4)
- OtV6 possess 9 tRNAs, with the unique tRNAs for Leucine, Arginine, and Proline (Tab. 1)

<table>
<thead>
<tr>
<th>Virus</th>
<th>Genome size (kb)</th>
<th>ORFs (No.)</th>
<th>GC content (%)</th>
<th>tRNAs</th>
</tr>
</thead>
<tbody>
<tr>
<td>OtV5</td>
<td>186</td>
<td>247</td>
<td>42</td>
<td>9</td>
</tr>
<tr>
<td>OtV6</td>
<td>189</td>
<td>250</td>
<td>45</td>
<td>9</td>
</tr>
<tr>
<td>OtV15</td>
<td>195</td>
<td>235</td>
<td>44</td>
<td>9</td>
</tr>
</tbody>
</table>

**2. Phylogeny among *Ostreococcus* viruses**

Maximum-likelihood phylogeny of *Ostreococcus* viruses (infecting *O. tauri*, *O. lucimarinus*, and *O. mediterraneus*) and two viruses infecting *Micromonas* (MpV1, MPWG) based on the full length of a major capsid protein. Bootstrap values were obtained from 1000 replicates.

**3. Specific genes of OtV6 and OtV15**

Highlighted genes of OtV15 with a putative function:

1. cell surface attached carbohydrate-binding domain protein -> probably involved in viral entry
2. beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase -> probably involved in anti-apoptosis

Highlighted genes of OtV6 with a putative function:

1. ammonium transporter derived from its host *O. tauri* -> probably involved in maintaining and perhaps enhancing nutrient uptake during infection
2. Alternative oxidase AOX potentially of host origin -> probably lowers ROS production
3. Thrombospondin type 1-like -> probably involved in proapoptotic activity