



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

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).

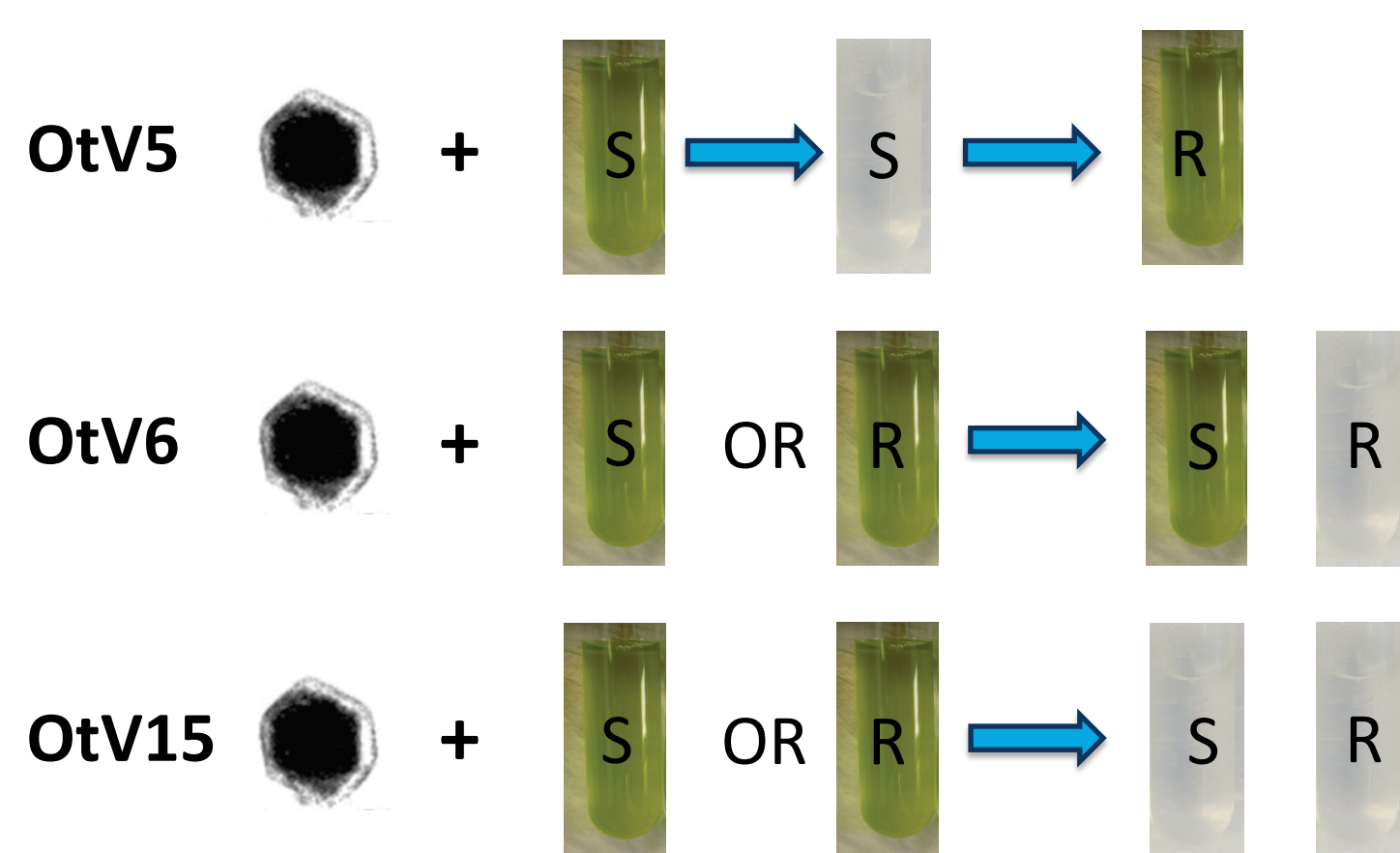


Figure 1: Infection pattern of the three *Ostreococcus tauri* viruses OtV5, OtV6, and OtV15 infecting *O. tauri* RCC745 (=S) or OtV5-resistant clones of the same strain (=R).

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)

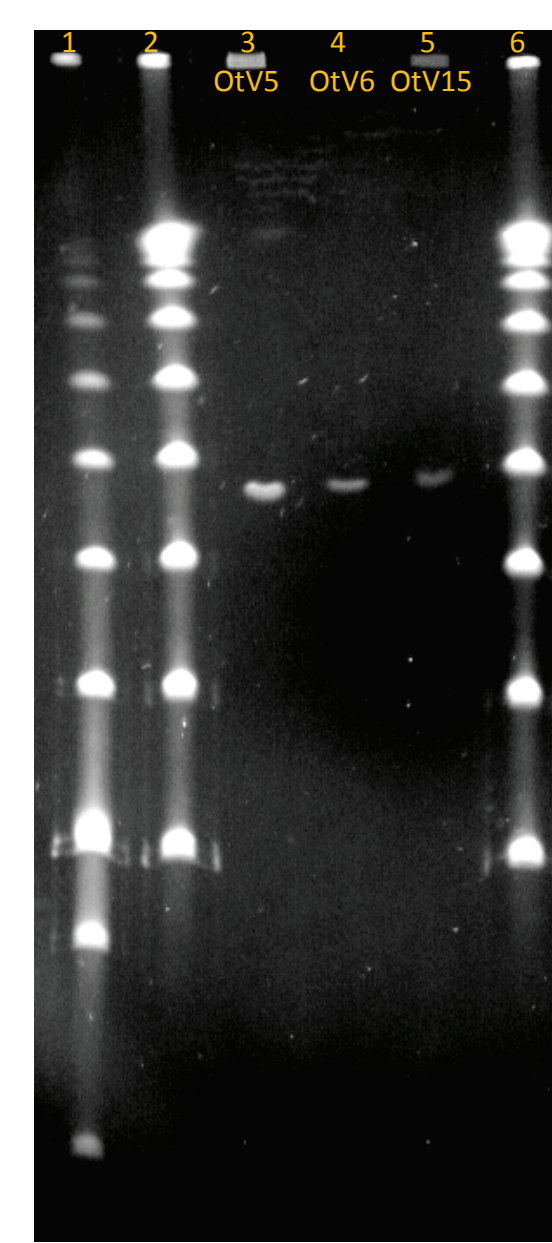


Figure 2: Pulsed-field gel electrophoresis of genomic DNA of the three *O. tauri* viruses OtV5, OtV6, and OtV15. Lane 1: A DNA low range, lane 2 and 6: A DNA ladder.

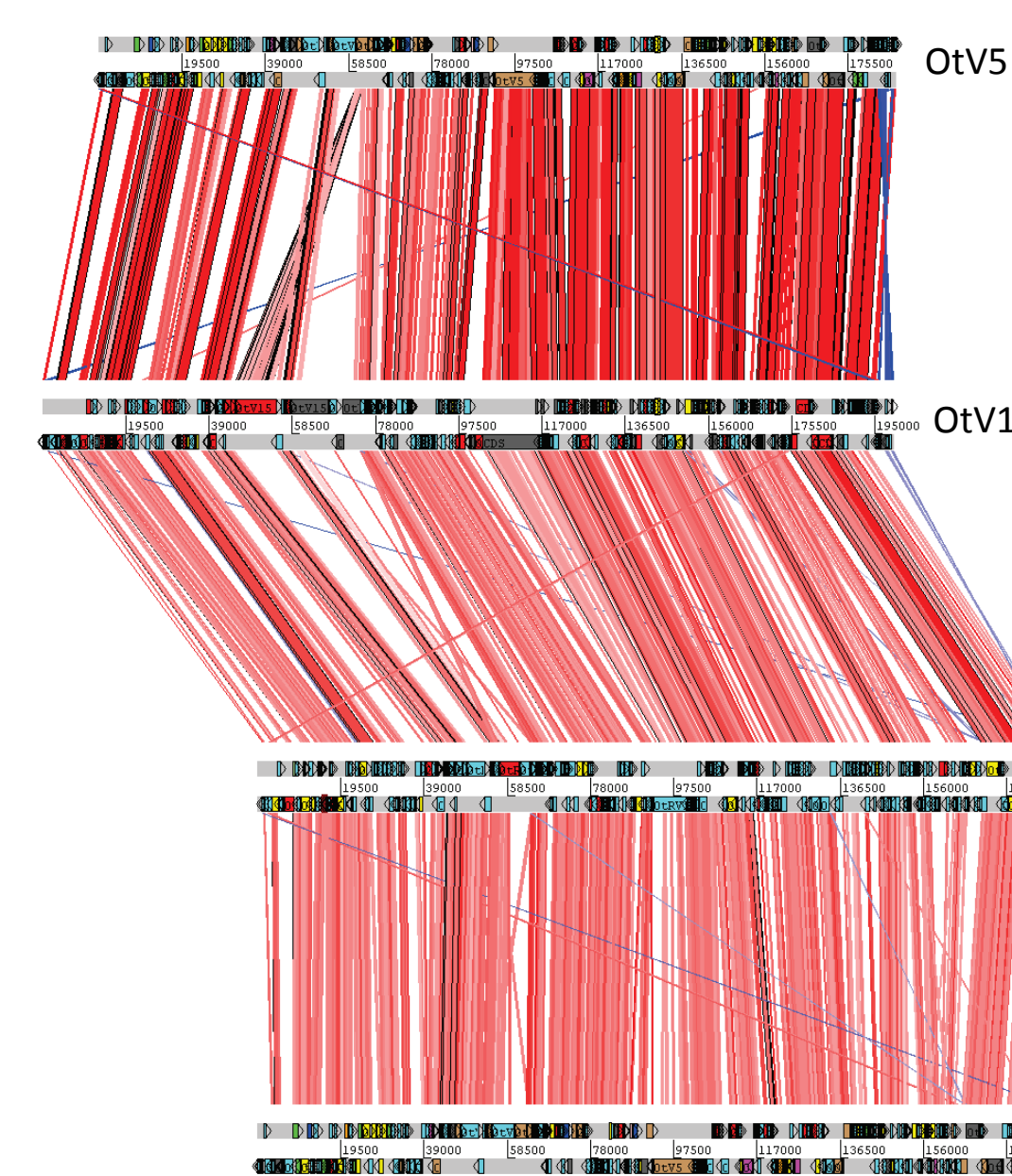


Figure 3: Synteny among the three *O. tauri* virus genomes based on pairwise alignment between predicted open reading frames translated into amino acids.

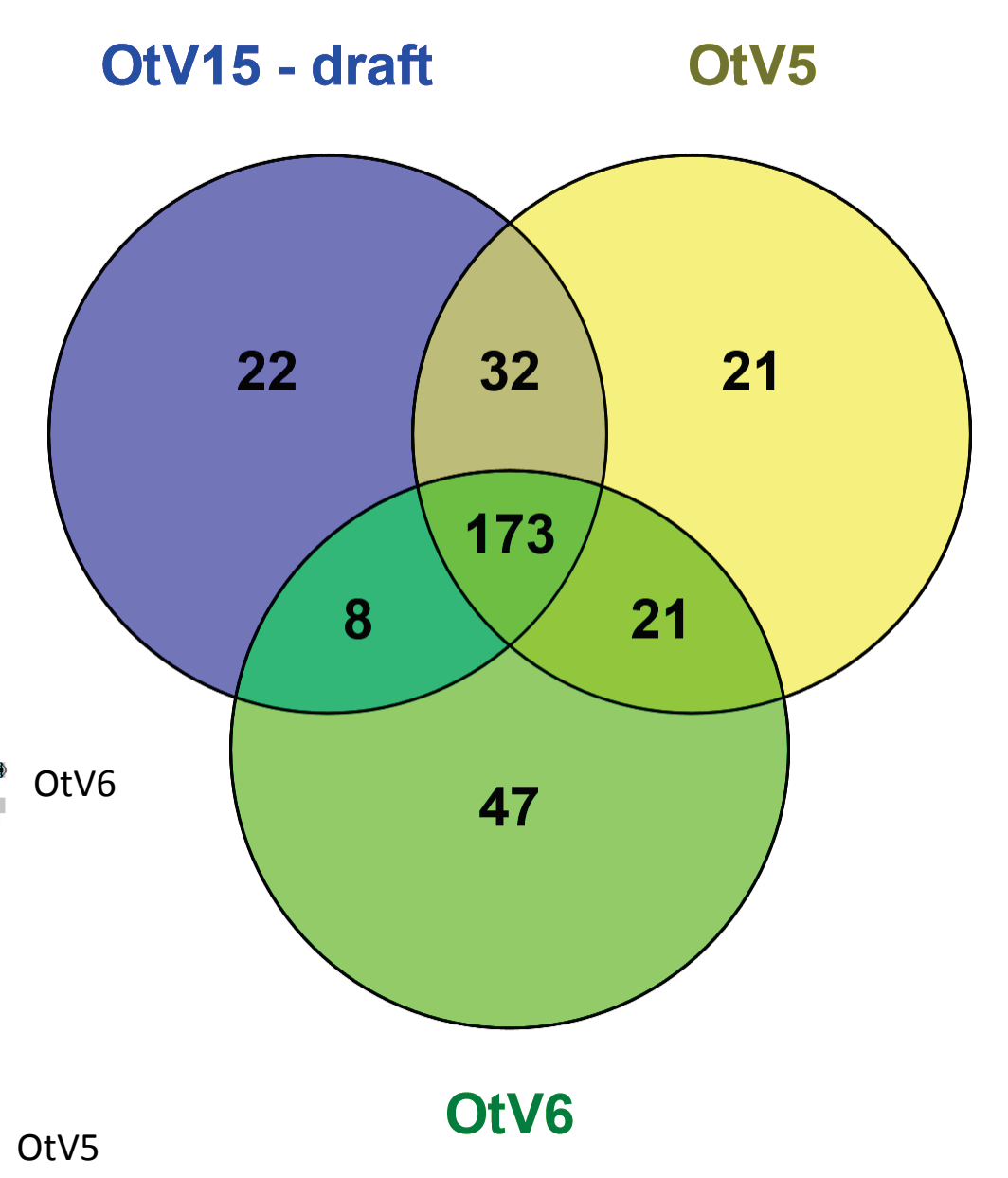
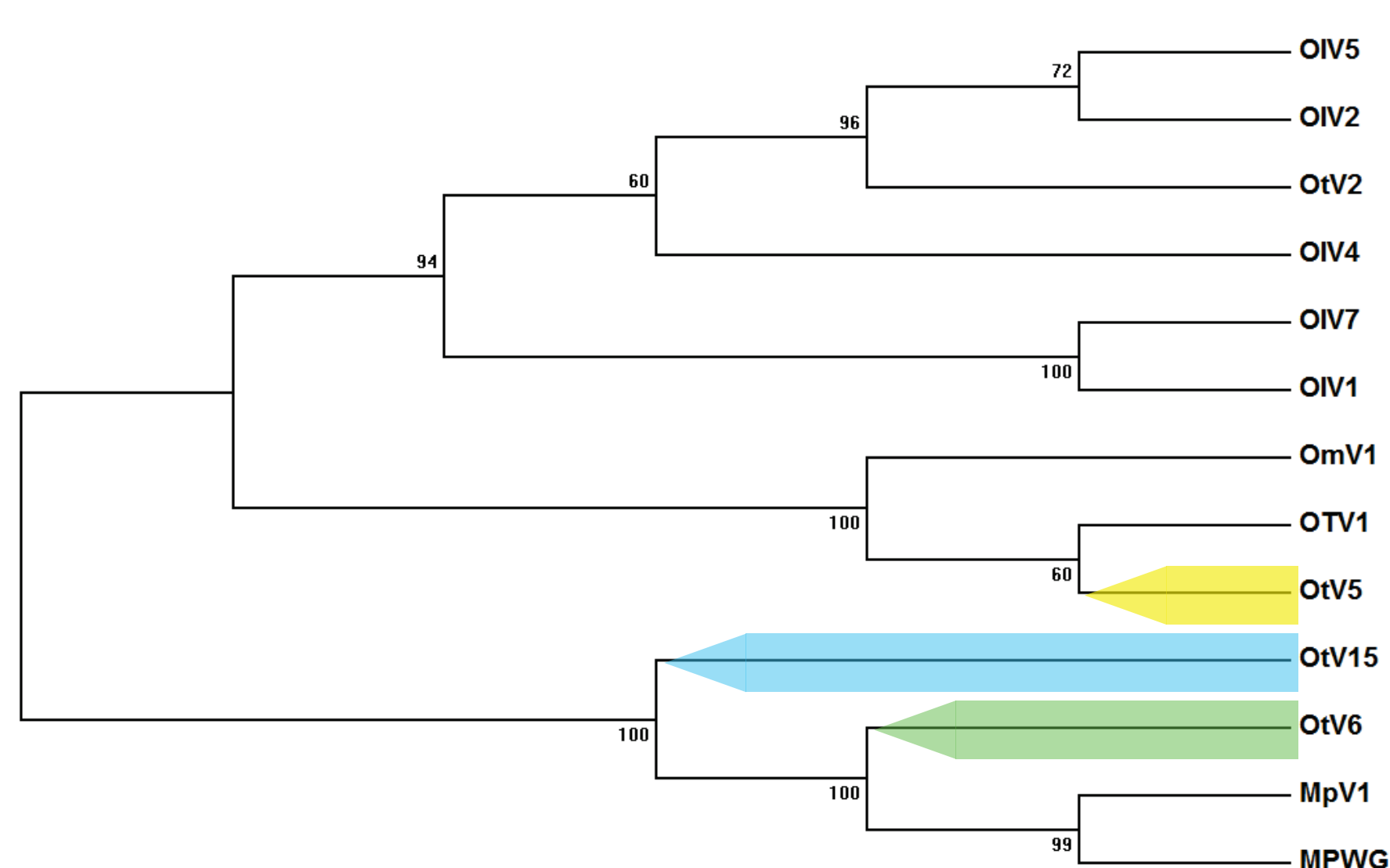


Figure 4: Diagram of orthologous ORFs of the three *O. tauri* viruses OtV5, OtV6, and OtV15.

Table 1: Genome properties of the three *Ostreococcus tauri* viruses OtV5, OtV6, and OtV15 infecting *O. tauri* RCC745 (=S) or OtV5-resistant clones of the same strain (=R).

Parameters	OtV5	OtV6	OtV15 - draft
Genome size (bp)	186	189	195
ORFs (No.)	247	250	235
GC content (%)	42	45	44
tRNAs	I,G,Ty,As,Th	I,G,Ty,As,Th,L,Ar,P,L	I,G,Ty,As,Th

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

SUMMARY: The two new *Ostreococcus* viruses OtV6 and OtV15 show a high synteny with OtV5 despite their significant phylogenetic 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.