A new phage satellite discovered in natural population of vibrio

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Résumé

In the marine bacteria from the *Vibrionaceae* family, many genomic islands are selected for and transferred by unknown mechanisms. We recently showed that numerous phage defense systems are encoded on genomic islands (Piel et al, Nat Micro 2022) but the mechanisms of transfer of these elements remained to be explored. Phage satellites are mobile genetic elements that exploit phages to ensure their own propagation and horizontal transfer into new bacterial hosts. We found that phage satellites are extremely abundant and broadly distributed in the vibrios and we discovered a new satellite family. Compared to known satellites, these elements are smaller in size, carried only 6 to 12 genes and are always integrated in the same recombination site (end of the Fis regulator gene). The activation of the element (excision and replication) is induced by specific virulent phage (or helper phage) and requires 4 genes encoding a putative excisionase (*alpA*), a tyrosine recombinase (*int*), a primase and a protein of unknown function, the latter being satellite-specific. Once excised and replicated, the element hitchhikes the capsid of the helper phage and can be transduced in a new host. We showed that this element is involved in the defense against other specific phages. We speculate that this "exclusion system" guarantees the helper phage a population of hosts to replicate.

Mots-Clés: Mobile genetic element. Phage defence. Natural population

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