This Word module should be used for all taxonomic proposals.

Please complete **Part 1** and:

either **Part 3** for proposals to create new taxa or change existing taxa

or **Part 2** for proposals of a general nature.

Submit the completed Word module, together with the accompanying Excel module named in Part 3, to the appropriate ICTV Subcommittee Chair.

The Word module explains and justifies your proposal. The Excel module is a critical document that will be used to implement the proposed taxonomic changes once they are approved and ratified. If proposals presented in the Word module are not presented accurately in the Excel module, the taxonomic changes cannot proceed.

For guidance, see the notes written in blue, below, and the Help Notes in file Taxonomic\_Proposals\_Help\_2019.

**Part 1:** **TITLE, AUTHORS, etc**

|  |  |  |  |
| --- | --- | --- | --- |
| **Code assigned:** | ***2019.061B*** | |  |
| **Short title:** Create one new order (*Tubulavirales*) including one new family (*Plectroviridae*), nineteen new genera and one new species | | | |
|  | | | |
| **Author(s) and email address(es):** | | | |
| List authors in a single line *Archives of Virology* citation format (e.g. Smith AB, Huang C-L, Santos, F) | | Provide email address for each author in a single line separated by semi-colons | |
| Knezevic P, Kropinski AM, Adriaenssens EM, Lavigne R | | [pknezevic20@gmail.com](mailto:pknezevic20@gmail.com)  [Phage.Canada@gmail.com](mailto:Phage.Canada@gmail.com); [Evelien.Adriaenssens@](mailto:Evelien.Adriaenssens@)quadram.ac.uk;  rob.lavigne@kuleuven.be | |
| **Corresponding author** | | | |
| Petar Knezevic | | | |
| **Author(s) institutional address(es) (optional):**   |  | | --- | | Provide institutional addresses, each on a single line followed by author(s) initials (e.g. University of Woolloomooloo [SAB, HCL]) | | University of Novi Sad, Serbia [PK]  University of Guelph, Canada [AMK]  Quadram Institute Bioscience, UK [EMA]  KU Leuven, Belgium [RL] | | | | | |
| **List the ICTV study group(s) that have seen this proposal:** | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | |  | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | |
|  | | | |
|  | | | |
| Date first submitted to ICTV: | | |  |
| Date of this revision (if different to above): | | |  |

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| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

**Part 3:** **PROPOSED TAXONOMY**

|  |
| --- |
| **Name of accompanying Excel module:** 2019.061B.A.v1.Tubulavirales\_1ord1fam19gen.xlsx |

The taxonomic changes you are proposing should be presented on an accompanying Excel module, 2019\_TP\_Template\_Excel\_module. Please enter the file name of the completed module in this box.

**Supporting material:**

| additional material in support of this proposal |
| --- |
| Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, please provide a tree where branch length is **proportional to genetic** distance, generated using an appropriate algorithm (Neighbour-Joining, Maximum Likelihood, or Bayesian) and provide evidence of the reliability of the branching (e.g., by bootstrapping).   Please refer to the Help Notes file (Taxonomic\_Proposals\_Help\_2019) for more information. |

| **Text of proposal:** | |
| --- | --- |
| **New species *Ralstonia virus RS551***  **Species demarcation criteria** We have chosen 95% DNA sequence identity as the criterion for demarcation of species in this new genus. Each of the proposed species differs from the others with more than 5% at the DNA level as confirmed with the BLASTN algorithm.  **Source of the name of this taxon:** Ralstonia phage RS551 is the first described strain of the species.  **Supporting evidence:**  Ralstonia phage RS551 infect *R.* *solanacearum* and can persist in the bacterial genome as a prophage. Virions are filamentous, approx. 7 x 1,200 nm. The genome size is 7,929 nt and contains 14 ORFs, including gene for resolvase and putative type-2 phage repressor. *R. solanacearum* infection with RS551 results in less EPS production and reduced motility, which decrease the bacterial virulence. It was proven that the phage integrates into the host genome at the sequence 5'- TGGCGGAGAGGGT-3' (Ahmad et al, 2017). This new species is a member of genus *Habenivirus*, as shows considerable DNA, proteome and core genes similarity to other members of this genus (Table 1; Fig. 1). Ralstonia phage RSIBR1(MF716957.1) should be considered as a strain of *Ralstonia virus RS551*, sharing 98% of DNA sequence identity.  **Table 1.** Properties of the three phages belonging to the genus *Habenivirus, Ralstonia virus RS551* and a peripherally related Ralstonia phage RSS1     |  |  |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | | **Ralstonia phage** | **GenBank accession No.** | **Genome length (bp)** | **Genome (mol%G+C)** | **No. CDS** | **DNA (% sequence identity)\*** | **Proteome (% homologous proteins)\*\*** | **Zot\*\*\*** | **CoatB** | **CoatA** | | **RSM1** | [**AB259123.2**](http://www.ncbi.nlm.nih.gov/nuccore/AB259123.2) | **9,004** | **60.0** | **15** | **100** | **100** | **100** | **100** | **100** | | **RSM3** | [**AB434711.1**](http://www.ncbi.nlm.nih.gov/nucleotide/209730235?report=genbank&log$=nucltop&blast_rank=4&RID=7YTTNT5N014) | **8,929** | **59.6** | **14** | **91** | **80** | **99** | **95** | **81** | | **RS603** | [**AB937974.1**](http://www.ncbi.nlm.nih.gov/nuccore/AB937974.1) | **7,679** | **59.4** | **13** | **56** | **60** | **93** | **100** | **75** | | **RS551** | **KX179905.1** | **7,929** | **60.8** | **14** | **48** | **67** | **90** | **93** | **72** | | RSS1 | [AB259124.1](http://www.ncbi.nlm.nih.gov/nuccore/AB259124.1) | 6,662 | 62.6 | 12 | 0 | 20 | 10 | 0 | 10 |   \* Determined using BLASTN; \*\* Determined using CoreGenes **\*\*\***Determined using BLASTP  **Fig. 1.** Phylogenetic analysis of the morphogenesis protein of phages from genus *Habenivirus* and an outlier RSS1, constructed using “one click” at phylogeny.fr (13). The "One Click mode" targets users that do not wish to deal with program and parameter selection. By default, the pipeline is already set up to run and connect programs recognized for their accuracy and speed (MUSCLE for multiple alignment and PhyML for phylogeny) to reconstruct a robust phylogenetic tree from a set of sequences (Anisimova and Gascuel, 2006).  result tree  **New genera**  **The creation of new genera based on existing species within the family *Inoviridae***  In Taxonomy Proposal 2016.080B.v3 a number of orphan species within the family *Inoviridae* were created, as they did not fit into any of the existing genera. As each of these species is sufficiently different from the others, we are now defining them as the type species of new genera.   1. **New genus *Infulavirus***   **Type species:** *Escherichia virus If1* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *infula, infulae*- woolen headband knotted with ribbons   **Supporting evidence:** Please see a TaxPro for the species   1. **Description:** The genome of the type species is 8.454 nt, GC 47.3% and encodes 10 ORFs. This phage is related to members of *Inovirus* and *Lineavirus*, considering amino-acid sequence of core genes, but there is a lack of DNA sequence similarity, which indicates evolutionary divergence. In addition, the members of the genus *Inovirus* attach to F pilus, while *Infulavirus* members attach to I pilus and there is a difference in infectivity mechanism, confirming evolutionary divergence (Lorenz et al, 2011). The host is *E. coli*, and the phage form turbid plaques, cause small host colony formation, cell death and lysis in a great extent.   New genus ***Restivirus***  **Type species:** *Ralstonia virus RSS1* as the only member of the genus.  **Source of the name of this taxon:** lat. *restis, restis*- a rope, cord  **Supporting evidence:** Please see a TaxPro for the species  **Description:** Ralstonia phage RSS1 contains genome of 6633 bp and 11 ORFs. The phage infect *Ralstonia solanacearum* and is able to integrate in bacterial genome (Nagata et al, 2007; Kawasaki et al, 2007). The filaments are approx. 1100 nm in length and 10 nm in width (Yamada, 2012). The infection activates expression of phcA, the global virulence regulator, enhancing extracellular polysaccharide (EPS) synthesis and twitching motility (Addy et al, 2012).  New genus ***Parhipatevirus***  **Type species:** *Ralstonia virus PE226* as the only member of the genus.  **Source of the name of this taxon:** lat. *parhypate, parhypatus* - second-top string/note, next to highest  **Supporting evidence:** Please see a TaxPro for the species  **Description:** The only member of the genus, *Ralstonia virus PE226*, was isolated from plant rhizosphere using *Ralstonia solanacearum* as a host. It has a genome of 5,475 bases (GC%: 61.7) that encodes 9 proteins. The phage is able to form clear plaques, and virion average length is 1050 ± 200 nm and width 6–9 nm (Murugaiyan et al, 2011).   1. New genus ***Primolicivirus***   **Type species:** *Pseudomonas virus Pf1* as the only member of the genus.  **Source of the name of this taxon:** lat. *primus*- first; lat. *licium, lici(i)*-thread  **Supporting evidence:** Please see a TaxPro for the species  **Description:** The representative of the genus, *Pseudomonas virus Pf1*, has virions approx. 2000x7 nm (Goldbourt et al, 2010), genome of 7,349 bases and encodes 14 OFRs (Hill et al, 1991). The phage is isolated from *P. aeruginosa* strain PAK and persists extrachromosomally.   1. New genus ***Tertilicivirus***   **Type species:** *Pseudomonas virus Pf3* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *tertius* – third; *licium, liciae* - a thread, leash or heddle in weaving   **Supporting evidence:** Please see a TaxPro for the species   1. **Description:** Pseudomonas virus Pf3 is approx.. 700nm long and its genome is 5,833 nt with 9 ORFs (Luiten et al, 1985).   New genus ***Suturavirus***  **Type species:** *Spiroplasma virus SVTS2* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *sutura, suturae*- seam, stitch, piece of sewing 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** The only member of the genus, *Spiroplasma virus SVTS2*, infects *Spiroplasma melliferum*. The genome is 6,825 bases (GC%: 22.7) and encodes 13 proteins (Sha et al, 2000).   1. New genus ***Psecadovirus***   **Type species:** *Stenotrophomonas virus PSH1* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *psecas, psecadis* - anointer of hair 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** Stenotrophomonas phage PSH1 is the only representative of the genus. It is isolated from a *Stenotrophomonas maltophilia* strain P2 and the virions are 2100 nm long. The genome consists of 6867 bases with 10 ORFs (Liu et al, 2012).  New genus ***Scuticavirus***  **Type species:** *Stenotrophomonas virus SMA6* as the only member of the genus.  **Source of the name of this taxon:** lat. *scutica, scuticae* – lash, whip, strap   1. **Supporting evidence:** Please see a TaxPro for the species   **Description:** Stenotrophomonas phage SMA6 is isolated from a *Stenotrophomonas maltophilia* strain Khak84, and has a genome of 7648. The phage possesses 11 open reading frames and is able to integrate into host genome (Petrova et al., 2014).  New genus ***Subteminivirus***  **Type species:** *Stenotrophomonas virus SMA7* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *subtemen, subtemini* - that which is woven in, a woof, weft 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** Stenotrophomonas phage SMA7 is isolated from a Stenotrophomonas *maltophilia* strain Khak84, and has a genome of 7069 bases. It possesses 11 potential open reading frames and is able to integrate into host genome (Petrova et al., 2014).  New genus ***Staminivirus***  **Type species:** *Stenotrophomonas virus SMA9* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *stamen, staminis* - warp in the loom, tread on distaff 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** Stenotrophomonas phage SMA9 is isolated from a strain c5 os *S. maltophilia* and it genome consists of 6907 bases and 7 ORFs (Hagemann et al, 2006).  New genus ***Versovirus***  **Type species:** *Vibrio VfO3K6 virus* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *versus, versus* - line, verse; row/string 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** The species *Vibrio virus VfO3K6* comprises 2 strains, VfO3K6 (sometimes designated as f237) and VfO4K8, isolated from a pandemic strains of *Vibrio parahaemolyticus*. The size of their genomes is in a range 6.9-8.8 kb (approx. 45% GC). The proteome contains 8- 10 proteins. The bacteriophage VfO3K6 has dimensions 2500 x 8 nm, while VfO4K68 has 1300 x 6 nm (Nasu et al, 2000; Chan et al, 2002); this morphological difference have to be further confirmed. It is reported that VfO4K68 is able to infect O3:K6 strain (Chan et al, 2002). The phage show similarity to Vf33 phages of *V. parahaemolyticus*, but only 21% at DNA and 30% at proteome level, with very low similarity of core genes.  New genus ***Capistrivirus***  **Type species:** *Vibrio virus KSF1* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *capistrum, capistri*- band for wines, halter/headstall 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** *Vibrio virus KSF1* is a virus of Vibrio cholera that uses MSHA type pili IV as receptors. Its genome contains 7,107 nucleotides, with 14 ORFs. Its virions are 1200 nm in length and 7 nm in width (Faraque et al, 2005).  New genus ***Vicialiavirus***  **Type species:** *Vibrio virus VCY* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *vicialia, vicialium* - [the](https://www.ultralingua.com/onlinedictionary/dictionary) [stalks](https://www.ultralingua.com/onlinedictionary/dictionary) [or](https://www.ultralingua.com/onlinedictionary/dictionary) [haulm](https://www.ultralingua.com/onlinedictionary/dictionary) [of](https://www.ultralingua.com/onlinedictionary/dictionary) [vetches](https://www.ultralingua.com/onlinedictionary/dictionary) 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** Vibrio phage VCY is a phage of Vibrio cholerae, 1600 nm long and 7 nm wide with the overall genome size of 7103 kb and 11 putative ORFs. The phage is able to integrate into host DNA (Xue et al, 2011).  New genus ***Bifilivirus***  **Type species:** *Propionobacterium virus B5* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *bifilum, bifili*- double thread 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** Propionibacterium phage B5 is the only member of the family that infect a Gram-positive bacterium (*Propionibacterium freudenreichii*). Its genome contains 5,806 bases (GC%: 64.3), encoding 10 proteins. The virions are 620 nm long and 12 nm wide (Chopin et al, 2002).  New genus ***Thomixvirus***  **Type species:** *Thermus virus OH3* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *thomix, thomicis*- a cord, string, line, thread 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** Thermus phage phiOH3 is isolated from a geothermal water sample and its host is a hyperthermophilic bacterium *Thermus thermophilus*. Virions are filamentous and flexible, 8 x 830 nm. Plaques are turbid and 0.5-1.1 mm in diameter. The virions are stable one hour at 70oC and in NaCl (1M), but sensitive to pH changes. The phage genome consists of 5,688 nt, with a GC% 69.5 and 8 ORFs predicted (Nagayoshi et al, 2016). The genome organization is characteristic for *Inoviridae* and key genes are present, although they show low percent of DNA and protein similarity to genes of other members of the family. There is also a Thermus phage phiOH16, which is a strain of species *Thermus virus OH3*.  **New genus *Xylivirus***  **Type species:** *Xanthomonas virus Xf109* as the only species in the genus.   1. **Source of the name of this taxon:** lat. *xylon, xyli*- cotton 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** The type species Xanthomonas virus Xf109 infects *X. oryzae* and can persist in the bacterium as a prophage. Virions are filamentous, approx. 8 x 1,210 nm. The genome is 7,190 nt in size and contains 12 ORFs. It was proven that the phage integrates into the host genome at the attB/attP sequence 5'-TATACATTATGCGAA-3' (Yeh, 2016). Xanthomonas phage Xf409 is considered as a strain of the species.  New genus ***Villovirus***  **Type species:** *Vibrio virus Vf33* as the only species in the genus.   1. **Source of the name of this taxon:** lat. *villus, villi*- shaggy hair, tuft of hair 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** *Vibrio virus Vf33*, as a representative species, is a filamentous phage that infects *V. parahaemolyticus* with K38 antigen. It is about 1,400 nm long and 7 nm wide, with the buoyant density in CsCl 1.292 g/cm3. The virus is resistant to heating below 80oC and to treatment with diethylether, acetone or methanol, but sensitive to chloroform. The nucleic acid of this phage is 8.4 kb in size (Taniguchi et al, 1984).   1. New genus ***Coriovirus***   **Type species:** *Xanthomonas virus Cf1c* as the only member of the genus.   1. **Source of the name of this taxon:** lat. *corius, cori(i)* – thong, strap, whip 2. **Supporting evidence:** Please see a TaxPro for the species   **Description:** *Xanthomonas virus Cf1c* is a type species, infecting *X. campestris* var. *citri.* It has a genome of 7,308 bases (Kuo et al, 1991). The strain Xantomonas phage XacF is 600nm long and cause phenotypic changes of host, including lower levels of extracellular polysaccharide production, reduced motility, slower growth rate, and a dramatic reduction in virulence. The phages integrate into host genome using cell XerC/D recombinase, and for Cf1c production of clear plaques is proven.  ***Affertcholeramvirus*** *- Vibrio virus CTXphi*  **Type species:** *Vibrio virus CTXphi* () which is the only member of the genus.  **Source of the name of this taxon:** lat. affero; affert – it brings, carries, produces, causes; lat. cholera, cholerae - cholera   1. **Supporting evidence:** Please see a TaxPro for the species   **Description:**  The genome size of CTXphi is approximately 7 kb and GC% is approx. 45%. The genome contains two regions: the RS2 sequence (rstR, rstA and rstB - replication, regulation, and integration) and the core region ( psh, cep, orfU (gIII), ace, zot and ctxAB). The phage integrates into the chromosome of *V. cholerae* at the *attB* (*dif*) integration site and in some strains appear as tandem repeat. The phage carries three genes for toxin production: *ace* (accessory cholera enterotoxin) which is a minor coat protein, *zot* (zonula occludens toxin) responsible for maturation and ctxAB without function, but which is responsible for cholera A-B toxin (CT) production. These genes are part of a virulence cassette of *V. cholera* O1, O139 and El Tor biotypes (Mantri et al, 2010; Faraque and Mekalanos, 2012).  **Family** ***Inoviridae***   1. **Supporting evidence:** Figure 2   **Description:** Family *Inoviridae* should be reorganized and to comprise members of genera ***Inovirus, Fibrovirus, Habenivirus, Lineavirus, Saetivirus***, and the following new genera:  ***Infulavirus*** – *Escherichia virus If1*  ***Restivirus***- *Ralstonia virus RSS1*  ***Parhipatevirus*** -*Ralstonia virus PE226*  ***Primolicivirus*** - *Pseudomonas virus Pf1*  ***Trilicivirus*** - *Pseudomonas virus Pf3*  ***Psecadovirus* -** *Stenotrophomonas virus PSH1*  ***Scuticavirus*** - *Stenotrophomonas virus SMA6*  ***Subtemenvirus*** - *Stenotrophomonas virus SMA7*  ***Staminivirus*** *- Stenotrophomonas virus SMA9*  ***Versovirus*** *- Vibrio virus VfO3K6*  ***Capistrivirus****- Vibrio virus KSF1*  ***Vicialiavirus***- *Vibrio virus VCY*  ***Bifilivirus*** *– Propionobacterium virus B5*  ***Thomixvirus*** *- Thermus virus OH3*  ***Affertcholeramvirus*** *- Vibrio virus CTXphi*  ***Villovirus*** *- Vibrio virus Vf33*  ***Coriovirus*** *- Xanthomonas virus Cf1c*  ***Xylivirus*** *- Xanthomonas virus Xf109*  The viruses of the family *Inoviridae* infect Gram-positive and Gram-negative bacteria. The virions are filamentous and (+)ssDNA genomes show similar organization. According to Fig. 2, the family comprises a coherent group of phylogenetically related viruses.  **New family** ***Plectroviridae***  **Source of the name of this taxon:** The name is given after first created genus belonging to the family (*Plectrovirus*)   1. **Supporting evidence:** Figure 2   **Description:** The new family *Plectroviridae* should comprise members of genera ***Plectrovirus, Vespertilliovirus***, and the new genus ***Suturavirus –*** *Spiroplasma virus SVTS2****.***  The viruses of the family *Plectroviridae* infect cell wall-less bacteria. The virions are rod-shaped and (+) ssDNA genomes show similar organization. According to Fig. 2, the family comprises a coherent group of phylogenetically related viruses.  **New order *Tubulavirales***  **Source of the name of this taxon:** lat. *tubula, tubulae* – pipe, tube  **Description:** The order *Tubulavirales* should comprises two families: *Inoviridae* and *Plectroviridae*. The phages infect Gram-positive, Gram-negative and cell wall-less bacteria. The members of the order *Tubulavirales* possess (+)ssDNA genome and have unique morphology, presented as flexible filaments or rigid rods. This combination of morphology and genome is unique among viruses, with an exception of representatives of family *Spiraviridae*, which are substantially different. The genomes are similarly organized, with modular structure and replicate by rolling circle (in some phages probably by transposition). Phage genomes persist extrachromosomally or can be integrate into bacterial chromosome. A prominent specificity of this order is that phages enter neither typical lytic nor lysogenic cycle and release from cells by extrusion, causing a chronic infection without host killing.  **Fig. 2.** The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model (Kimura, 1980), based on whole genomes’ alignment of members *Tubulavirales*. The tree with the highest log likelihood (-360619.65) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 57 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. There were a total of 22338 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kimura et al, 2018), with bootstrap 100. The green frame represents family *Plectroviridae*, while red represents *Inoviridae*. Different genera are framed with various colors, while uncolored phages are unapproved species. | |
| **References:** |
| [Addy, H.S](https://www.ncbi.nlm.nih.gov/pubmed/?term=Addy%20HS%5BAuthor%5D&cauthor=true&cauthor_uid=22085298)., [Askora, A](https://www.ncbi.nlm.nih.gov/pubmed/?term=Askora%20A%5BAuthor%5D&cauthor=true&cauthor_uid=22085298)., [Kawasaki, T](https://www.ncbi.nlm.nih.gov/pubmed/?term=Kawasaki%20T%5BAuthor%5D&cauthor=true&cauthor_uid=22085298)., [Fujie, M](https://www.ncbi.nlm.nih.gov/pubmed/?term=Fujie%20M%5BAuthor%5D&cauthor=true&cauthor_uid=22085298)., [Yamada, T](https://www.ncbi.nlm.nih.gov/pubmed/?term=Yamada%20T%5BAuthor%5D&cauthor=true&cauthor_uid=22085298). 2012. The filamentous phage ϕRSS1 enhances virulence of phytopathogenic *Ralstonia solanacearum* on tomato. [Phytopathology.](https://www.ncbi.nlm.nih.gov/pubmed/22085298) 102(3):244-51.  Ahmad, A.A., Stulberg, M.J., Huang, Q. 2017. Prophage Rs551 and Its Repressor Gene orf14Reduce Virulence and Increase Competitive Fitness of Its Ralstonia solanacearum Carrier Strain UW551. Front. Microbiol. 8: 2480.  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