Comment on “The complete nucleotide sequence and genome organization of pea streak virus (genus *Carlavirus*)”

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Dear Editor,

It has come to my attention that the recently published paper by Li Su et al., “The complete nucleotide sequence and genome organization of pea streak virus (genus *Carlavirus*)” claims that the authors determined “the first complete genome sequence of PeSV” (Arch Virol DOI [10.1007/s00705-015-2467-2](https://doi.org/10.1007/s00705-015-2467-2); submitted March 13th, accepted May 23rd, 2015 – as seen in the online version of the paper published on June 21, 2015).

However, the complete genomic sequence of the virus (*Alfalfa latent virus*, a strain of PeSV) was freely available from GenBank since March 1th, 2015 which was two weeks before Li et al. submitted their manuscript to Archives of Virology and almost four months before it was published (please see history of the submission here: <http://www.ncbi.nlm.nih.gov/nuccore/KP784454.2?report=girevhist>).

Since Li Su et al studied phylogeny of the members of the genus *Carlavirus*, it is likely that the group worked extensively with GenBank data. It is therefore hardly possible that the available complete genome sequence of the virus escaped their attention.

I also refer you to the publication in Genome Announcements freely available to the public since April 16, 2015 (Nemchinov LG, Shao J, Postnikova OA.

Complete Genome Sequence of the *Alfalfa latent virus*. Genome Announc. 2015 Apr 16;3(2). pii: e00250-15. doi:[10.1128/genomeA.00250-15](https://doi.org/10.1128/genomeA.00250-15)). This publication was available to the authors, the Editor assigned to the Li Su et al article, and the Reviewers, while the manuscript was under review in Archives of Virology. Please also note that Genome Announcements will not consider manuscripts for publication “until the availability of the sequence(s) in GenBank/ENA/DDBJ has been verified”.

It appears that it might have been a personal decision of the authors of the Li Su et al paper to ignore the already available genome sequence of the virus belonging to the same species and claim priority rather than adjust their data accordingly and give credit to their colleagues.

The obvious facts would not change, regardless of Li Su et al’s explanation and justification of this incident. What is important, however, is to assure that in the future Dr. Xiang and his co-authors will not treat other colleagues’ work in the same way.

It is critical for the scientific community that research is built upon principles of mutual respect, honesty, and responsibility.

Thank you for your time.

Yours sincerely,
Lev Nemchinov

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