Comments to the Author

In this study, the authors describe a one-off assessment of aphid monitoring and presence of pea enation mosaic virus on alternative hosts to legume crops in the Palouse Prairie and adjacent shrup-steppe region adjacent to it (USA). Different sites were monitored between May to July 2018 for aphid abundance, plant diversity and PEMV presence along a 10 m transect at each side.

The authors concluded that hairy vetch was not only the most abundant plant species from the Fabaceae family but also had the highest abundance of pea aphids. In addition, PEMV was only detected in hairy vetch and dry peas but not in other hosts. They concluded that early detection of PEMV in hairy vetch poplulations could be an indicator for PEMV outbreaks in legume crops later in the season.

Although I acknowledge the effort and work that has been put into this study, I feel that I cannot recommend it for publication in its present form.

Firstly, a one season snapshot is not enough to draw any meaningful conclusions, as vague as they might have been described.

*Well there is nothing I can do about that at the moment. We found a needle in a haystack and were just describing where we found the needle. I added a section to the discussion about this in my revisions and its actually right in the first paragraph of the conclusions.*

Secondly, I am missing a lot of technicial details that would describe the methodology better; also, a lot of information in not separated correctly.

*I need more guidance on what technical details the reviewer is looking for.*

~~E.g., describing PEMV symptoms (l75ff) would fit better to the introduction (by the way, the more typical PEMV symptoms are translucent patches which is quite a distinct symptom when compared to other legume viruses);~~

~~the numbers of sites and transects should be indicated in the M&M section.~~

In the manuscript, no details on the long-term trapping network can be found (l82), the relevant information is only mentioned in the figure legend of Fig S1.

*I added this and also checked in with Sanford on whether some more details can/should be added.*

I wonder if the aphid collection method is really the best one for A. pisum, as these aphids drop off plants at the slightest movement.

*I can’t go back and change the sampling methodology and an alternative is not proposed, so I won’t bother to address this.*

In figure legend S2 it is mentioned, that there was quite a disturbance of plants by setting up the transect and removing flags...

*Again. Its what we did and we still got plenty of aphids so I’m not sure how to address this criticism.*

The sentence in line 116ff sounds very strange; perhaps there should be a separation between primer design and setup of PCR reaction? In line 119 it should be PCR program as the reverse transcription had been carried out before with the Bio-Rad kit (line 114 ff).

The term "disturbed habitat fragments" in line 125 is not defined.

*This part was too vague, so I just stated that we resampled it and validated that PEMV was present in nearby live vetch.*

When presenting the results, it is unclear if the authors refer to A. pisum when they mention aphids (e.g., line 143).

*Its pea aphids! We got a lot and this ameliorates any concern I have that the plant transects knocked a handful of aphids off plants. It’s a drop in the bucket, metaphorically peaking.*

One can only assume that the total number of aphids is mentioned here but that for Fig 2 A. pisum density was used? Or how was the probability of pea aphid presence in Fig. 4 determined? Neither in the M&M section nor in the Results section is a clear description given.

*Added to the statistical methods section.*

As this is only a one-off study, it is very difficult to substantiate the conclusion. I agree that the likelyhood of crop infection increases by higher density of alternative hosts, PEMV infection and vectors, but these are very vague conclusion.

*Ok I added this:*

*“Our surveys of plant communities in habitats adjacent to pea fields suggest that there are at least 23 potential hosts that can be resampled in future years, and the absence of aphids or PEMV does not rule them out as compatible hosts for either.”*

I doubt that the use of qRT-PCR techniques as suggested in line 198ff would add any meaningful results to forthcoming studies as PEMV infection is in general associated with high viral titres (own experience using DAS-ELISA for PEMV detection), **so sensitivity would not be seen as an issue here.**

*I told Saumik this comment and we both agreed its total nonsense. ELISA is not sufficient for the type of work completed in this study and has far too many false negatives. For surveying weeds, we need a more sensitive technique and qRT-PCR is the way to go.*

Minor errors:

~~line 40: host patches not hosts patches~~

~~line 45: Latin name for American barberry desirable~~

~~line 48: The role of legumes in providing green manure, alternative crops for crop rotation and soil sanitation and organic farming are not mentioned her; not only weeds are important virus reservoirs~~

~~line 68: pea enation mosaic virus as it is a virus here and not a species~~

~~line 70. add "," before common vetch~~

~~line 183: reduce not reducing~~

~~line 204: rephrase the second part of the sentence~~

~~line 206: give Latin name for banner pea (I am unfamiliar with this term and google only gave results for poster banners :-))~~

~~line 271: Capitalise Disease line~~

~~350: italicise Luteoviridae: Polerovirus~~

~~line 357f: small letters for latency, impact and plants~~