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In terms of feeding mechanism, persistently (PT) or semi-persistently (SPT) transmitted viruses require relatively long vector feeding periods for an effective uptake, but they can either bind to the infectious insect foregut or circulate within its hemocoel, often making vectors competent for transmission throughout several days or their remaining lifetime. Plants infected with PT or SPT viruses often express disease symptoms associated with a “honest” syndrome that attract, arrest, and increase performance and survival of vectors to ensure effective acquisition and transmission. Non-persistently transmitted (NPT) viruses are acquired by vectors faster (long feeding periods are not required), but virions remain only in the insect mouthparts and transmission competence is lost within hours. Infections of NPT viruses express symptoms that trigger a “deceptive” syndrome which induce attraction of vectors, but neither arrestment nor performance is granted, so as to favor quick insect movement from infected to healthy hostplants after acquisition. There are three additional syndromes which involve attraction to infected hostplants depending on the infective/non-infective status of vectors (“conditional”), differential attraction of vectors across the disease progression (“dynamic”), and the induction of changes in vector feeding behavior after virus acquisition (“consumption related”).

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Clones with designation PK are pink and those with designation GN are green; clones with designation OR were collected in Oregon those with designation ID were collected in Idaho.

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We found that pea aphid performance largely matched host preference and varied as expected as a function of hostplant, with some exceptions. Pea aphid biotypes grouped as “pea” performed better on pea and hairy vetch plants, which matches the results of previous work in the Palouse region (PNW) (Clark et al., 2023). However, their increased performance in pea plants did not match their preference for this plant, but it did for hairy vetch. This result supports the hypothesis of “fundatrix specialization”, which states that evolution of aphids is constrained by the selective pressures exerted on the morph that hatches after the winter. These morphs are heavily adapted to prefer and perform better in hostplants that are available in early spring (Moran, 1988, Moran, 1994). Hairy vetch emerges early, is widely dispersed across the Palouse region, and has been proposed as a “stopover” host for aphid alates before they build up dense populations that will eventually infest pea crops (Clark et al., 2023). Thus, we suggest that pea plants are alternate hosts for “pea” pea aphids, which are adapted to prefer and perform best in hairy vetch, the plant that fundatrix individuals encounter when they hatch after the winter. Subsequent morphs may have to switch to pea plants as hairy vetch populations senesce and become scarce. Pea aphid biotypes grouped as “alfalfa” do not need a “stopover” host because alfalfa is a winter-hardy plant, which grows in both crop and non-crop areas and is fairly available through the growing season.

Another exemption to the performance-preference correlation rule was “alfalfa” pea aphids, which preferred pea plants to a similar extent as “pea” pea aphids, despite their performance being significantly lower in these plants. We also found that pea plants were not as poor hosts for “alfalfa” pea aphid biotypes as alfalfa plants were to “pea” pea aphids, which matches Eigenbrode et al. (2016) observation that “pea” and “alfalfa” clones may reduce their performance by 93% and 17-52% when feeding on alfalfa or pea plants, respectively. Thus, it looks like pea aphid “alfalfa” biotypes are better adapted to use pea plants as hosts, than “pea” biotypes are to shift to alfalfa. We can only speculate that the preference for and ability to exploit host pea plants by “alfalfa” biotypes is a plesiomorphy shared among pea aphid biotypes, and that the host shift to alfalfa is a more recent apomorphy only evolved in the “alfalfa” biotypes. To our knowledge, there are no studies investigating the phylogenetics of pea aphid biotypes in the PNW, but Moran (1988) notes that related species of aphids tend to share hosts used by sexual generations and their immediate descendants (i.e., primary hosts), and quite different secondary hosts which have been recently acquired.

One of the most important findings of this study is that vector manipulation by plant viruses appears to be restricted to maximizing intraspecific transmission, and to have little influence on interspecific transmission and patterns of vector’s hostplant specialization. These results differ from those described by Lee et al. (2022) with BCTV-carrying beet leafhoppers [*Circulifer tenellus* (Baker)], which seem to increase their probing behavior on different hostplant species, compared to their non-viruliferous conspecifics, to apparently maximize interspecific transmission. Similarly, Shoemaker et al. (2019) found that BYDV-PAV-carrying bird cherry-oat aphids (*Rhopalosiphum padi* L.) exhibited a stronger preference for perennial grasses, compared to non-viruliferous aphids, which showed no preference for any of the offered hostplants. Phytophagous insects use specific ratios of relatively common plant volatiles to recognize and locate suitable hostplants (REF). Furthermore, the complexity associated with the ability to detect a wide range of such compounds provides the required plasticity to adapt to a greater range of potential hostplants (Bruce et al., 2005). Soluble proteins, known as odorant binding proteins (OBP), have been identified as key carriers of odorants through the insect body and responsible of olfactory recognition of and behavioral responses to semiochemicals in insects (Pelosi et al., 2006). Pea aphids are equipped with efficient mechanisms to recognize and respond to a wide range of plant volatiles, which includes at least 18 OBPs, most of which presumably related with hostplant recognition and location (Shih et al., 2023, Robertson et al., 2019). Moreover, there is evidence that indicates that OBPs are differentially expressed as a function of hostplant-biotype interaction in pea aphids, and that such profiles are hardwired and heritable (Eyres et al., 2016). In contrast, both leafhoppers and bird cherry-oat aphids seem to exhibit much simpler mechanisms of hostplant location and recognition. To date, there are no specific characterizations of the beet leafhopper OBPs, but related species may exhibit between three and 16 OBPs (He et al., 2019, He et al., 2011, He and He, 2014) [one exception with 40 OBPs (Bian et al., 2018)], of which only a few seem to be involved in hostplant recognition and location (Hu et al., 2019, He et al., 2018). Bird cherry-oat aphids also have a simpler OBP complex, compared to that exhibited by pea aphids, although the function of most of them remain to be characterized (Kang et al., 2018, Wang et al., 2019). Furthermore, neither beet leafhoppers nor cherry-oat aphids appear to be under a host-driven speciation process such as that widely documented for pea aphids (Via et al., 2000, Via, 1999, Peccoud et al., 2008, Eigenbrode et al., 2016). Although some genetic differences have been reported for different populations of both beet leafhoppers (Young and Frazier, 1954) and bird cherry-oat aphids (Simon and Hebert, 1995), they either seem to be caused by allopatry rather than by sympatric host specialization (Hudson et al., 2010, Morales-Hojas et al., 2020). We hypothesize that the complexity behind the hostplant recognition and location by pea aphids and the reproductive isolation derived from hostplant specialization prevents parasites from triggering “consumption related” syndromes that alter the preference and performance of viruliferous pea aphids for different hostplant species.