

presence of an endosymbiont bacterium (*Cardinium*), which results in the production of only haploid females. Although in recent years several aspects of the biology of this mite have been elucidated, little is known about its genetics. However, collaborative efforts from Brazilian, Canadian, French and Belgian research groups are leading towards an international initiative to sequence the genome of *B. phoenicis*. The objective of this study was to estimate the genome size of the mite to provide basic information for this sequencing project. Flow cytometry analyses were run on a Particle Analysing System (Partec, Münster, Germany) using *B. phoenicis* females and males. *T. urticae* mites (females and males) were used as internal controls. The nuclear DNA content was stained with DAPI fluorescent dye and C-value was estimated based on their fluorescent intensity. Male and female cells of *B. phoenicis* showed similar frequency distribution with a single peak at the same fluorescent intensity and DNA content value was estimated in 86 Mbp. These values reveal that the *Brevipalpus* genome size is similar to that of diploid *T. urticae*, estimated in 90 Mbp. Studies using quantitative real-time PCR (qRT-PCR) should be carried out to validate the flow cytometry results. Financial Support: Fapesp, CNPq, Embrapa.

*Biological Control*

### Survey of phytoseiids and mite-transmitted viruses in weeds from an organic sweet orange orchard in Brazil

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Despite the fact that Brazil is the largest sweet orange producer in the world, it is affected by several pests and pathogens that hinder production and increase costs; among them *Citrus leprosis virus C* (CiLV-C). This is considered the most important virus infecting sweet oranges currently in the country, where it causes approximately US\$ 70 million in losses every year. Leprosis is also present in other countries in South, Central and North America. The virus is efficiently transmitted by *Brevipalpus phoenicis* Geijskes (Acari: Tenuipalpidae), a cosmopolitan and polyphagous vector. In this study we conducted a survey in an organic sweet orange commercial orchard with the objective to determine whether or not weeds naturally occurring in citrus agrosystem could host CiLV-C, its vector, and predaceous mites. We assessed the presence of *B. phoenicis* and phytoseiids on weeds of a Westin citrus orchard with high incidence of leprosis in Borborema, São Paulo State, Brazil, from June 2010 to April 2011. We identified 33 weed species, including five perennials. *B. phoenicis* specimens were found in *Amaranthus deflexus* L., *Agerantum conyzoides* L., *Alternanthera tenella* Colla, *Bidens pilosa* L., *Solanum americanum* Mill., *Ipomea quamoclit* L., *Ipomea* sp., *Panicum maximum* Jacq., *Merremia cissoides* (Lam.) Hallier f., and *Commelina benghalensis* L. The latter was the most favorable to the leprosis vector, and CiLV-C infection was confirmed by RT-PCR. No other plant species was found as viral host in this survey. The prevalent phytoseiid species identified, representing 58% of all the phytoseiids found, was *Iphiseiodes zuluagai*, a known *B. phoenicis* predator. It was followed by *Euseius concordis* (21%) and *Amblyseius composites* (13%). Most of the phytoseiids were found on *Agerantum conyzoides*, *S. americanum* and *A. tenella* with 22%, 21% and 18% of specimens, respectively. Our data suggest that *C. benghalensis* should be eliminated from citrus orchards, since it can serve as source of CiLV-C and its mite vector. On the other hand, *A. conyzoides* has a potential to be reservoir for phytoseiid predators of *B. phoenicis* and could probably be considered an ally in IPM programs. Financial Support: Fapesp/Embrapa.