



## Seasonal abundance of cotton thrips (Thysanoptera: Thripidae) across crop and non-crop vegetation in an Australian cotton producing region

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### ABSTRACT

The spatio-temporal relationships of thrips populations across weeds and cotton (*Gossypium hirsutum* L. (Malvales: Malvaceae)) crops were studied across the agricultural landscape of the Namoi Valley, New South Wales, Australia. In a structured sampling program, the seasonal patterns of host plant use by *Thrips tabaci* Lindeman, *Frankliniella occidentalis* Pergrande and *F. schultzei* Trybom (Thysanoptera: Thripidae) were quantified in relation to their invasion of cotton crops. Plants of 69 species (in 20 families) were sampled; *T. tabaci* was the most numerous thrips species and was recorded from 31 plant species, *F. occidentalis* was less numerous but recorded from 35 plant species, and *F. schultzei* was present at very low densities on 25 plant species. Both *T. tabaci* and *F. occidentalis* were mostly collected from weeds flowering in spring and summer, when these plants were most abundant. The seasonal composition of thrips populations on cotton changed from predominately *T. tabaci* on seedling cotton to *F. schultzei* and *F. occidentalis* on mature flowering cotton later in the season. High *T. tabaci* abundance on early season cotton was attributed to the abundance of *T. tabaci* on the surrounding weed species, because the weed hosts on which it was recorded were plentiful then. In contrast, the patterns of *F. occidentalis* and *F. schultzei* abundance on cotton were not correlated with their abundance on weeds, but rather with the emergence of cotton flowers. The genetic relationships and cryptic species identity of thrips on cotton relative to those on the other host plant species sampled was investigated through the analysis of mitochondrial CO1 gene sequences. *Thrips tabaci* and *F. occidentalis* collected from cotton were genetically identical to conspecifics collected from weeds. This is consistent with these insects moving onto cotton plants from nearby source populations on weeds. *Frankliniella schultzei* is a species complex in Australia, two members of which are present in this region, but only the black species was found in these surveys. This study demonstrates that (i) weeds play an important role in the population ecology of thrips, particularly in *T. tabaci* infesting early season cotton crops, (ii) the role of weeds warrants consideration in relation to pest management strategies, and (iii) without considering the surrounding landscape (which needs definition relative to each pest species) invasions cannot be readily understood mechanistically.

### 1. Introduction

Understanding the sources of crop infestation by pests that use multiple host species is important in developing effective integrated pest management strategies. The information can be used to predict likely future pest abundance, thereby assisting in developing pro-active management plans, or may allow the sources to be manipulated to reduce the magnitude of the infesting pest population, thereby reducing the risk that it will need to be controlled (Wilson, 1995). In many cotton-producing regions, thrips (Thysanoptera: Thripidae) are often abundant and damaging (Atakan et al., 1998; Toews et al., 2010; Cook

et al., 2003). In Australia three species of thrips, *Thrips tabaci* Lindeman, *Frankliniella occidentalis* Pergrande and *F. schultzei* Trybom are regarded as pests of cotton crops (Williams et al., 2011).

Thrips generally feed on the undersides of the cotton leaves, causing damage that can lead to dramatic deformation of seedling leaves (Williams et al., 2011). In extreme cases thrips damage can result in the death of the plant terminal; plant development and the production of fruiting bodies may then be delayed and can result in reduced yield and/or delayed maturity (Sadras and Wilson, 1998; Lei and Wilson, 2004). Thrips sometimes damage plants in mid to late season crops, causing distortion of the upper leaves, but this damage does not usually

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result in economic loss (Williams et al., 2011).

The Namoi valley, New South Wales, is a major cotton producing region and *T. tabaci* has been recorded as the most abundant thrips species on cotton early in the season; this is typically followed by a rapid decline in abundance during mid-December, while the abundance of *F. schultzei* increases after this period (Wilson and Bauer, 1993). The processes behind the decline in *T. tabaci* abundance and the later increase in *F. schultzei* abundance are poorly understood. Further, *F. occidentalis* entered Australia some years ago and it has spread to cotton producing regions since the report of Wilson and Bauer (1993) was published. Little is known of its seasonal abundance, host use or ecology. Indeed, the ecology of thrips in relation to cotton crops more broadly is not well understood, despite their pest status.

The three species of thrips that invade seedling stage cotton are generally regarded as polyphagous (Milne and Walter, 1998, 2000). Many pest thrips have wide host ranges that include both non-cultivated and cultivated plants; the relative attraction of the different host plant species, which changes with their phenology, is important during periods of dispersal (Doederlein and Sites, 1993). Movement of individuals of any particular species from one locality to another can be brought about by unfavourable conditions in the habitat of origin or in response to certain environmental stimuli (Walter, 2003; Loxdale and Lushai, 1999; Dingle and Drake, 2007). For example, North and Shelton (1986) demonstrated that populations of *T. tabaci* developed on cereal and forage crops and colonized nearby cabbage fields when the original hosts were harvested or became senescent.

These studies suggest that thrips populations can shift from one host type to another and that movement can be driven by deterioration in host plant quality. Wilson and Bauer (1993) suggested that the influxes of thrips to seedling cotton, primarily *T. tabaci*, probably came with migration from nearby senescent winter weeds and cereal crops. Milne and Walter (1998) confirmed the presence of high densities of *T. tabaci* adults and larvae on inflorescences and vegetative parts of five common weed species near cotton fields. However, there is no direct evidence that the thrips on nearby weeds or crops subsequently colonize cotton crops, in Australia or elsewhere. Further, the relationship between host plant use and the impact of seasonal conditions on the abundance and the species composition of the thrips pest complex in cotton remains unclear.

Polyphagous insects are frequently found to be suites of cryptic species (Walter, 2003; Raftar et al., 2013; Perring, 2001; Loxdale et al., 2011) and indeed cryptic species have been detected within *F. occidentalis* (Rugman-Jones et al., 2010), *T. tabaci* (Jacobson et al., 2016) and *F. schultzei* (Gikonyo et al., 2017). This situation confounds the analysis of host plant relationships because each cryptic species within a complex may well have its own specific host plant interactions. The inference of thrips movement between weed hosts and crops in cases where cryptic species may be present therefore also requires that the identity of the insects is confirmed by some means other than morphological identification alone.

In this study we quantified the relative importance of the major host species of *T. tabaci*, *F. occidentalis* and *F. schultzei* in the Namoi Valley, by sampling insects across various crop and weed species over a wide area. Specifically we aimed to determine (1) on which weeds and crops the different thrips species were found, (2) which host plants were the most important for reproduction of the thrips, (3) how the abundance of thrips was affected by the abundance of a particular host plant species, (4) how the species composition of the thrips complex, and the relative abundance of each species, changes with crop phenology, (5) how the abundance of thrips on weed or non-crop host plants was related to their abundance in cotton crops, and (6) the genetic relationships and species identity of thrips on cotton relative to those on weeds (by analysing mitochondrial CO1 gene sequences). This approach allowed us to assess the landscape level interactions of the three thrips species with confidence.

## 2. Materials and methods

### 2.1. Sampling sites and methods

A structured sampling program was conducted in the Namoi valley, near Narrabri, New South Wales, Australia. Sampling was conducted for two days in each of the following months: October and November 2011, February, August, October, November and December 2012, February, April, May, June, July, September and November 2013. Twelve sample sites (GPS coordinates see Suppdata Table 1) spread along a transect of about 35 km from east to west were selected across the Namoi valley and all sites were sampled on each sampling occasion. Each site contained a variety of different uncultivated native and introduced broad-leaf species (predominantly introduced weed species), native and introduced grass species, and five sites also had cultivated crops. The availability of plants changed across sampling events, with rainfall and other seasonal factors, as well as stage of the cropping cycle. At each site 10 samples of inflorescences and 10 samples of leaves (when leaves were small,  $\approx 20$  cm long sections of stems with associated leaves were collected) of each plant species available, including crops, were collected without bias. All the inflorescences from a given plant species were pooled and stored together in 70 ml vials with 100% ethanol, leaf samples were similarly pooled and stored together in ethanol. For some weed species it was not practical to separate inflorescences and leaves, so in these cases sections of stem ( $\approx 20$  cm long including leaves and flowers) were collected.

### 2.2. Thrips and plant identification

Thrips were extracted from plant material by vigorously shaking the storage vials. The ethanol and plant parts were then searched for thrips under a dissecting microscope. Larval thrips were separated from the adults for identification. Adults were initially sorted into suborder, Terebrantia or Tubulifera; Tubulifera were not processed further. In samples that contained more than 50 terebrantian larvae or adults, 10% of individuals were sub-sampled for identification. In samples that contained < 50 Terebrantia all individuals were identified. Individual adults and larvae were slide mounted and morphologically identified to species (Mound et al., 2014; Kirk, 1987; Milne et al., 1997). The number and stage of each thrips species associated with each sample was counted and recorded. All plant specimens were identified to species.

### 2.3. Seasonal abundance of potential host plants

On each sample date the abundance of each plant species at a given site was estimated visually and assigned a score based on percentage ground cover. This was achieved by observing plant species from the edge of each site and giving an abundance score (1–6) for each plant species present; 6, plant species present over > 60% ground cover; 5, present over 40–60%; 4, present over 20–40%; 3, present over 10–20%; 2, present over 5–10% and 1, present but less than 5%. To provide an accurate estimate of overall plant abundance for each site on a given date the total abundance across all hosts sampled was summed for each site. This accounted for both the abundance of each plant species and the number of plant species present. As all sites were on fertile black soils (Isbell, 1996) that support many plant species, we predicted that higher rainfall would support relatively larger numbers of species than would lower rainfall. Monthly rainfall data were obtained from the Australian Cotton Research Institute, which is located roughly central to the study sites. Total plant abundance was regressed against monthly rainfall; rainfall was offset by 1 month to allow for the delay in seed germination and plant growth following rain. The number of plant species recorded was regressed against total plant abundance for each sample site for each sample event.

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