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ORIGINAL CONTRIBUTION

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# Mediterranean fruit fly subplot hot spots prediction by experts' experience

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## Abstract

The Mediterranean fruit fly (medfly), *Ceratitis capitata* (Wiedemann), is a major pest, infesting hundreds of crop types. Since current field monitoring is mostly manual, understanding the spatiotemporal patterns of pest emergence at the fine scale can optimize precise trap placement and site-specific treatment activities, also within area wide integrated pest management projects. We carried out a three-year study in deciduous orchards in Israel, testing for the existence of subplot hot spots in which medfly populations display small-scale aggregations over consecutive seasons, beyond the expected spatial variability resulting from host type and ripening sequence. medfly population increase in these locations often preceded or was parallel to infestations in surrounding orchards, suggesting that hot spots can provide an important tool for effective prediction and control of pest emergence. We also examined the use of expert knowledge to predict hot spot locations and suggest a methodology for verifying them.

KEYWORDS
area wide IPM, expert knowledge, integrated pest management, medfly microscale aggregations, site-specific treatment, spatial variability

## 1 | INTRODUCTION

The Mediterranean fruit fly (medfly), *Ceratitis capitata* (Wiedemann), is ranked at the top of economically important fruit fly pests, infesting over 300 different species of fruits, citrus, vegetables and nuts (Papadopoulos, 2014; White & Elson-Harris, 1992). Due to its ability to tolerate cool climates and expand its habitat, export quarantine restrictions were developed to prevent further dispersion to regions where it is not yet present or has already been controlled, mostly in North America, Asia and Australia (Malacrida et al., 2007; Papadopoulos, 2014).

Medfly control targets range from eradication to suppression and maintaining its populations under an economic threshold (Suckling et al., 2014). The use of medfly Integrated Pest Management (IPM) practices increases continuously, and in recent years, area-wide IPM (AW-IPM) practices were developed, supporting also environmentally friendly techniques such as SIT (Sterile Insect Technique) and mass trapping which depend on large area application (Hendrichs, Kenmore, Robinson, & Vreysen, 2007). A major component of IPM projects is continuous monitoring of pest populations (Barzman et al., 2015) using traps; thus, optimizing trap location to improve detection of temporal and spatial trends is important in order to improve the efficacy of medfly control projects (Lance, 2014).

Medfly monitoring and control in the Mediterranean region are based upon understanding fly biology: its life cycle is normally completed within 25 to 35 days, there are several generations per year, and during the season, it moves to new fruit hosts as they ripen (Bodenheimer, 1951; Escudero-Colomar, Vilajeliu, & Batllori, 2008; Papadopoulos, 2014). Thus, efficient planning, implementation and evaluation of AW-IPM programmes require information on the spatiotemporal distribution of medfly population at the landscape level, in relation to host plants, geography and climate (Hendrichs et al., 2007; Midgarden, Lira, & Silver, 2014).

Various studies of medfly spatiotemporal dynamics have been carried out to evaluate the effects of landscape elements and host–plants on pest distribution, including the formation of hot spots (with high medfly aggregations) at the orchard scale (compared to their surroundings), which should potentially be the focus of monitoring and pesticide applications. These studies proposed that the abundance and distribution of host trees and availability of ripe fruit are the major factors determining medfly population growth and spatial dispersion patterns. In addition, spatiotemporal effects of other factors were also found, such as climate conditions (mostly temperature and wind) and environmental heterogeneity (Israely, Ziv, & Galun, 2005; Israely, Ziv, & Oman, 2005; Katsoyannos, Kouloussis, & Carey, 1998; Nestel et al., 2004; Papadopoulos, Katsoyannos, & Nestel, 2003; Pimentel, Lopes, Mexia, & Mumford, 2014; Sciarretta & Trematerra, 2011).

There is a long experience and practice of trap array planning according to predefined goals, factoring in also the effect of host trees and geographical conditions (International Atomic Energy Agency [IAEA], 2003; International Atomic Energy Agency [IAEA], 2013; California department of food and agriculture [CDFA], 2013; Meats, 2014; Midgarden et al., 2014). However, commonly traps are still placed at the orchard or grid (recommended distances between traps) level. In order to further optimize the time and effort-consuming practice of medfly field monitoring and even to promote more site-specific pesticide applications, there is a need for more accurate within-orchard trap placement.

We asked whether medfly trap placement can be fine-tuned by identifying subplot hot spots at the scale of a small cluster of trees. This scale is at a finer resolution than the previously studied existence of hot spots at the plot scale which relates to all trees of the same cultivar in an orchard as identical attractants of medfly, and it also differs from the known occurrence of individual exceptional trees (e.g., a different crop) that may be heavily infested. Both scales are affected by host species and ripening sequence. However, the causes of hot spot formation at a small cluster of trees level and the parameters that cause the formation of such precise hot spots are still not fully understood. Therefore, such fine-scale spatial distributions are currently almost impossible to foresee and require in situ studies for their detection (Van Helden, 2010). Since current understanding of medfly short distance dispersal and aggregation is mostly based on managed MRR (Mark-Release-Recapture) and caged trees studies, our study aimed to improve understanding of wild medfly aggregations in commercial field situations.

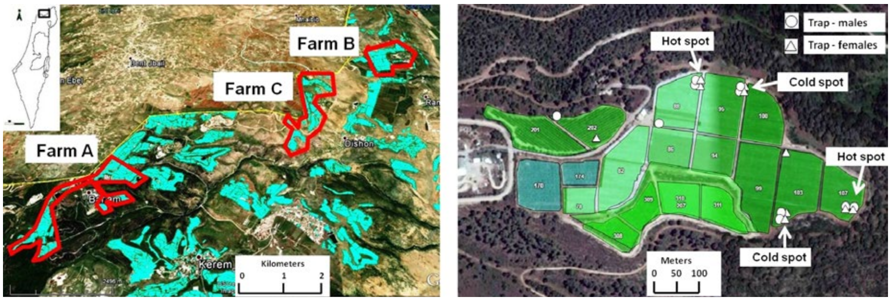
We asked whether small-scale hot spots can be characterized based on historical experience of growers and pest scouts, and then be verified for future reference. The study was located in northern Israel, where in recent years, most of the medfly control in deciduous orchards shifted to advanced AW-IPM, with regional management projects encompassing thousands of plots. This practice includes centrally managed online field monitoring, providing a vast database of trappings and an option to use standardized data for marking suspected subplot medfly hot spots. The goal of this study was to verify the repeatability and characteristics of suspected medfly hot spots and to develop a field methodology to verify them.

## 2 | MATERIALS AND METHODS

### 2.1 | Study area

The study sites are part of a regional medfly management programme in northern Israel, encompassing 7,000 ha of deciduous orchards. The project includes *ca.* 9,000 plots and *ca.* 750 growers. The average plot size is 0.8 ha. Field monitoring is performed according to a standard protocol by pest scouts who were trained by the project professional team. In 2014, about 65% and in 2015/2016, over 80% of the project plots were managed using mass trapping of various manufacturers based on synthetic food attractants, with around 100 traps per ha.

The study was undertaken in three cooperative farms ("Kibbutzim") in a mountainous area (Figure 1a), managed with mass trapping. Apples (*Pyrus malus*) are the main crop, in addition to pears (*Pyrus domestica*) and stone fruits—peaches/nectarines (*Prunus persica*), plums (*Prunus domestica*) and cherries (*Prunus avium*). In all farms, plots are arranged in clusters, surrounded by natural grassland and small Mediterranean maquis or isolated trees, mostly terebinths (*Pistacia palaestina*) and



**(a)** Case study areas **(b)** Partial view of farm A

**FIGURE 1** Maps of the study areas (delineated with black line on the map on Israel [top left]), the locations of the three farms (delineated with red line), and deciduous plots in northern Israel (in cyan) (1a) and a zooming to part of farm A, showing the locations of hot and cold spots and the routinely monitored traps, representing common dispersal also in the other sites (1b). White circle and triangle represent male and female traps, respectively [Colour figure can be viewed at wileyonlinelibrary.com]

**TABLE 1** Details of the study farms

| | Total farm area (ha) | | | | | Total number of traps | |
|---|---|---|---|---|---|---|---|
| Farm | Apples | Pears | Stone fruits[a] | Total | Altitude (m) | Males | Females |
| Farm A | 104 | 9.5 | 5.5 | 119 | 650-750 | 32 | 32 |
| Farm B | 49.5 | 27 | 9.5 | 86 | 400-450 | 22 | 23 |
| Farm C | 62.5 | | 12.5 | 75 | 650-700 | 21 | 17 |

[a] Farm A – peaches and nectarines; Farm B – plums; Farm C – nectarines, plums and cherries.

Palestine oaks (*Quercus calliprinos*). The three farms, further detailed in Table 1, are as follows:

1. Farm A—33$^0$03′N, 35$^0$26′E is partially surrounded also by pine (*Pinus*) plantations.
2. Farm B—33$^0$07′30′′N, 35$^0$33′E is partially surrounded also by fruit plots of other farms growing apples, pears and grapes (*Vitis vinifera*).
3. Farm C—33$^0$06′N, 35$^0$30′30′′E is partially surrounded also by Kiwi (*Actinidia chinensis*) plots which are not hosts of medfly (White & Elson-Harris, 1992; UF-IFAS (University of Florida, Institute of Food and Agricultural Sciences), 2017).

## 2.2 | Data collection

Medfly populations were continuously monitored in the project area using two trap types—Trimedlure para-pheromone baited Steiner (Gruvias, Israel) for males and Biolure food baited Tephri (Utiplast, Spain) for females. On average, one Steiner trap was positioned per 5 ha and one Tephri trap per 10 ha, considering also the crop types and landscape elements. In plots with several cultivars, the traps are set in the cultivar which is the earliest to ripen, such as "Golden" apples. Using the project database, historical data of 2012-2013 trapping and infestation level were used as the baseline for the study which started in 2014.

Suspected hot spots were marked based on historical experience of growers and pest scouts, as groups of a few trees in which infestation levels seemed higher, and/or were infested earlier in the season, compared with the other trees in the same plot and in similar neighbouring plots. In each suspected hot spot, two Steiner and two Tephri traps were positioned in a 4 × 3 metres array of two tree pairs in adjacent rows, with a 4-metre distance between rows and a 3-metre distance between trees in a row (Figure 1b).

In 2014, three suspected hot spots (HS) were marked and monitored in farm B and farm A, and two in farm C based on expert experience of local pest scouts and farmers. In 2015 and 2016, five suspected hot spots were marked in each study site according to updated expert advice, four of them in the same locations as in 2014 (two in farm A and two in farm C) following 2014 results and technical constraints of uncertainty regarding optional future uprooting in farm B. In 2016, two of the inspected plots were uprooted due to unexpected circumstances in farm B, and thus, three new hot spots were added and monitored instead. In farm A, two new hot spots were added in 2016 to the already monitored five. In addition, respective "cold spots" (CS) were marked in parallel to the hot spots in 2015 and 2016. These CSs were also selected based on local experts' experience, and they represent areas with normal medfly population and infestation (Figure 1b). In each cold spot, two Steiner and two Tephri traps were positioned in a 4 × 3 metres array similarly to the hot spots array. All cold spots were marked in areas with similar characteristics of the relevant hot spot such as altitude, soil and blend of cultivars, and location within the plot, such as distance from plot edges and other hosts. In farm B, the cold spots were marked in the same plots of the hot spots, in farm A in adjacent plots and in farm C in further distant plots.

All traps, including those positioned in hot and cold spots were examined on a weekly basis throughout the season. Medfly infestation was monitored by scouting ripe plots' entire area weekly and randomly sampling a minimum of 100 fruits in each plot every weekly visit. Field data were routinely uploaded to AgriTask online farm data management system (AgriTask, Israel), for real-time presentation to advisory staff and growers. Required data for this study were exported from AgriTask for further analysis.

## 2.3 | Data analysis

Trap counts were converted to FTD units (Flies per Trap per Day), and when needed square root transformed to homogenize the variance, and infestation counts converted to percentage of infected fruits. Statistical analysis was performed using JMP 10 (SAS Institute). Spatial analysis was performed with ArcGIS 10 (ESRI) and Surfer 12.5 (Golden software).

Analysis of suspected subplot hot spots was based in 2014 on comparing them to other traps in the neighbouring plots' cluster within a radius of about 250 m and to the entire farm. In 2015 and 2016, each subplot hot spot was compared to its respective cold spot, except for Farm C in which every hot spot was compared to the average of all of farm C's cold spots due to the selected trap placement methodology in this site.

The analysis focused on evaluating the continuity of medfly populations and infestation throughout the season stages and of similar stages through the years by comparing their FTD averages (annual weeks 20-25, 26-37 and 38-44). These three time intervals represent three distinct stages with distinct management implications: in the early season, if medfly population was low, only hot spots might be treated; during mid-season, higher attention should be given to the hot spots that are outside the areas of ripe fruit; hot spot monitoring during the end of season was mostly indicators of poor fruit sanitation.

Hot spot analysis in 2014 was performed by multigroup comparison in each study site of the hot spots to the surrounding traps in the near plots' cluster and entire farm using a single factor ANOVA, followed by post hoc Tukey HSD test. Hot spot analysis in 2015 and 2016 was performed by comparing the hot spots to their respective cold spots, using paired t tests of weekly FTD levels and assessment of medfly population rise vs. infestation patterns. The predictions were assessed by calculating the proportions of various factors, based on the understanding that since our method is focused at identifying only true and false positives, these proportions are identical to the precision of prediction (PPV-positive predictive value).

Assessment of repeatability between years was carried out using the proportion of HSs with repeated patterns in both years, which represents the precision of prediction in that respect. Further analysis of experts' prediction capabilities was performed using Matthews correlation coefficient, relating to patterns I and/or II in HSs and pattern III in CSs as positives.

In addition, spatial autocorrelation of medfly populations, during the entire season and during the week of first medfly population peak in 2013-2015, was tested using global Moran's *I* statistic. As the total number of male and female traps in farm B and farm C was lower than 30 in each study site (Table 1), the geographical area of these neighbouring farms was combined to meet Global Moran's *I* best practice requirements of minimal features number for a reliable spatial autocorrelation analysis. Medfly population spatial patterns were also modelled in 2014 using kriging interpolation.

## 3 | RESULTS

### 3.1 | Medfly temporal dynamics

On a multiyear basis, three major seasonal phases in medfly population temporal patterns were noticed in both genders: initial population rise with first available ripe fruits around early June, gradual increase along the July–September ripening period and a substantial increase at the season end and after harvest, especially in males (Figure 2). There were interannual variations, both in exact timing of the seasonal phases and levels, and in the relationship between timings of FTD rise and infestation, which was also variable.

### 3.2 | Hot spot analysis

The 2014 initial evaluation of suspected subplot hot spots (published in Mendelsohn et al., 2015) demonstrated non-consistent differences in population levels FTD between them and other traps in the same cluster of plots, as well as the entire farm; variations in the results were found both in terms of gender and between seasons. Based on the 2014 results, a significantly higher FTD during mid-season was set as an initial verification factor for a suspected HS. In total, four of eight suspected HSs could be verified in at least one of the medfly genders in 2014.

The relationship between FTD and infestation at hot and cold spots was classified into three general patterns as demonstrated in Figure 3: a peak in FTD (female or male) before first detection of infestation (pattern I); no earlier increase, but a peak in FTD in parallel to the first detection of infestation (pattern II); and no increase in FTD before or during first detection of infestation (pattern III). Patterns I

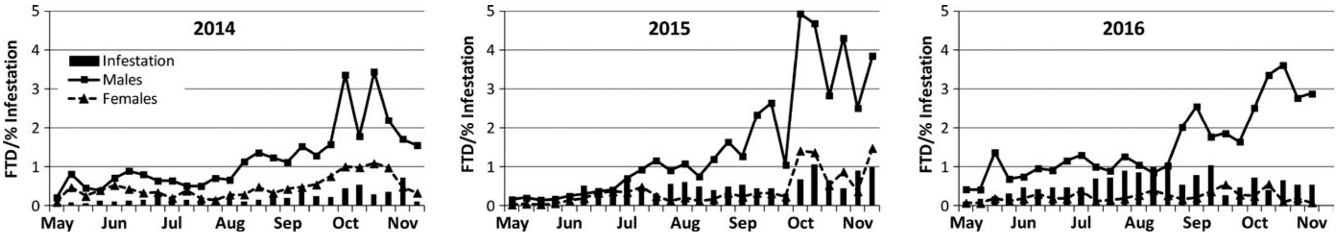


**FIGURE 2** Medfly trends temporal dynamics in 2014-2016—General average trapping (FTD—lines) and infestation rate (% of infested fruits—bars) including all the traps and plots in the study area

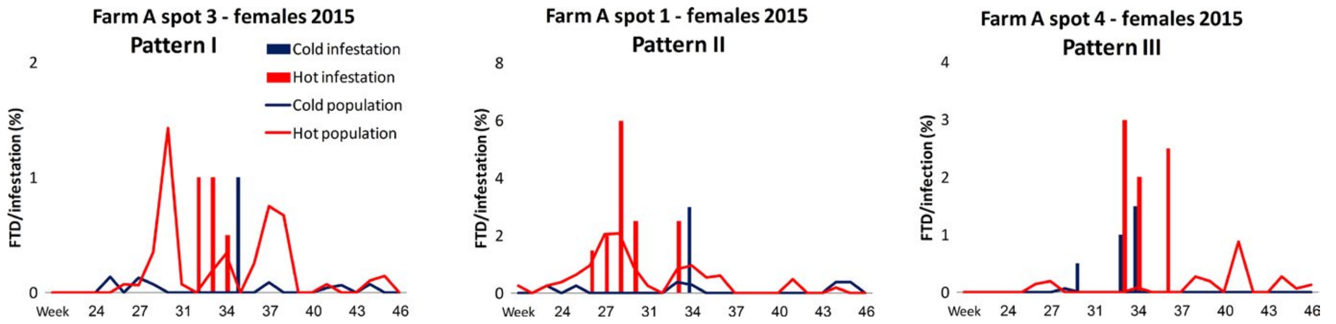


**FIGURE 3** Samples of three medfly female populations and infestation patterns in pairs of hot and cold spots in farm A in 2015 [Colour figure can be viewed at wileyonlinelibrary.com]

and II which can allow timely treatment will be named hereafter "effective patterns".

In 2015 and 2016, the majority of suspected hot spots in farms A and B had significantly higher FTD compared to the respective cold spots in at least one of the medfly genders in each trap array, except for Farm B in 2016 (Table 2). The proportion of patterns in the suspected hot spots was 85% for an effective pattern (I or II) and 58% for pattern I only for males, and for females only 55% for an effective pattern and 33% for pattern I only (Table 2). The proportion of patterns I and II was substantially lower in cold spots compared to hot spots, especially for females, except for male and female traps in farm C in 2016 (Table 2). In most cases, the proportion of effective patterns (I and II) was similar in both fractions of all HSs with higher FTD than the respective CSs (significant and not significant) and only locations with a significantly higher FTD, but in the case of pattern I only, the proportion was higher in the fraction of locations with only significantly higher FTD (Table 3).

No false-negative predictions of infestation by average mid-season FTD (higher male/female FTD in the respective cold spot but pattern I or II in the hot spot) were found in any of the cases (Figure 4). Only about a quarter of the cases, and none for Farm A males in 2015, were classified as false positive (higher male or

**TABLE 2** Summary of 2015 and 2016 results - Number of marked hot spots (HSs) in each farm, precision of prediction for verified (significant higher Flies per Trap per Day (FTD) in hotspot compared to respective coldspot) hot spots from at least one gender, and proportion of effective pattern (pattern I or II) and pattern I only for hot spots and coldspots (CSs)

| | | | Precision of prediction (PPV-positive prediction value) | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | Total | Male patterns | | | | Female patterns | | | |
| | | | | HSs | | CSs | | HSs | | CSs | |
| Year | Farm | Number of marked HSs | Verified HSs | I+II | I | I+II | I | I+II | I | I+II | I |
| 2015 | Farm A | 5 | 1.00 | 1.00 | 0.80 | 0.20 | 0.00 | 0.80 | 0.60 | 0.00 | 0.00 |
| | Farm B | 5 | 0.80 | 0.40 | 0.20 | 0.00 | 0.00 | 0.80 | 0.20 | 0.00 | 0.00 |
| | Farm C | 5 | NA | 0.80 | 0.40 | 0.40 | 0.00 | 0.80 | 0.20 | 0.20 | 0.00 |
| | Total | 15 | 0.90 | 0.73 | 0.47 | 0.20 | 0.00 | 0.80 | 0.33 | 0.07 | 0.00 |
| 2016 | Farm A | 7 | 0.86 | 0.86 | 0.57 | 0.29 | 0.29 | 0.43 | 0.14 | 0.00 | 0.00 |
| | Farm B | 6 | 0.33 | 1.00 | 0.67 | 0.17 | 0.17 | 0.17 | 0.17 | 0.00 | 0.00 |
| | Farm C | 5 | NA | 1.00 | 0.80 | 1.00 | 1.00 | 0.40 | 0.20 | 0.60 | 0.40 |
| | Total | 18 | 0.62 | 0.94 | 0.67 | 0.44 | 0.44 | 0.33 | 0.17 | 0.17 | 0.11 |
| Total | Farm A | 12 | 0.92 | 0.92 | 0.67 | 0.25 | 0.17 | 0.58 | 0.33 | 0.00 | 0.00 |
| | Farm B | 11 | 0.55 | 0.73 | 0.45 | 0.09 | 0.09 | 0.45 | 0.18 | 0.00 | 0.00 |
| | Farm C | 10 | NA | 0.90 | 0.60 | 0.70 | 0.50 | 0.60 | 0.20 | 0.40 | 0.20 |
| | Total | 33 | 0.74 | 0.85 | 0.58 | 0.33 | 0.24 | 0.55 | 0.33 | 0.12 | 0.06 |

**TABLE 3** Summary of 2015 and 2016 results – Proportions of hot spots (HSs) with higher and significantly higher Flies per Trap per Day (FTD) than their respective coldspot (CS) from all marked hot spots, and proportion of HSs with an effective pattern (I or II) and pattern I only within each fraction of higher or only significantly higher FTD

| | | Precision of prediction (PPV - positive prediction value) | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | 2015 | | | | | | 2016 | | | | | |
| | | FTD in HS higher than CS | | | FTD in HS significantly higher than CS | | | FTD in HS higher than CS | | | FTD in HS significantly higher than CS | | |
| | | | Pattern | | | Pattern | | | Pattern | | | Pattern | |
| Gender | Farm | HSs total | I+II | I | HSs total | I+II | I | HSs total | I+II | I | HSs total | I+II | I |
| Male | Farm A | 1.00 | 1.00 | 0.80 | 0.60 | 1.00 | 0.67 | 0.86 | 1.00 | 0.67 | 0.57 | 1.00 | 0.75 |
| | Farm B | 1.00 | 0.40 | 0.20 | 0.40 | 0.50 | 0.50 | 0.86 | 1.00 | 0.67 | 0.33 | 1.00 | 1.00 |
| | Total | 1.00 | 0.70 | 0.50 | 0.50 | 0.80 | 0.60 | 0.86 | 1.00 | 0.67 | 0.46 | 1.00 | 0.80 |
| Female | Farm A | 1.00 | 0.80 | 0.60 | 0.80 | 1.00 | 0.75 | 0.71 | 0.60 | 0.17 | 0.57 | 0.50 | 0.25 |
| | Farm B | 1.00 | 0.80 | 0.20 | 0.60 | 0.67 | 0.33 | 0.50 | 0.33 | 0.33 | 0.00 | NA | NA |
| | Total | 1.00 | 0.80 | 0.40 | 0.70 | 0.86 | 0.57 | 0.62 | 0.50 | 0.22 | 0.31 | 0.50 | 0.25 |

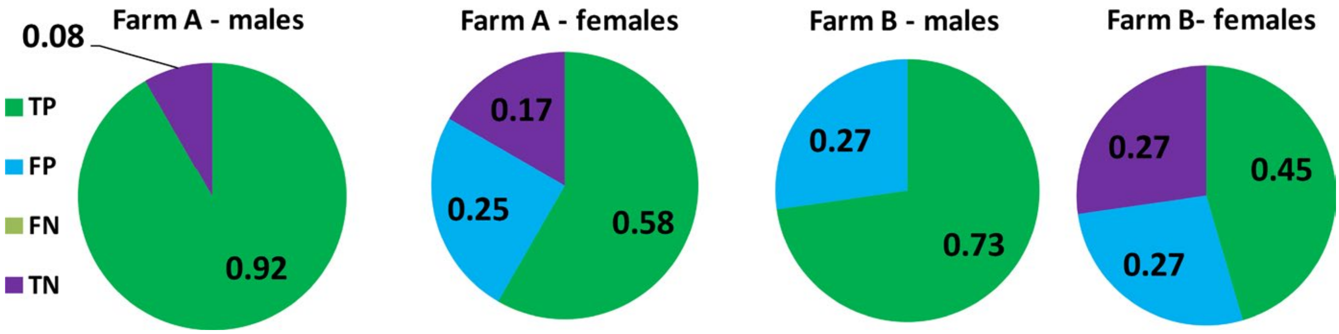


**FIGURE 4** Proportions of predictions in farm A and farm B aggregated male and female for 2015 and 2016: True positive (TP) with hot spot Flies per Trap per Day (FTD) higher than cold spot and an effective pattern; True negative (TN) with hot spot FTD lower or equal to cold spot and a type III pattern; False positive (FP)—with HS FTD higher than cold spot and a type III pattern; False negative (FN)—with hot spot FTD lower or equal to cold spot and an effective pattern [Colour figure can be viewed at wileyonlinelibrary.com]

**TABLE 4** Matthews correlation efficient of male and female patterns, relating to patterns I and/or II in HSs and pattern III in CSs as positives

| | Matthews correlation coefficient | | | |
|---|---|---|---|---|
| | Male patterns | | Female patterns | |
| Farm | I+II | I | I+II | I |
| Farm A | 0.68 | 0.51 | 0.64 | 0.45 |
| Farm B | 0.65 | 0.41 | 0.54 | 0.32 |
| Farm C | 0.25 | 0.10 | 0.20 | −0.60 |
| Total | 0.52 | 0.34 | 0.45 | 0.24 |

female FTD in the hot spots, including non-significant differences, and pattern III).

Assessment of repeatability between years demonstrated that of the HSs classified to effective patterns (I or II) in 2015, nine of 10 (90%) for male and four of 10 (40%) for female retained one of these patterns also in 2016 (Tables S1-S3). In only part of all cases (10 of 15 in 2015 and five of 18 in 2016), males and females had both effective (I or II) or non-effective (III) patterns (Tables S1-S3).

Further analysis of experts' prediction capabilities using Matthew's correlation coefficient (Table 4) demonstrated relatively strong positive relation (0.41-0.69) for farms A and B, except for pattern I for females in farm B. The low values for farm C, which affect also the overall values, can be partly explained by the high proportion of patterns I and II in the CSs, especially in 2016 (Table 3).

## 3.3 | Medfly spatial patterns

Large-scale spatial autocorrelation analysis of medfly population in the entire season and the peak week in the study sites for 2013-2015 showed very low spatial correlation (Global Moran's *I* close to zero) and no aggregation, as summarized in Table 5. All results, except for seasonal female dispersal in the combined Farms B and C, showed random dispersal. However, when analysing the only mid-season female FTD averages in farms B and C, the results showed random dispersal.

# 4 | DISCUSSION

We analysed suspected medfly hot spots at the resolution of several trees in deciduous orchards plots, identified based on expert experience, by comparing them to nearby control spots with similar characteristics for two consecutive years. The results showed a large percentage of higher medfly populations in the suspected hot spots, and also a substantially higher ratio of increase in medfly populations before or parallel to infestation, with no false-negative results. These

**TABLE 5** Global Moran's *I* autocorrelation analysis of Flies per Trap per Day (FTD) in all farms in three stages of the season

| | Males | | Females | | |
|---|---|---|---|---|---|
| Farms | Peak week | Seasonal average | Peak week | Seasonal average | Mid season average |
| Farm A 2013 | −0.154 | 0.181 | −0.041 | 0.085 | |
| Farm A 2014 | −0.034 | −0.035 | −0.067 | −0.009 | |
| Farm A 2015 | −0.117 | 0.188 | −0.006 | 0.029 | |
| Farms B+C 2013 | 0.058 | 0.023 | −0.021 | 0.391* | 0.099 |
| Farms B+C 2014 | 0.138 | 0.067 | −0.045 | 0.252* | −0.015 |
| Farms B+C 2015 | 0.119 | 0.027 | 0.024 | 0.004* | −0.012 |

Results with * have significant aggregation ($p < .05$).

results were more evident for medfly males, and in the majority of cases were repeated along 2 years.

In Israel, as in other countries in the Mediterranean region, medfly eradication is considered impractical, and the control policy is based on suppression and maintaining medfly populations and infestation levels below an economic threshold. Thus, in Israel, the majority of the host orchards are already managed under large-scale AW-IPM projects.

The study sites, like most of the project plots, are managed mostly by mass trapping, but there may still be a need for occasional complementary ground spraying. Minimizing ground spraying is preferred, and deeper understanding of local medfly spatiotemporal dynamics is necessary for high-resolution mapping of medfly presence and infestation risk as support for more precise decision-making.

A major part of the field data necessary for formulating spraying decisions is gathered weekly by manual trap monitoring as the most common, fast and cost-effective method for medfly population monitoring. It also requires lower pest scouts' expertise compared with field detection of infestation. Our goal in this study was to improve the resolution and optimization of trap placement beyond targeting of plots with ripe hosts in general, by specifically identifying early and/or highly infested locations within the ripening orchards, preferably at the level of small groups of trees.

According to field data collected in recent years, first medfly adults are usually trapped in the study area after overwintering at the end of April. Their annual temporal dynamics in the study area (Figure 2) matched the known medfly biology that follows fruit ripening sequence and development of new generations during the season, with some differences between years in timing and population levels due to environmental factors, mostly climate conditions. There was a relationship between male and female populations, with a higher increase in male populations at the end of season, although lower female trappings may be also due to the different types of attractants in the traps. There was not always an immediate relationship between timings of medfly population rise and infestation level increase which may serve as an important factor for decision support (Figure 2), as demonstrated also by other works (Pimentel, Lopes, Mexia, & Mumford, 2017).

In terms of large-scale spatiotemporal trend dynamics, we observed large variations in medfly population size between the different study sites, although they are in the same region and grow a similar variety of crops. It was also modelled by us in 2014 using interpolation of medfly population spatial patterns (kriging) throughout the season, presenting a variable pattern with formation of large-scale temporary hot spots (Mendelsohn et al., 2015). In this study, we found also that medfly population presented a random dispersal in the studied farms (Table 5).

These large-scale random and the variable medfly spatiotemporal population dynamics highlight the need to further formulate a methodology to locate and verify small-scale medfly concentrations beyond those expected from host variations and topography. In addition, the random dispersal also demonstrates that attracting medfly adults by traps did not affect natural dispersal.

The large-scale spatiotemporal variation depends on the combined effects of plant phenology, local climate, pest behaviour, population dynamics and farmers' activities (Van Helden, 2010). Alternating periods of clumped and random patterns have also been observed to be recurrent for medfly and other pests (Sciarretta & Trematerra, 2014). Due to cross-pollination and marketing requirements, in Israel, there are frequently a few cultivars of the same species in the same plot, especially in pome fruits, leading to even greater variability and a long alternating ripening period of a few months even in a single plot. The wide variety of host species and ripe fruit availability also affects medfly adult dispersal, which can reach long distances of 1-1.3 km (Gavriel, Gazit, Leach, Mumford, & Yuval, 2012; Meats & Smallridge, 2007; Navarro-Llopis, Vacas, Zarzo, & Primo, 2014).

Initial uncertainty regarding existence of subplot hot spots and their parameters required a simple and cost-effective methodology for their identification and verification, and different evaluation methods were examined in this study. The first stage of this study, carried out in 2014, compared suspected hot spots to their surrounding plots' cluster and to the entire farm, verifying half of them to be hot spots. It also demonstrated that hot spots may be active only during a certain part of the season and may be significant only locally compared with the near plots and not in comparison with the entire farm. Considering the multi-annual variability in timing of fruit ripening and medfly population and infestation trends (Figure 2), we selected to focus on the fixed mid-season period of weeks 26-37 (late June-mid September) as the time frame for verification.

Following the initial validation of the subplot hot spot concept in 2014, the locations of suspected hot spots were reassessed in 2015. Additionally, a new, simpler and more precise evaluation methodology was implemented. We compared suspected hot spots to similar traps in a nearby location representing the plot in general as a control (termed cold spot), and this way we avoided the high variability of heterogenic plots clusters. The 2015 and 2016 results demonstrated again variability in hot spots activity along the season, but verified most of the hot spots (Tables 2-3) in farm A and farm B for at least one of the medfly genders; due to the placement method, we could not technically verify them also in farm C.

The repeatability of results over 2 years in many of the locations further supports the concept of subplot hot spots as a recurrent phenomenon. At the same time, the level of prediction's precision and correlation (Tables 2-4) was different between study sites; this difference may be explained by variability between pest scouts and farmers' expertise and experience in locating suspected hot spots, or by the fact that in farm A the cold spots were located in an adjacent plot while in farm B mostly in the same plot as the hot spots. This should be further studied with more data.

Relationship between increase in medfly population and first detection of infestation is important for decision support, and in this study, we analysed the population/infestation patterns to find out whether hot spots demonstrate also better correlation in that respect. An increase in medfly populations before detection of infestation (pattern I) allows implementation of preventive control measures; an increase in medfly populations parallel to first infestation (pattern II) can also assist in medfly control decisions, especially by allowing more focused infestation field monitoring. The results demonstrated substantially higher percentage of hot spots with effective pattern (I or

II), especially in males, compared with the cold spots (as controls) in which we found a high percentage of pattern III (Tables 2-3). In that respect, non-existence of false-negative correlations and low percentage of false positives in hot spots also demonstrate the efficacy of the methodology (Figure 4).

The explanation of the phenomenon of hot spots in medfly populations at the subplot level can be attributed to various small-scale factors such as microclimate, exposure to other hosts, and higher vigour or early fruit maturation in specific trees. It may also reflect the individual fly foraging behaviour, and local dispersal of essential resources for medfly adults such as food, mating sites, mating partners, oviposition sites and refugia (Papadopoulos, Kouloussis, & Katsoyannos, 2006).

There may also be differences between the two sexes because of their different ecological and behavioural needs (Papadopoulos et al., 2006). Both sexes exhibit an aggregated distribution pattern in deciduous orchards. While in females it is tightly related to host fruit availability and maturity which are mostly relevant at the plot scale, in males, it is not necessarily closely related to these factors and can differ from that of females in various times of the season (Papadopoulos et al., 2003).

Subplot hot spots may be related to patchy large-scale lek formation, which can form male aggregations at the scale of a few trees and may also indirectly affect female distribution through attraction to the male sex pheromone. The higher number of verified hot spots based on male trapping and their higher correlation with infestation in the study (Tables 2-3, Figure 4) support the hypothesis that males contribute more to formation of subplot hot spots.

A combination of ecological factors was suggested to drive medfly male mating activity, first away from host fruit and second to become concentrated in certain trees within the habitat. Such ecological factors were suggested to form a composite predation and hot spot effect, modulated by microclimate preferences in habitat selection, such as trees with denser canopies that provide better shade and shelter (Field, Kaspi, & Yuval, 2002). Medfly male spatial distribution might often be affected also by plant volatiles, especially the male attractant terpene α-copaene (Juan-Blasco et al., 2013; Quilici, Atiama-Nurbel, & Brévault, 2014; Shelly, 2001), which can demonstrate high variability both between individual trees and even within trunk and branches of specific trees (Shelly & Villalobos, 2004).

## 5 | CONCLUSIONS

This study provides the first support to the concept of locating subplot medfly hot spots, and using them to optimize medfly trap placement. In addition, the relationship between trapping at subplot hot spots and infestation, especially for males, further demonstrates the advantage of using fewer traps in verified hot spots for decision support in medfly control.

In addition, the study demonstrated a potential verification methodology, based on comparing data from the suspected hot spot to a respective nearby cold spot. It also demonstrated the potential of expert knowledge, which was not tested methodically to date, to be a useful practice in locating subplot hot spots. This still requires more study due to the variability in results between the study sites, which may be due to variability in pest scout experience and hot spots prediction capabilities.

At the next stage, evaluation should also focus on better understanding of hot spot characteristics, to improve prediction and verification, such as analysis of volatiles (like α-copaene) levels, canopy characteristics and ripe fruit properties. Identifying the characteristics of subplot hot spots and the reasons for their formation may allow developing technical solutions, such as fruits and volatile field sensing and automated traps for optimization of manual monitoring.

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## AUTHOR CONTRIBUTION

SA, MS and OM designed experiments and study. SA, MS and VO conducted field work. OM, LB, VO and TD analysed the data. OM wrote the manuscript. All authors read and approved the manuscript.

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