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Preliminary study on micro area based spatial distribution of *Monilinia fructigena* in an organic apple orchard

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Summary: In this study, we aimed to report a preliminary study on micro area based spatial distribution of *Monilinia fructigena* in an organic apple orchard. Results showed that number of symptomatic fruit ranged between 22 and 42 in 2013 and between 25 and 35 in 2014. Number of asymptomatic fruit ranged between 111 and 187 in 2013 and between 119 and 167 in 2014. Disease incidence of fruit ranged between 19.7 and 23.2% in 2013 and between 19.1 and 26.5% in 2014. Disease aggregation index ranged between 0.111 and 0.335 in 2013 and between 123 and 401 in 2014. Three of the four trees showed significant within canopy aggregation of disease for fruit brown rot symptoms in both years. However, the remaining one tree exhibited random patterns during both years. Disease aggregation indicated a disease spread by fruit-to-fruit contact and/or an aggregated pattern of insect damage.

Keywords: *Monilinia fructigena*, spatial pattern, organic apple

Introduction

Spatial aspects of brown rot development in fruit orchards have received considerably less attention than temporal dynamics. Two-dimensional spatial patterns have been investigated by van Leeuwen *et al.* (2000) and Xu *et al.* (2001) in pome fruits. In general, these studies showed that infected trees were spatially clustered within orchard rows, with variable intensity of disease among individual trees. Although spatial patterns were more pronounced in pear (*Pyrus communis*) than in apple (*Malus domestica*) orchards, wounding of the fruit by birds, insect damage or growth cracks was considered an influential source of the spatial pattern in both species. In a separate study, Elmer et al. (1998) examined the two-dimensional spatial pattern of *Monilinia fructicola* strains resistant to dicarboximide fungicide in peach and nectarine orchards, reporting that resistant strains were mostly restricted to individual trees with no spatio-temporal correlations from year to year of trees harbouring resistant strains.

Previous studies examining spatial disease patterns within tree canopies either divided the canopy into layers (Holb and Scherm, 2007) or quadrats (Batzer *et al.*, 2008; Spósito *et al.,* 2008). However, an important limitation of using such stratification is that the associated grouping of data may fail to capture fine-scale patterns within each block. In a recent pilot study, Everhart *et al.* (2011) used a digitizer to map different brown rot symptom types (blossom blight, shoot blight, and twig cankers) caused by the fungal plant pathogen *M. laxa* in individual sour cherry canopies.

In this study, we aimed to report a preliminary study on micro area based spatial distribution of *M. fructigena* in an organic apple orchard.

Materials and methods

Orchard site

The experiment was carried out in an organic orchard located at Eperjeske, Hungary. The orchard was planted with cultivars Mutsu, Jonathan, Prima on M26 rootstocks in 1997. The distance between rows was 5 m, and the distance between trees within a row was 2. The orchard was treated according to the Hungarian Organic Growing Guidelines derived from the IFOAM guidelines. The micro-area based spatial experiment was set in 2013 and 2014.

Assessment of spatial pattern of symptoms

At harvest, fruit symptom caused by *M. fructigena* was present and readily distinguishable. Four trees (Table 1) of different sizes and with varying levels of disease incidence were selected for digitizing. The x, y and z co-ordinates of all symptomatic elements were digitized, as were all asymptomatic (healthy) fruit (Table 1). Each digitized canopy element was tagged with coloured tape to ensure that points were not measured twice and that no relevant point was omitted. Disease incidence of fruit was also measured also for each tree.

Spatial pattern analysis

Spatial patterns of aggregation for fruit symptom within the canopy were characterized based on nearest neighbour distances, i.e. the shortest Euclidian distance between

symptoms derived from the x, y and z co-ordinates of points. The frequency distribution of nearest-neighbour distances within each tree could then be used to determine deviation from randomness.

Disease aggregation index (dw) was also determined. The test statistic dw, the maximum departure of the observed cumulative frequency distribution. Values of dw represents the index of disease aggregation and is calculated based on the cumulative frequency distribution of nearest-neighbour distances among brown rot-affected fruit. Significant positive values indicate aggregation, whereas significant negative values correspond to a more regular distribution compared with the random simulation.

Results

Disease pattern

The range of the data point was between 133 and 229 in 2013 and between 146 and 199 in 2014 for the four digitized trees (Table 1). Number of symptomatic fruit ranged between 22 and 42 in 2013 and between 25 and 35 in 2014. Number of asymptomatic fruit ranged between 111 and 187 in 2013 and between 119 and 167 in 2014. Disease incidence of fruit ranged between 19.7 and 23.2% in 2013 and between 19.1 and 26.5% in 2014.

Table 1. Summary of symptomatic patterns and fruit disease incidence of brown rot on 4 apple trees within the tree canopy (Eperjeske 2013 and 2014)

No of tree	No of symptomatic fruit	No asymptomatic fruit	Disease incidence (%)
2013			
I	34	146	23.2
II	31	157	19.7
III	42	187	22.4
III	22	111	19.8
2014			
I	35	132	26.5
II	32	167	19.1
III	25	124	20.1
IV	27	119	22.7

Disease aggregation

Disease aggregation index ranged between 0.111 and 0.335 in 2013 and between 0.123 and 0.401 in 2014 (Table 2). Three of the four trees showed significant within canopy aggregation of disease for fruit brown rot symptoms in both years (Table 2). However, the remaining one tree exhibited random patterns during both years.

Table 2. Summary of disease agrregation index and spatial patterns for brown rot symptoms on 4 apple trees within the tree canopy (Eperjeske 2013 and 2014)

No of tree	Disease aggregation index (dw)	P value	Spatial pattern
2013			
I	0.298	0.022	aggregated
II	0.231	0.044	aggregated
III	0.335	0.008	aggregated
IV	0.111	0.234	random
2014			
I	0.401	0.003	aggregated
II	0.356	0.005	aggregated
III	0.123	0.119	random
IV	0.279	0.028	aggregated

dw represents the index of disease aggregation and is calculated based on the cumulative frequency distribution of nearest-neighbour distances among brown rot-affected fruit. Significant positive values indicate aggregation, whereas significant negative values correspond to a more regular distribution compared with the random simulation. Significant dw values ($P \leq 0.05$) are in bold.

Conclusions

Spatial disease incidence caused by *M. fructigena* is high (around 20%) in organic apple orchard which are due to high frequency of insect damage in these orchards. Most diseased fruit are aggregated within the tree which indicate a disease spread by fruit-to-fruit contact and/or an aggregated pattern of insect damage.

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