

Biotic resistance and the spatiotemporal distribution of an invading woodwasp, *Sirex noctilio*

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Abstract Quantifying the strength of interactions among introduced and native species across space and time is critical in understanding biological invasions as they can attenuate or amplify the magnitude of impact. The European woodwasp, *Sirex noctilio* F., a global threat to pines, is a recent invader to North America. It attacks and kills primarily *Pinus resinosa* and *Pinus sylvestris*, and encounters a diverse assemblage of potential competitors for this resource. We quantified spatial colonization patterns of this woodwasp and resident competitors including scolytine bark beetles, woodboring cerambycid and buprestid beetles, and the fungal root rot diseases *Armillaria* and *Heterobasidion* across an 80 year old pine plantation over 4 years. All xylophages were spatially aggregated, but only on a localized scale of 15–20 m. Colonizers occurred non-randomly within trees, with *S. noctilio* negatively or neutrally associated with all other colonizing agents, whereas all other insect and root rot colonizers were mostly positively co-

associated. An autologistic regression with spatially-weighted variables indicated the probability of a dead tree exhibiting symptoms of *S. noctilio* attack was positively associated with tree density, host species (*P. sylvestris*), and density of *S. noctilio*-attacked trees from the current and previous year. Interspecific stand patterns were weaker; probability of attack was negatively associated only with root rot pathogens. Across spatial scales, there were mixed (woodborers) and neutral (bark beetles) associations between *S. noctilio* and other co-colonizing insects. Our results suggest that competitive interactions with resident species may be contributing to the limited success of *S. noctilio* in North America, but are unlikely to be driving it by themselves.

Keywords Aggregation · Auto- and cross-correlation · Autologistic regression · Non native insect · *Pinus*

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Introduction

A poorly understood component of invasion biology is the interaction among invaders and native biota, particularly across space and time (Denno et al. 1995; Niemelä and Mattson 1996; Keane and Crawley 2002; Parker and Hay 2005; Carlsson et al. 2009). Collectively, the role native species play in impeding establishment and spread of an invasive species is

termed biotic resistance (Elton 1958). While extensive research has focused on biotic resistance of native plants to invaders in plant communities, relatively few studies have looked at other organisms. Competitive biotic resistance, in particular, is poorly represented in studies of non-plant invasions.

Among bark and woodboring insects, direct or indirect interspecific competition can drive distribution, abundance, and population dynamics (Graham 1925; Coulson et al. 1976; Light et al. 1983; Miller 1986; Rankin and Borden 1991; Hofstetter et al. 2005; Davis and Hofstetter 2009). These interactions are often asymmetrical and can be mediated by biotic and abiotic factors, such as plant host, microbial associates, natural enemies, disturbance, and climate (Price et al. 1980, 1986; Paine et al. 1981; McClure 1984; Denno et al. 2000; Erbilgin and Raffa 2000; Aukema et al. 2004). For primary tree-attacking insects, co-colonization with heterospecifics can exert negative feedback via competition for resources or intraguild predation (Coulson et al. 1976; Rankin and Borden 1991; Schlyter and Anderbrant 1993; Schroeder and Weslien 1994; Dodds et al. 2001; Aukema et al. 2010).

In 2005, *Sirex noctilio* F. (Hymenoptera: Siricidae), the European woodwasp, was identified from a 2004 survey trap in central New York State, USA (Hoebeke et al. 2005). Discovery of this non-native insect was of particular concern because of its history as a devastating introduced pest in plantations of North American pine across the Southern Hemisphere (Madden 1988; Slippers et al. 2015). Female *S. noctilio* inoculate hosts with phytotoxic mucus and a mutualist fungus, *Amylostereum areolatum*, both of which aid in weakening and killing trees (Coutts 1969a, b). Developing larvae are dependent upon *A. areolatum* as a nutritional substrate, extracting nutrients from colonized tissue and cellulases produced by the fungus that facilitate xylem digestion (Francke-Grosman 1939; Parkin 1941; Buchner 1965; Thompson et al. 2012).

Confounding early predictions, *S. noctilio* has caused limited tree mortality in North America, with successful attacks restricted primarily to suppressed *Pinus resinosa*, a native pine, and *Pinus sylvestris*, a naturalized pine from Europe (Dodds et al. 2010; Ayres et al. 2014). A diverse guild of native parasitoids have readily adopted *S. noctilio* as a host since its advent in North America (Long et al. 2009; Eager et al. 2011; Standley et al. 2012; Ryan et al. 2012b; Foelker et al. 2016a). However, levels of

parasitism exhibit large spatial and temporal variations, as do the component members of this guild attacking *S. noctilio* (Foelker et al. 2016b; Haavik et al. 2016). While not definitive, inconsistent and often relatively low levels of overall parasitism suggest that by themselves, parasitoids are not acting as a strong regulating force limiting the success of this invader.

In North America, unlike anywhere else in its invaded range, *S. noctilio* has encountered a large assemblage of native co-colonizing insects associated with *Pinus* spp. (Graham 1925; Savely 1939; Erbilgin et al. 2002; Dodds et al. 2012). Unfortunately, relationships between *S. noctilio* and competing insects are largely uninvestigated in its native range in Europe due to its lack of economic importance, whereas these interactions are absent entirely in the Southern Hemisphere. Thus, an understanding of these multipartite species interactions is lacking, even though they may be a significant driver of the invasion ecology of *S. noctilio* in North America.

The suite of pine colonizers is extensive in eastern North America. *Ips pini* (Coleoptera: Curculionidae) is the most prevalent of a large contingent of scolytines that colonize all portions of the tree (Ayres et al. 2001) and are active across a wide temporal window that extends into early fall (Aukema et al. 2004). In addition, multiple woodboring beetles (Cerambycidae) feed deep in the xylem tissue (Erbilgin and Raffa 2002; Erbilgin et al. 2002) and can even facultatively feed on *S. noctilio* as larvae (Thompson 2013). Adding to the complexity, interactions among *S. noctilio*, bark beetles, and woodborers are likely indirect, mediated through their respective fungal associates (Hurley et al. 2012; Ryan et al. 2012a; Yousuf et al. 2014a). This array of competitors may be more analogous to what *S. noctilio* encounters in its native range in Eurasia and North Africa where it is largely a secondary mortality agent (Chrystal and Myers 1928; Spradbery and Kirk 1978; Ayres et al. 2014).

While spatiotemporal attack patterns of *S. noctilio* have been described for some invaded regions of the Southern Hemisphere (Tribe and Cillie 2004; Corley et al. 2007; Corley and Villacide 2012; Lantschner and Corley 2015), analysis of dispersal and colonization is lacking for North American populations. Though *S. noctilio* is a large robust insect, it is suggested that long distance dispersal is fairly limited, as these events present a substantial risk for these insects (Corley et al.

2007; Corley and Villacide 2012). Generally, dispersal by insects in forest settings is influenced by predation risk, parasites, energetic reserves, and abundance/quality of host material (Capinera and Barbosa 1976; Barbosa et al. 1981; Villacide and Corley 2008). Empirical and theoretical work indicate a majority of bark and woodboring insects are located in close proximity to their emergence site and only a small proportion actually fulfill their full dispersal potential (Raffa and Berryman 1980; Safranyik et al. 1992; Turchin and Thoeny 1993; Cronin et al. 2000; Smith et al. 2001; Corley et al. 2007).

Here, we investigate stand-level colonization patterns of *S. noctilio*, co-occurring bark and woodboring insects, and root rot disease fungi at a *P. resinosa* and *P. sylvestris* plantation in New York State from 2011 to 2014. Planted stands of similar composition and age are ubiquitous across the Northeastern USA and indeed, appear to represent the majority of habitat occupied by *S. noctilio* since its arrival (Dodds et al. 2010). We specifically investigated the independent distributions and aggregation patterns of five typical and prominent colonizing agents to pine mortality in the region: bark beetles (Coleoptera: Curculionidae: Scolytinae), woodborers (Coleoptera: Cerambycidae and Coleoptera: Buprestidae), Armillaria root disease, Annosum root disease, and *S. noctilio*. Our main objectives were to explore: (a) patterns of aggregation, (b) co-occurrence within trees, and (c) spatiotemporal patterns of *S. noctilio* attack in relation to density of co-colonists (both current and previous year) and to other stand-level factors.

Methods

Pack Demonstration Forest (43.549753°N, -73.821885°W), near Warrensburg, NY in the southeastern corner of the Adirondack Park, is comprised primarily of 80–90 year old *P. resinosa*, *P. sylvestris*, and *P. strobus* plantations. The 48.5 ha site was historically used for soil nutrients and silviculture research in the 1940–1950s, but has not been thinned for over 30 yr (Buxbaum et al. 2005). We conducted a full stand census of all *P. resinosa* and *P. sylvestris* compartments in late summer from 2012 to 2014 (15 Aug–30 Aug 2012, 25 Aug–5 Sep 2013, and 25 Aug–5 Sep 2014). We marked all dead/dying trees from the previous summer using a handheld GPS (Garmin Rino

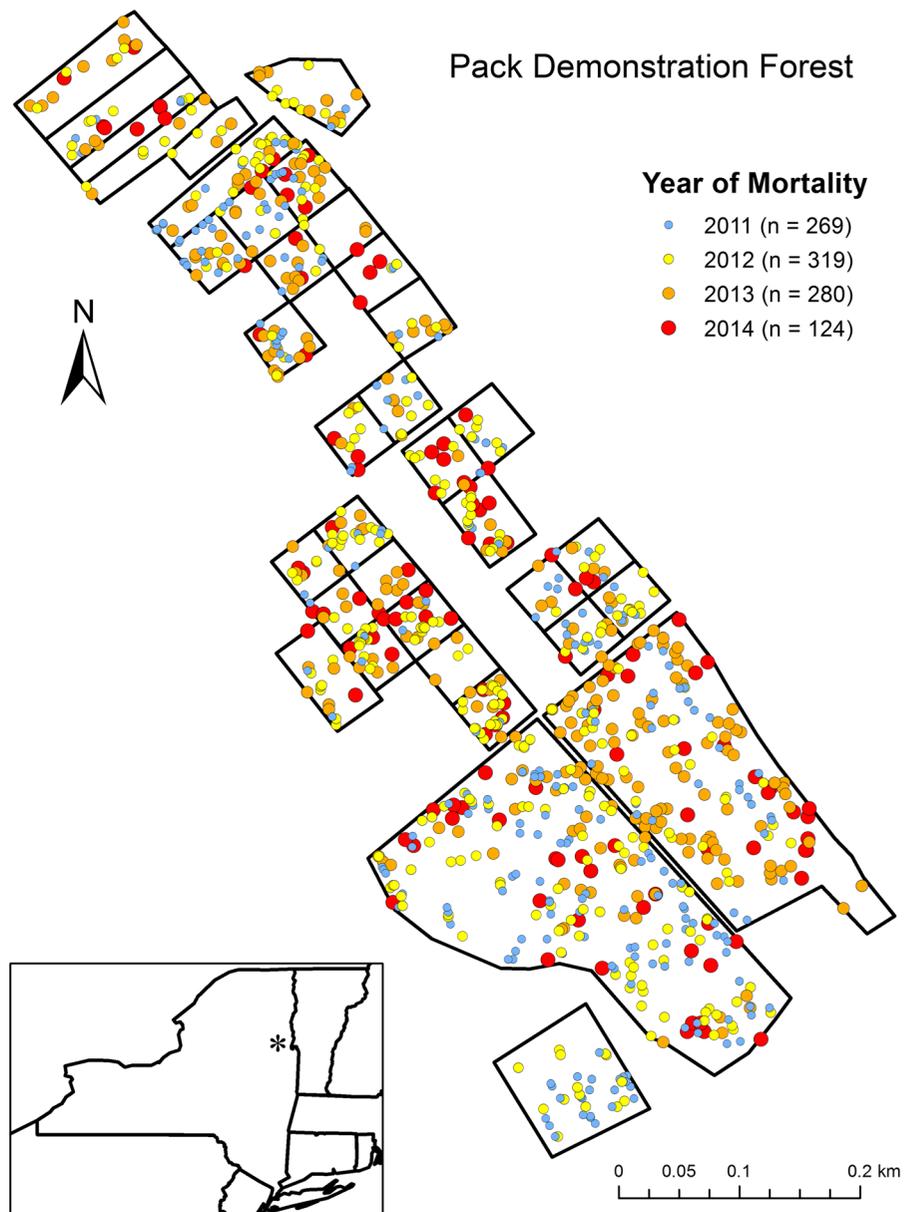
520HCx; accuracy < 3 m), recorded DBH and species (*P. resinosa* or *P. sylvestris*), and established boundaries for all compartments using GPS coordinates (Fig. 1).

Chronology of *S. noctilio* colonization can be reconstructed reliably for the current and previous attack year based on two diagnostic features: resin beads and exit holes. Siricid exit holes are distinguishable from other woodborers as they are circular, angled perpendicular to the direction of the main bole, and are usually clustered together in groups of 10–20 (Ayres et al. 2014). *Sirex noctilio* exit holes and resin beads are indistinguishable from those of native siricids. However, native siricids are much less abundant than *S. noctilio* in attacked trees (Eager et al. 2011; Ryan et al. 2012b; Foelker et al. 2016b).

We recorded visual evidence (exit holes and frass) of insect co-colonizers along the lower 3 m of the tree as either being from woodborers and/or bark beetles and confirmed observations by removing the outer bark. Prevalent bark beetles were *I. pini*, *Tomicus piniperda* (a non-native European species), and *Dendroctonus valens*.

We also inspected the root collar for presence of two ecologically and economically important root rot diseases, Armillaria and Annosum. There is a lack of taxonomic consensus on the causal agents of these diseases in North America, at least at the species level (Ross-Davis et al. 2011; Garbelotto and Gonthier 2013), so we hereafter refer to each as *Armillaria* sp. (Basidiomycota: Agaricales) and *Heterobasidion irregulare* sensu lato (s.l.) (Basidiomycota: Russulales). Bark was peeled at three equidistant points along the perimeter of the root collar to a depth of ~ 30 cm. *Armillaria* sp. was identified via presence of thick white mycelial fans or black rhizomorphs (Omdal et al. 2004; Bendel and Rigling 2008). *Heterobasidion irregulare* s.l. was diagnosed using fruiting bodies, but also by the presence of a paper-thin mycelium with pustules, lamination (separation of the growth rings), and pitting (spotted bleaching of the wood caused by oxidation) (Omdal et al. 2004; Bendel and Rigling 2008; Garbelotto and Gonthier 2013). Dead trees in known areas of root rot disease, particularly *H. irregulare* s.l., were checked the following year for signs because fruiting bodies are often not present during the year of mortality (Woodard et al. 1998). We collected binary data (yes/no) for each dead tree on the presence of each of

Fig. 1 All stand compartments containing *P. sylvestris* or *P. resinosa* dead trees ($n = 992$) recorded from 2011 to 2014 at Pack Demonstration Forest in the Adirondack Park of New York State



these five colonizing agents and allowed for multiple agents simultaneously in the same tree.

Site variable measurements included a modified version of Morisita's ordered distance protocol (Nielson et al. 2004) where each compartment was sampled with two, randomly placed, 50 m transects. We ran three transects in the two largest compartments in the southeastern portion of the site. At 10 m intervals along the transects, the third nearest tree was located, its distance measured to the transect point, and

diameter at breast height (DBH) recorded. We used these data to estimate stand density (trees/ha) by Morisita's equation. At three points along the transect (10, 30, and 50 m), we measured basal area (m^2/ha) with an English BAF 10X prism.

Statistical analysis

We analyzed within-tree correlations of presence/absence of colonizing agents using phi (ϕ) coefficients

(a derivative of Pearson's correlation used for binary data). Ten dying/dead trees exhibited no symptoms of the investigated colonizing agents and were removed from the analysis.

We tested the individual aggregative pattern of each colonizing agent using Ripley's inhomogeneous K function with border correction (Ripley 1976). This function tests the null hypothesis of complete spatial randomness using an expanding search radius centered on each event. The inhomogeneous component of the model allows for scaling based on the intensity of points (i.e. stand density). We set a maximum search radius of 50 m to test if the density of events occurring inside the circle was significantly different from the global density of events using 2500 bootstrap replicates.

The spatial autocorrelation for *S. noctilio* and cross-correlation for pairwise comparisons of *S. noctilio* and all other colonizing agents was estimated using a non-parametric covariance function with 1000 iterations of bootstrap resampling (Bjørnstad and Falck 2001). We used this pairwise comparison method on data pooled from all years to establish a region of influence for *S. noctilio* specifically (autocorrelation) and between *S. noctilio* and each individual colonizing agent (cross-correlation).

To investigate spatial and temporal patterns of *S. noctilio* and colonizing agents, we conducted an autologistic regression on all dead trees using symptoms of *S. noctilio* (resinosis) as the response variable and separate spatially lagged variables for each co-colonizer: density of trees killed in the current year (t) and in the previous year ($t - 1$). The spatially lagged variable was calculated as the density of trees attacked by an individual co-colonizer within a fixed radius of each tree. Unique radii (r) were calculated for each colonizing agent based on the spatial autocorrelation (for *S. noctilio*) and cross-correlation function (see above). Extent of spatial cross-correlations (radii) was calculated based on the maximum distance over which covariance was detectable (range) (i.e. covariance $>$ or $<$ 0). Density of trees was standardized based on established boundaries that only included sampled stands (Fig. 1). A parameter for bark beetles was not included in the model as the covariance function indicated an absence of spatial association between this factor and *S. noctilio*.

Stand-level variables of trees species (*P. resinosa* or *P. sylvestris*), density (stems/ha), and basal area

(m²/ha) were included in the model. Analysis was conducted only on dead trees sampled from 2012 to 2014 ($n = 723$) to include both colonization from the current (t) and previous year ($t - 1$). Data from 2011 ($n = 269$) were omitted as response variables and only used as previous year ($t - 1$) variables for 2012. We constructed one full model with all spatially-lagged and stand-level variables. All input variables were standardized ($x_i/2\sigma_i$) to facilitate comparison among predictors (Gelman 2008). We calculated log odds ratios on untransformed parameter coefficients to present a magnitude of effect. All data were managed in ArcGIS (v10.2.2 ESRI) and analyses were conducted in R using the packages 'nfc', 'spatstat', 'MBA', and 'lme4.'

Results

Over the duration of this study, 992 dead trees were identified (Fig. 1). The most prevalent colonizing agents were *S. noctilio* and bark beetles, collectively associated with 88.7% of all dead trees (Fig. 2). The root rot diseases *Armillaria* sp. and *H. irregulare* s.l. were recorded in 24.2% of dead trees, however, they were never found in the same tree. All colonizing agents, independent of each other, exhibited a degree of spatial aggregation, but it was limited to a moderate spatial scale, exhibiting significant aggregation only within a radius of 15–20 m (Fig. 3). *Heterobasidion irregulare* s.l. differed in that it was strongly aggregated, but there was considerable variability with this species given its limited abundance at the site (Fig. 2).

Sirex noctilio exhibited strong negative interspecific associations for within-tree colonization patterns. It was negatively associated with all other colonizing agents except bark beetles, with which it was neutral (Table 1). *Armillaria* sp. and *H. irregulare* s.l. had a weak but significant negative correlation and these two agents were never identified in the same dead tree. All other colonizing agents had significant positive associations, except for bark beetles, which had a negative association with *Armillaria* sp. and a neutral association with *H. irregulare* s.l.

The degree of spatial autocorrelation and cross correlation was variable for all pairwise comparisons against *S. noctilio* (Fig. 4). Positive spatial autocorrelations of *S. noctilio* and negative cross correlation of *S. noctilio* and woodborers exhibited the greatest

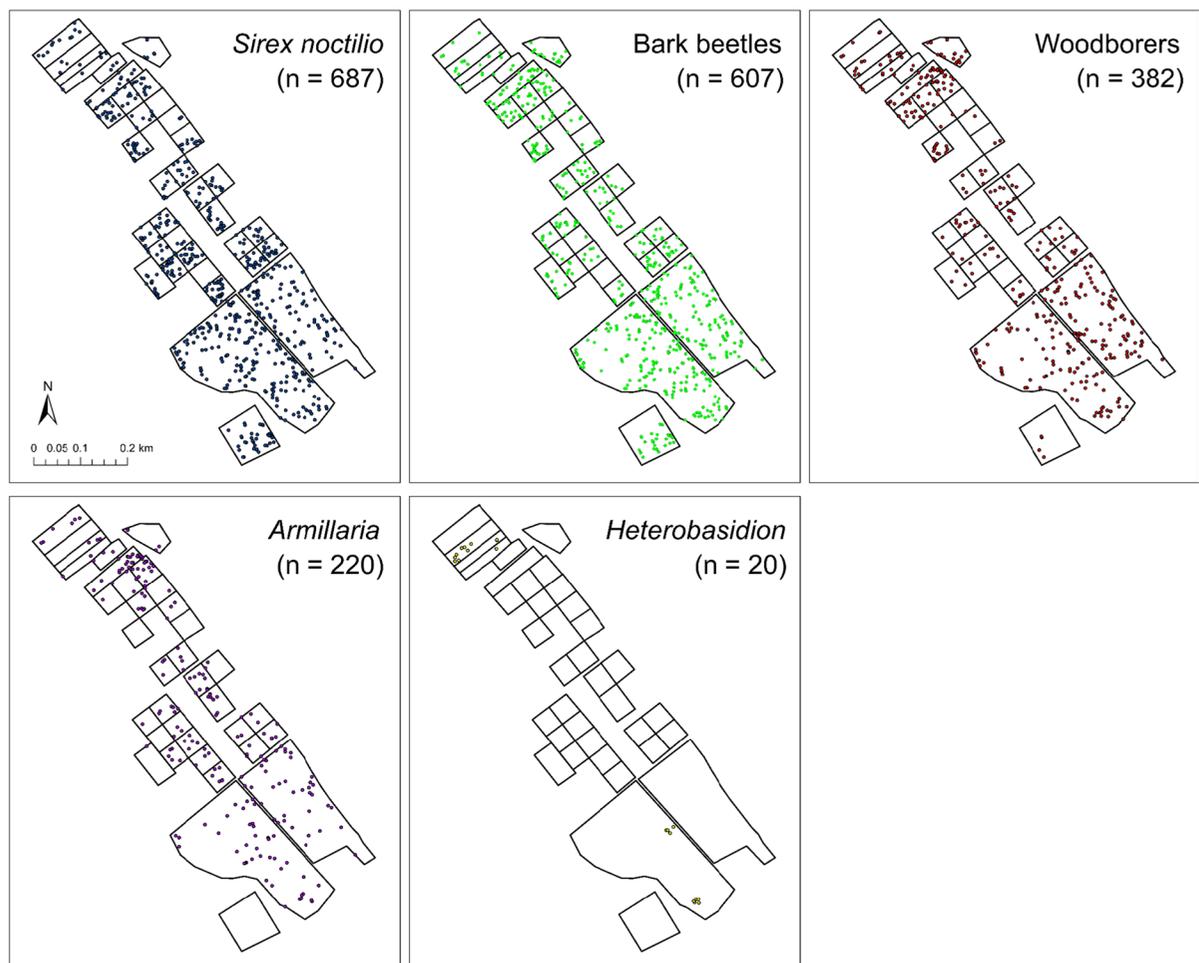


Fig. 2 Distributions of five pine colonizing agents across Pack Demonstration Forest, NY. Counts represent the total number of trees from 2011 to 2014 colonized by each agent. Multiple agents could be present in the same tree

distance of correlation ($r = 185.7$ and $r = 188.7$, respectively). Similar to within-tree correlations, *S. noctilio* exhibited negative interspecific associations in stand-level colonization patterns, again with the exception of bark beetles (neutral). Subsequently, we did not include bark beetles as a factor in the autologistic regression model as there were no within-tree correlations and the spatial cross correlation was not significantly different from zero.

The autologistic regression model indicated probability of *S. noctilio* attack increased significantly with *S. noctilio* attack density from the current and previous year, density of woodborer attack from the previous year, stem density, and if the pine host was *P. sylvestris* (Table 2). Presence of root rot disease (both *Armillaria* sp. and *H. irregulare* s.l.) from the current

year were significantly negatively associated with evidence of *S. noctilio* attack. Comparisons among standardized variables indicate the three strongest factors were density of current year *S. noctilio* attack (positive effect), host species (*P. sylvestris*) (positive effect), and density of current year *Armillaria* sp. attack (negative effect). The strongest factor, current year *S. noctilio* attack, had almost a fourfold greater impact than the two weakest significant factors (density of previous year woodborer attack and density of current year *H. irregulare* s.l. attack).

Patterns of *S. noctilio* attack were highly aggregated both in space and through time, with an increase of one attacked tree within the range (i.e. radius when spatial autocorrelation = 0) in the current and previous year increasing the probability of attack by *S.*

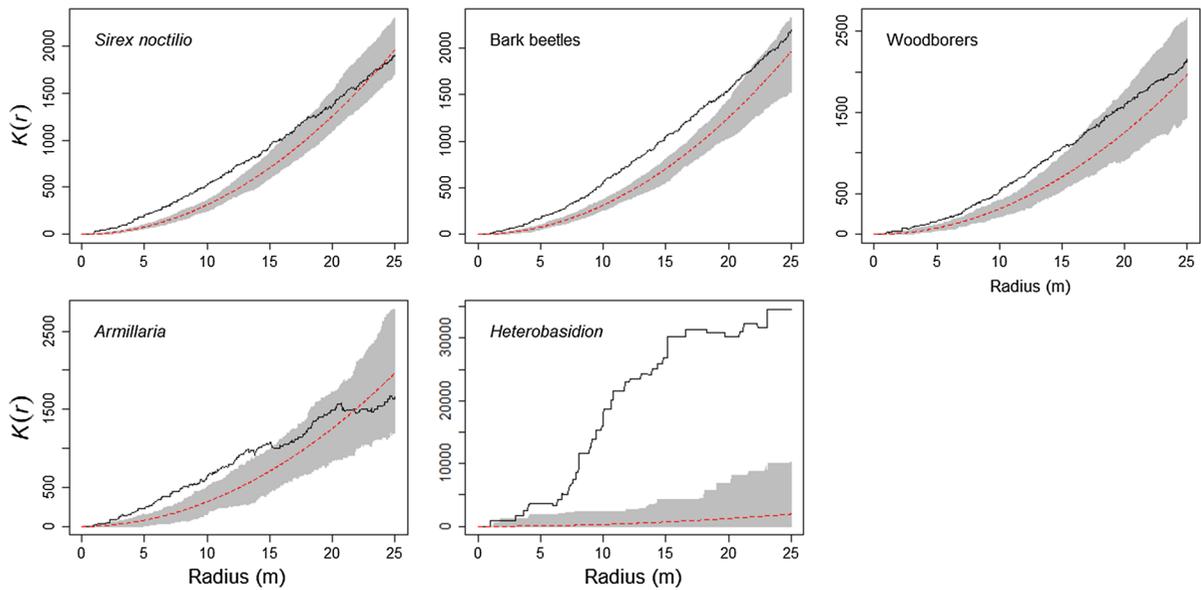


Fig. 3 Spatial aggregation of colonizing agents at Pack Demonstration Forest, NY using Ripley’s inhomogeneous K function with borders correction. The red dashed line indicates complete spatial randomness and the grey envelope indicates a 95% confidence envelope calculated from 2500

bootstrapping replications. The black line indicates the degree of aggregation for each colonizing agent. The space above the grey envelope indicates aggregation and the space below indicates regularity

Table 1 Phi (ϕ) coefficients for within-tree associations for all pine colonizing agents in 992 dead trees identified at Pack Demonstration Forest in northeastern New York State in 2011–2014

	Scolytinae	Cer/Bup ^a	<i>Armillaria</i> sp.	<i>H. irregulare</i> s.l.
<i>Sirex noctilio</i>	– 0.03	– 0.35**	– 0.42**	– 0.14**
Scolytinae		0.35**	– 0.12**	0.01
Cer/Bup ^a			0.24**	0.06*
<i>Armillaria</i> sp.				– 0.08*

* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$

^aCerambycidae/Buprestidae

noctilio by 13.4 and 9.7%, respectfully (Table 2). Log odds indicated an increase of 100 stems/ha translated to a 15.1% increase in probability of a dead tree being symptomatic for *S. noctilio*. A density increase of one tree attacked by either root rot diseases in the current year decreased probability of *S. noctilio* attack by ~ 18%. However, the log odds confidence interval ranges for density of current year *H. irregulare* s.l. attack as well as previous year woodborer attack were almost twice as wide as that of other significant variables with both intervals nearly encompassing 1, indicating they were more variable and less predictive than other significant factors.

Discussion

This study is the first to investigate the spatial dynamics of *S. noctilio* in North America and one of the first on spatial pattern of *S. noctilio* mortality in a stand through multiple years (Corley et al. 2007). Aggregation of this insect appears to operate across space and through time, with different factors driving distributions at different spatial scales (Levin 1992). A strong aggregative pattern by *S. noctilio* at broad spatial scales has been shown in South America (Corley et al. 2007), but this dissipates as *S. noctilio* populations become epidemic (Lantschner and Corley

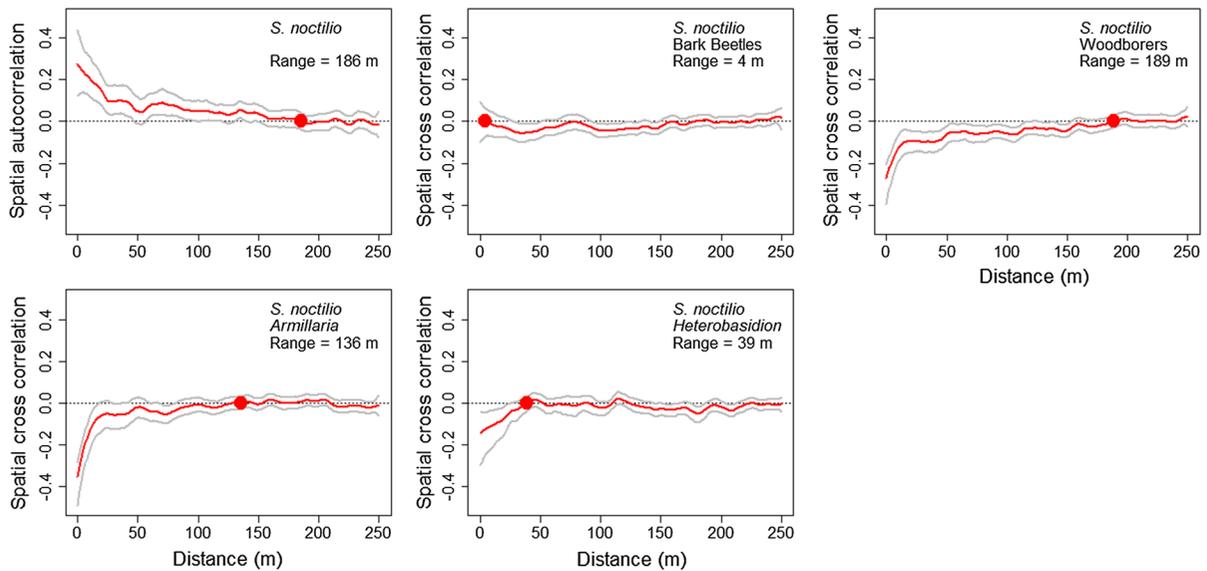


Fig. 4 Spatial nonparametric covariance function estimates of autocorrelation of *S. noctilio* attack and cross correlation of *S. noctilio* and other colonizing agents at Pack Demonstration Forest. Red lines indicate the true data and the grey lines indicate a 95% confidence envelope based on 1000

bootstrapping replicates. The red point is the range (covariance = 0) or the maximum distance over which a spatial relationship is detectable. The range was used to calculate spatially lagged variables

Table 2 Full autologistic regression models testing effects of spatially lagged colonizing agents from the current (*t*) year and previous year (*t* - 1) and stand-level variables

Factor	Estimate (SE)	z-value	P value	Log odds	95% CI
Intercept	- 2.26 (0.78)	- 2.89	0.004	0.104	0.022, 0.474
<i>S. noctilio</i> _{<i>t</i>}	1.51 (0.28)	5.49	< 0.001	1.134	1.085, 1.187
<i>S. noctilio</i> _{<i>t</i>-1}	0.81 (0.22)	3.70	< 0.001	1.097	1.045, 1.153
Woodborers _{<i>t</i>}	0.45 (0.28)	1.59	0.113	1.083	0.982, 1.196
Woodborers _{<i>t</i>-1}	0.38 (0.19)	2.02	0.044	1.092	1.003, 1.191
<i>Armillaria</i> sp. _{<i>t</i>}	- 1.05 (0.27)	- 3.83	< 0.001	0.852	0.784, 0.924
<i>Armillaria</i> sp. _{<i>t</i>-1}	- 0.24 (0.23)	- 1.03	0.305	0.964	0.898, 1.034
<i>H. irregulare</i> s.l. _{<i>t</i>}	- 0.38 (0.19)	- 2.00	0.046	0.844	0.709, 0.991
<i>H. irregulare</i> s.l. _{<i>t</i>-1}	- 0.13 (0.18)	- 0.71	0.475	0.957	0.848, 1.078
Density (stems/ha)	0.46 (0.23)	1.99	0.047	1.000	1.000, 1.002
Basal area (m ² /ha)	- 0.29 (0.23)	- 1.23	0.220	0.995	0.987, 1.003
Species (<i>P. sylvestris</i>)	1.15 (0.27)	4.20	< 0.001	3.154	1.866, 5.470

Log odds ratios and 95% CI are calculated on unstandardized coefficient variables

2015). It is notable that *S. noctilio* displays a high degree of aggregation at small spatial scales even though this insect is a large, effective flier as indicated by flight mill studies showing potential dispersal of healthy females can exceed 30 km (Villacide and Corley 2008). Abiotic factors can also impact *S. noctilio* aggregation at larger spatial scales, such as aspect and elevation (Lantschner and Corley 2015); all of which can be compounded by acute or chronic stressors like drought (Madden 1988).

Co-colonizing insects play a role in patterns of *S. noctilio* mortality, but these effects are strongest at the tree level rather than the stand. Stand-level interactions were important for root rot diseases though, with *S. noctilio* exhibiting negative associations with both *Armillaria* sp. and *H. irregulare* s.l. This may stem from the relative immobility and strong aggregative nature of root rot diseases due to their below-ground vegetative spread. Hanson (1939) and Parkin (1942) suggest interactions between these two agents hinges

on fungal colonization of xylem tissue, with developing siricid larvae avoiding or failing to develop on wood tissue infected or altered by *Armillaria* or *Heterobasidion* sp. The negative association documented in our study may be driven by avoidance, with ovipositing *S. noctilio* avoiding these trees during host selection. Siricid ovipositors have complex sensory structures (Fukuda and Hijii 1996; Hayes et al. 2015), which facilitate precise host selection by females as they are able to distinguish subtle changes in tree moisture content and plant secondary chemistry.

There are surprisingly mixed co-colonization patterns for *S. noctilio* and bark and woodboring beetles at the tree and stand level. All insects in this study (*S. noctilio*, bark beetles, and woodborers) are effective fliers in pine stands at the scale analyzed in this study and limitations due to dispersal were likely minimal. The negative or neutral associations with these insects suggest *S. noctilio* may be targeting a different subset of trees for colonization. Because of its unique ability to weaken or condition a tree by injecting phytotoxic mucus and fungal arthrospores, *S. noctilio* may be avoiding co-colonization by attacking trees healthier than those targeted by most bark and woodboring beetles. Whether these insects then attack trees weakened by *S. noctilio* may be contingent upon local populations, timing of initial attack, tree condition, and attack intensity. This could explain the neutral association between *S. noctilio* and bark beetles, with some *S. noctilio* attacked trees appearing early enough in the season to incite colonization by late summer generations of bark beetles (e.g., *I. pini*), but some being attacked so late in the fall that they enter winter with only *S. noctilio* colonization and are then unsuitable for bark beetles in the early spring due to their deteriorated condition.

Indirect interactions with bark beetles are hypothesized to negatively affect *S. noctilio* (Dodds and de Groot 2012; Ryan et al. 2012c; Yousuf et al. 2014a). The results of our research provide no evidence that these two agents strongly co-occur or partition resources though; as there was a lack of association between *S. noctilio* and bark beetles as indicated by the whole-tree (Table 1) and stand-level analyses (Fig. 4). Meaningful interactions with bark beetles (and their associated fungi) are likely contingent on the spatial scale of analysis. Within-tree patterns may yield more representative outcomes for these relationships. This could have implications for *S. noctilio*'s population

dynamics though, as negative associations at the individual insect level do not appear to translate to patterns at the broader spatial scales addressed in this study. This is important because it could function as a negative feedback mechanism if *S. noctilio* attacked trees are in close proximity to bark beetle attacked trees.

Interestingly, Ayres et al. (2014) found similar patterns in host colonization associations for *S. noctilio* and insect assemblages in Galicia, Spain, with *S. noctilio* having neutral relationships with scolytines, excluding *T. piniperda* (with which it has a positive association). Unfortunately, fall surveys for this project occurred long after *T. piniperda* colonization and reasonable species level identifications could not be determined via gallery systems. Ayres et al. (2014) also found similar patterns of association among all species (Scolytinae, Buprestidae, Cerambycidae, *Armillaria* sp.) when compared to this study (Table 1), suggesting major insect and root pathogen assemblages in North America are a suitable analog to its native habitat in Eurasia.

Recent studies in North America present evidence that biotic resistance from native insect assemblages may hamper the success of *S. noctilio* (Ryan et al. 2012c; Haavik et al. 2015) and that these assemblages are similar to those present in Europe, where it is a non-pest (Ayres et al. 2014). The strongest mechanistic explanation for this hypothesis is that competition for xylem tissue between *A. areolatum* and bark beetle-vectored fungi (*Ophiostoma* and *Lep-tographium* spp.) does not favor *S. noctilio*'s symbiont and can compromise development. This has support from emergence studies (Ryan et al. 2012c), in vitro competition assays between these fungi (Ryan et al. 2011; Hurley et al. 2012; Yousuf et al. 2014b), exclusion manipulations (Haavik et al. 2015), and in situ comparisons of survivorship (Foelker 2016). However, it is unknown if this mechanism is acting alone or in concert with other factors.

Biotic resistance is multifaceted and may be operating through multiple mechanisms across spatial scales. A possible additional limitation is that native insects are removing potential host trees early in the season before *S. noctilio* emergence—over 30% of dead trees in this study showed no evidence of *S. noctilio* attack. When *S. noctilio* does emerge, it likely rejects trees already colonized by woodborers and bark beetles due to an aversion to host infected with

bluestain fungi (Ryan et al. 2012a), a pattern noted in the Southern Hemisphere (Clarke et al. 2016). These native insects thus narrow the pool of potential hosts across a stand. This scenario is not present in the Southern Hemisphere, where trees may persist in a weakened state for an extended time since there are very few mortality agents.

Bottom-up factors also can influence patterns of mortality attributed to *S. noctilio*. More attacks occurred on *P. sylvestris*, an ancestral Eurasian host naturalized to North America, as has been found in other studies of *S. noctilio* (Dodds et al. 2010; Zylstra et al. 2010; Ayres et al. 2014). The basis for this pattern is unclear and could involve several factors, including preference for a familiar host, variation in defensive responses, or environmental stressors. There is considerable interspecific variation in secondary chemistry and the composition of co-colonizing insects among pine species (Thoss et al. 2007; Zylstra et al. 2010; Böröczky et al. 2012; Dodds et al. 2012), but it is uncertain if this is biologically meaningful for *S. noctilio*. Additionally, *P. sylvestris* stands across northeastern North America are largely unmanaged and often overstocked, senescing, and located at sites with poor growing conditions (Dodds and de Groot 2012).

Due to its size and high vagility, *S. noctilio* may function over larger spatial scales than other forest insects. This is particularly important in comparisons between the invaded regions of North America and the Southern Hemisphere, as one of the key differences is the extent, distribution, and homogeneity of host across the landscape (Dodds and de Groot 2012). Increasingly homogeneous landscapes in terms of host composition have intrinsic properties that can positively affect insect population dynamics, such as increasing patch size and decreasing distance among patches (Dunning et al. 1992). Each patch can subsequently support a larger population and dispersants have a higher likelihood of encountering a host and a shorter distance to travel. The distribution and amount of suitable pine for *S. noctilio* across northeastern North America is dispersed and limited, which may be an underlying factor limiting its population growth in the region. This, in concert with parasitoids and competition from native insects, is likely exerting a strong degree of biotic resistance. It is uncertain how this scenario could be altered as *S. noctilio* invades southern forests, where climate and host composition

and homogeneity are more closely aligned with Southern Hemisphere conditions.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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