

1 **Research Note**

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4 **First documented pest outbreak of the herbivorous springtail *Sminthurus***
5 ***viridis* (Collembola) in Europe**

6 F. V. Crotty^{1*}, R. Fychan¹, C. M. Benefer², D. Allen³, P. Shaw⁴ and C. L. Marley¹,

7 ¹ Institute of Biological, Environmental and Rural Sciences, Aberystwyth University,
8 Aberystwyth, UK.

9 ² School of Biological Sciences, Plymouth University, Plymouth, UK.

10 ³ FERA Science Ltd, Sand Hutton, York, UK.

11 ⁴ Centre for Research in Ecology, University of Roehampton, London, UK.

12 *Correspondence to:* Dr Felicity Crotty, Current address: Game & Wildlife
13 Conservation Trust, Loddington House, Main Street, Loddington, LE7 9XE, UK.

14 E-mail: fvcrotty@gmail.com

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19 Running header: Outbreak of *Sminthurus viridis* in Europe

20 **Abstract**

21

22 *Sminthurus viridis* (Collembola: Sminthuridae) is a native of grasslands across Europe
23 and feeds preferentially on clover (*Trifolium* spp.) and lucerne (*Medicago sativa*),
24 although its abundance does not normally reach damaging pest levels (as occurs in
25 Australasia). This research note describes the first quantitative assessment of a pest
26 outbreak of this springtail in Europe, which occurred within an existing experiment
27 investigating the effects of cultivation practices on forage establishment. Using sticky
28 traps to assess the incidence of *S. viridis* we found a significant outbreak consisting of
29 catches that were ten-fold greater than background levels in nearby, undamaged fields.
30 Within the experimental area, lucerne established by direct drilling with herbicide had
31 the highest incidence (105 (\pm 4.9) individuals per trap) compared to other treatments (79
32 (\pm 3.9)). Results are discussed in terms of how cultivation practice may have
33 imbalanced the ecosystem; for example, herbicide use may have diminished potential
34 refugia for predators during forage establishment. This paper highlights the potential of
35 a currently innocuous, widely established invertebrate to become present at damaging
36 levels in agricultural crops.

37

38 **Keywords:** agricultural pest, clover springtail, lucerne flea, Collembola, lucerne, direct
39 drilling.

40 **Introduction**

41 The clover springtail, *Sminthurus viridis* L. (or lucerne flea), is an economically
42 damaging invasive agricultural pest in Australasia (Bell and Willoughby, 2003), having
43 been accidentally introduced from Europe in the 1880s (Hopkin, 1997). A pest outbreak
44 is defined to have occurred when an insect population erupts to high densities, causing
45 damage (Berryman, 1982). Herbivorous pest outbreaks often occur in non-native
46 habitats; however, it is less likely for this to occur where they are native, because of the
47 biological controls already in place (Berryman, 1982).

48 *Sminthurus viridis* feeds on clover (*Trifolium* spp.), lucerne (*Medicago sativa*) and
49 other legumes and has a ubiquitous distribution across the Palaearctic, South Africa
50 and North America (CAB International, 1973) but is not considered an agricultural pest
51 in these regions. It has been found to occur at densities of up to 60 per 0.5 m² (through
52 suction sampling) in agricultural fields in the UK (Alvarez *et al.*, 2000) and up to 70 per
53 m² (in soil samples) in southern France (Renaud *et al.*, 2004). Historically, field damage
54 by *S. viridis* alone has rarely been observed, quantified or monitored in Europe (Davies,
55 1928), with *S. viridis* referred to as an insect of 'minor economic importance' (Jones and
56 Jones, 1984). However, some studies investigating the general effect of invertebrate
57 herbivores, on clover have found damage caused by *S. viridis* (Mowat and Shakeel,
58 1989a, b; Wiech and Clements, 1992).

59 In Australasia, *S. viridis* can reduce stocking density by 0.6 sheep ha⁻¹ through
60 lost plant material (Wallace and Mahon, 1963) and is still causing more than \$A28
61 million annum⁻¹ of damage to cereals and brassica crops there (Murray *et al.*, 2013).
62 The abundance of *S. viridis* reported to cause economic damage is highly variable,

63 ranging from 215-1300 per m² (Cleland, 1955; Bishop *et al.*, 2001) with some
64 populations in untreated Tasmanian pastures reaching 50,000 per m² (Ireson, 1984).
65 While this research note represents only one field site, in one location, it is the first
66 quantitative assessment of a pest outbreak of the springtail *S. viridis* in Europe. The
67 outbreak was captured within an experiment investigating different cultivation
68 techniques, showing the wider implications of the phenomenon of pest outbreaks in
69 native, widespread and common invertebrates in agricultural land, and suggesting a
70 need for greater awareness and surveillance of new outbreaks globally.

71

72 **Materials and methods**

73 In June 2013, an experiment was set up in a 2 x 2 factorial structure, with a randomized
74 complete block design, to evaluate the effect of different cultivation techniques
75 (ploughing versus direct drill; with/without a pre-cultivation herbicide) on the yield of
76 lucerne (n = 3). Each replicated plot was 10 x 2.7m, 0.5 m apart within block and each
77 block was 7 m apart. The experimental field site was located near Aberystwyth, Mid-
78 Wales, UK (52°26'2N, 4°1'W; elevation 30 m a.s.l.) on a silty clay loam. Previously the
79 area had supported a perennial ryegrass sward, sown in 2007. Plots were randomly
80 allocated for herbicide application and were treated on 10 June 2013 with 360 g L⁻¹
81 glyphosate (Clinic Ace, Nufarm UK Ltd, Belvedere, Kent, UK) at a rate of 4 L ha⁻¹. Plots
82 allocated for ploughing were ploughed to a depth of 150 mm, power-harrowed and
83 rolled on 18 June, prior to surface sowing using a Fiona D784 seed drill (Westmac
84 Maskinfabrik A/S, Bogense, Denmark) then lightly harrowed and rolled using a flat
85 roller. Plots that had been randomly allocated for direct drill were sown with a Duncan

86 Eco Seeder direct drill (Willow Farm Machinery Ltd., Ludford, UK) into slots 15 mm
87 deep. All plots were sown with lucerne (cv. Timbale) at a rate of 22 kg ha⁻¹ on 19 June.

88 On 3 July 2013 an increased abundance of a jumping invertebrate was observed
89 on the plots and damage to leaves was visible. This damage was characteristic of *S.*
90 *viridis* with the epidermis stripped off the leaf and underlying mesophyll eaten,
91 skeletonizing the leaves (Barker, 2006) (Figure 1). Two groups of specimens were
92 randomly collected using an aspirator (Pocket Pooter, Watkins and Doncaster,
93 Leominster, UK), from the 'outbreak' and identified. One group were identified using
94 morphology (Hopkin, 2007) and confirmed by the UK recorder of Collembola as *S.*
95 *viridis*. A second group were taken for molecular identification, by comparing individual
96 cytochrome c oxidase subunit I (COI) sequences to known, publically available
97 sequences for *S. viridis* (following the methods of Shaw and Benefer (2015)) to assess
98 similarity to known 'pest' *S. viridis* from Australasia and determine whether they may be
99 a separate pest morph – potentially explaining why this species does not usually reach
100 pest proportions in Europe.

101 The unusually high abundance observed led to an assessment of numbers to
102 ascertain whether this was comparable to any other reported outbreak. To assess
103 abundance, a modified method previously used for assessment of hopping insects
104 (Norment, 1997; Matsukura *et al.*, 2011) and which did not require destructive sampling
105 of experimental plots, was set up on 4 July 2013. Yellow sticky boards (Silvandersson,
106 Sweden) were cut in half (12.5 cm x 5.5 cm) and the halves placed centrally within each
107 plot, ~2m apart (n = 24). The boards were horizontal, with one side adhering to the soil
108 surface and staked centrally, whilst the other sticky side could catch jumping

109 Collembola, akin to pitfall trapping. These sticky boards were left in the field overnight
110 (~15h) before removal. On 5 July, cypermethrin insecticide was applied at a rate of 200
111 ml ha⁻¹ to salvage the original experiment (results of original experiment reported in
112 Marley et al., 2015). Invertebrates attached to the sticky boards were identified and
113 counted under a microscope.

114 To establish whether the outbreak could be considered of pest proportions, an
115 area of established lucerne (sown 2011) of the same cultivar (approx. 100 m from the
116 experimental plots) was used to compare populations (this site had no reported pest
117 problems in the previous two growing seasons). Here, the same sticky board method
118 was implemented (n = 12), over the same time scale and area. In addition, soil cores
119 (5.7 cm diameter; n = 3) were taken from the outbreak, in the replicated herbicide
120 treated (plough/direct drill) plots, prior to the application of the insecticide, to obtain an
121 estimate of abundance per m² for comparison to previous estimates of damaging
122 population levels. These were placed upside down on Tullgren funnels following Crotty
123 *et al.* (2014) and the results transformed to per m² (by multiplication of 97.97) for
124 comparison with other published results.

125 All data were analysed using GenStat (v14, VSN International, Hemel
126 Hempstead, UK), *S. viridis* counts per trap were normally distributed (tested within
127 GenStat) and assessment of the effect of treatment on catches was performed by a
128 general analysis of variance (ANOVA) as a 2 x 2 factorial in a randomized complete
129 block design, multiple comparisons were made using the Student Newman Keuls test.

130

131 **Results**

132 There was a ten-fold difference in the number of *S. viridis* caught in the newly planted
133 lucerne crop (mean 86.8 (\pm 3.53) n=24) compared with a 'normal' population (mean 6.2
134 (\pm 1.28) n=12) in an established lucerne crop ($P < 0.001$). There were also significant
135 differences among management treatments ($P = 0.005$). More *S. viridis* were caught in
136 the direct drill-with-herbicide plots (mean average 105.5 (\pm 4.92)), compared to the
137 other treatments (DD without herbicide 74.5 (\pm 5.22), plough without herbicide 82.3 (\pm
138 10.19), plough with herbicide 81.3 (\pm 4.19)). No significant difference was found when
139 comparing the cultivation method alone (plough 81.8 (\pm 5.26) vs direct drill 90.0 (\pm
140 5.79)) ($P = 0.072$). However, herbicide usage was significant when considered
141 singularly ($P = 0.007$; mean catches in herbicide plots were 93.4 (\pm 4.77) compared to
142 78.4 (\pm 5.58) in plots without herbicide). There was a mean of 261 (\pm 130.6) *S. viridis*
143 per m² extracted from the soil cores.

144 COI sequences were obtained for seven individuals, ranging from 593–681bp in
145 length (GenBank accession numbers KJ155509–KJ155515). They produced a 92.6–
146 98.7% match to *S. viridis* sequences on BOLD (Barcode of Life Database), all to
147 individuals collected from New Zealand, (Figure 2). At this time there are no other UK
148 sequences for *S. viridis* on BOLD/GenBank.

149

150 **Discussion**

151 Our study shows *S. viridis* at pest levels in its native environment, with results showing
152 ten-fold greater catches in the affected area than a 'normal' population and damage
153 being caused (Figure 1). We have measured this infestation within an experiment with

154 replicated treatments showing the potential effects of agricultural management on pest
155 abundance. Prior to the outbreak, the weather conditions over the previous 12 months
156 had shown large fluctuations from the long-term average. Data provided by the Met
157 Office, for the weather station located at Gogerddan Aberystwyth, showed that 2012
158 was wetter than the 50-year average, whilst spring 2013 was drier and colder than the
159 50-year average. These extremes were experienced across the UK (Met Office 2013a;
160 2013b), and may have been a contributing factor to this pest outbreak. This study is
161 limited by being representative of only one field site, during the first establishment year
162 of a *S. viridis* host plant; however, we are aware of at least one other occurrence in a
163 different location during the same growing season (R. Fychan, personal
164 communication). Our findings highlight the need for greater awareness and surveillance
165 of potential pest outbreaks, especially where these may be exacerbated by changing
166 weather conditions as projected for the UK by current models (IPCC, 2014).

167 Comparisons between an established crop ('normal' population) and the affected
168 experimental plots confirmed that there was an outbreak of *S. viridis* with an order of
169 magnitude difference between catches (mean average of 6.2 (\pm 1.28) in a 'normal'
170 population, compared to 86.8 (\pm 3.53) in the outbreak). It also verified that sticky boards
171 could be used to test the incidence of *S. viridis* in the field. This method was previously
172 found to be comparable to pitfall trapping of surface-active arthropods (Norment, 1987);
173 is already used for other hopping pests of crops (e.g. plant and leaf hoppers (Matsukura
174 *et al.*, 2011)), and is easier to use than a sticky trap corer (Taverner *et al.*, 1996). Sticky
175 traps set in the direct-drill-with-herbicide treatment caught the greatest numbers overall;
176 possibly due to the reduced plant cover diminishing refugia for surface dwelling

177 predators, whilst also stimulating crop growth through reduced competition (Wardle,
178 1995). In comparison, the direct drill without herbicide treatment had the most 'intact'
179 ecosystem, with the lucerne competing with existing ryegrass and potentially allowing
180 greater numbers of predators to reside within these plots, thereby reducing *S. viridis*
181 abundance.

182 The abundance of *S. viridis* reported to cause economic damage is highly
183 variable, although can be as little as 215 per m² (Cleland, 1955). If this is true, without
184 the immediate application of insecticide substantial yield reductions would have
185 occurred here (results from soil cores estimated 261 (± 130.6) individuals m²). The few
186 individuals of *S. viridis* obtained via soil cores demonstrates that this is not the most
187 appropriate method for ascertaining abundance of an epigeic springtail because of its
188 ability to jump away from the soil core during sampling. Here, the sticky board method
189 has been shown to be a useful 'farmer friendly' tool that could be implemented in the
190 field to quickly assess population size of *S. viridis*. However, the methods of Alvarez *et*
191 *al.* (2000) or use of other suction-based methods may provide a more accurate
192 assessment as they provide a per-m² measure of abundance.

193 The COI sequences obtained were a high match to other COI sequences
194 available on BOLD and were in agreement with the morphological identifications,
195 confirming the identity of the species causing the infestation. All individuals matched
196 either haplotype 1B (98.6–98.7% match) or haplotype 2B (92.6% match) from New
197 Zealand (Vink and Brown, 2013; Figure 2). Due to the paucity of UK and European
198 sequences published for *S. viridis*, we could not ascertain whether a 'pest morph' was
199 present, as opposed to a 'normal' ubiquitous European morph.

200 In European grasslands, persistence of forage legumes can be unreliable.
201 Historic studies and surveys have found 90% of clover leaves with pest damage at
202 some sites, and up to 30% of this damage was due to unidentified pests (Lewis and
203 Thomas, 1991). The addition of a pesticide was also shown to increase dry matter
204 yields of white clover, although not of lucerne, however the pests were not identified
205 (Clements and Henderson, 1983). It is possible that this unreliability is because of
206 undiagnosed *S. viridis* outbreaks occurring, as suggested by Mowat and Shakeel
207 (1989b), but due to lack of research and publicity they remain undetected. Overall, it
208 was found that crop management can alter the abundance of a ubiquitous, usually
209 harmless springtail, to pest proportions. These findings highlight the need for further
210 understanding of the different agricultural and environmental interactions affecting *S.*
211 *viridis* populations globally. This outbreak could be a rare localized occurrence or the
212 harbinger of future pest outbreaks, and only greater awareness and surveillance will
213 help to understand this issue within agricultural ecosystems globally.

214

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218 laboratory at Plymouth University for genetic analyses.

219

220 **References**

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312 **FIGURE LEGENDS:**

313 Figure 1: Photograph of damage to lucerne leaves caused by *S. viridis*.

314 Figure 2: Phylogenetic tree using maximum likelihood in MEGA v5 (Tamura *et al.*, 2011)

315 of cytochrome c oxidase I subunit I (COI) sequences of *Sminthurus viridis*

316 using the TN92+G model (LogL = -2019.18) using the obtained sequences

317 and those for *S. viridis* downloaded from the Barcode Of Life Database

318 (BOLD) and GenBank to determine intraspecific relationships between

319 samples collected in Europe and Australasia. The percentage of trees in which

320 the associated taxa clustered together is shown next to the branches, and

321 branch lengths are representative of the number of substitutions per site.

322 There were 428 positions in the final dataset. C169-C175 represent *S. viridis*

323 individuals collected from the infested field site in Aberystwyth (accession

324 numbers KJ155509 – KJ155515). All other sequences were downloaded from

325 BOLD (accession numbers K150049 – KC150080) and GenBank (accession

326 numbers EU016192, JN970939 and HM355586 – HM355589). *Sminthurinus*

327 *trinotatus*, *S. aureus* and *S. elegans* were included as outgroups (accession

328 numbers pending; Shaw and Benefer, 2015).