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1 **Comparison of viral infection risk between organic and conventional crops**
2 **of tomato in Spain**

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12 **Keywords:** *Tomato mosaic virus, Cucumber mosaic virus, Tomato spotted wilt virus*

13

14 **Abstract**

15 The harmful effects of conventional agriculture on the environment and human health have been an
16 increasing concern, resulting in the search for alternative and more sustainable agricultural systems in
17 the last decades. Organic farming is the fastest growing system worldwide, but there is a controversial
18 debate on the ability of the agroecological practices to cope with diseases and pests and produce food for
19 the world population. However, comparative studies on the effect of organic farming on plant disease are
20 almost non-existent particularly concerning plant virus diseases. In this work, a survey of *Tomato mosaic*
21 *virus* (ToMV), *Cucumber mosaic virus* (CMV) and *Tomato spotted wilt virus* (TSWV) was performed in
22 tomato crops under organic or conventional management by sampling 40 small farms in Eastern Spain.
23 ToMV had the highest incidence whereas few plants were infected by CMV and none by TSWV. Viral
24 infection risk was estimated as the probability of a plant being infected by at least one of the three viruses
25 or by each virus separately according to a Bayesian logistic regression model. Our analysis showed that
26 the infection risk by these viruses was lower in organic than in conventional farms in two nonconsecutive
27 years.

28

29 Over the past century, the development of intensive agriculture enabled a remarkable increase in
30 crop production worldwide, becoming the predominant agricultural system. Intensive or conventional
31 agriculture relies on monocropping of high-yielding cultivars obtained by plant breeding or genetic
32 engineering, as well as high external inputs of water, fossil fuel, synthetic fertilizers and pesticides.
33 However, the negative effects on the natural environment (e.g. greenhouse gases, biodiversity loss, soil
34 degradation and water contamination), as well as human health (food contamination by pesticides or
35 other chemicals) have raised concerns about the sustainability of this agricultural system (van Bruggen
36 et al. 2018).

37 Main challenge of the agriculture in this century is to achieve an alternative system to produce
38 nutritious food for the growing world population in a sustainable manner while protecting environment
39 and the human health (Wezel et al. 2014). Organic agriculture is the most popular and the fastest growing
40 one, having almost tripled the dedicated land in the last decade (Crowder and Reganold 2015). The
41 agroecological system is based on the design and management of sustainable agroecosystems by
42 understanding and manipulating ecological interactions and processes for I) enhancing recycling of
43 biomass and nutrients; II) securing favorable soil conditions by managing organic matter and biotic
44 activity; III) promoting plant diversification in time and space favoring beneficial biological interactions
45 such as predator/prey, competition and symbiosis (Altieri 1995; Finckh et al. 2015).

46 Damages caused by pests and diseases have a considerable negative economic impact in
47 agriculture, not only because of the yield reduction but also by the requirement of costly inputs to combat
48 or control them undermining sustainability (Pretty et al. 2010). Viral diseases constitute a major threat to
49 the large-scale production of crops worldwide, accounting up to several billion dollars in losses every
50 year (Hull 2009). This situation is aggravated by the frequent cases of emergence of viral diseases as a
51 result of climate change, international trade and the great ability for viruses for fast evolution and
52 adaptation (Jones 2009; López et al. 2011; Elena et al. 2014; Dennehy 2017).

53 Conventional agriculture tries to eradicate or control diseases with the use of resistant cultivars
54 obtained by plant breeding and high chemical or biological inputs. In contrast, the agroecological
55 paradigm argues that pests and pathogens can be under control, but not eliminated, by antagonistic
56 ecological processes promoted by genetic diversity of crops and vegetation as well as soils rich in organic
57 matter and biotic activity (Van Bruggen et al. 2016). Currently, there is a controversy over the ability of
58 organic agriculture to stand against diseases and being profitable and adequate for the world food demand
59 (Reganold & Wachter 2016). However, comparative studies on plant pathology between organic and
60 conventional farming are very scarce, mainly on soil-borne diseases by bacteria, fungi and nematodes
61 with variable outputs, whereas the impact of these farming practices on viral diseases has been neglected
62 (Van Bruggen 1995; Berkelmans et al. 2003; Van Bruggen et al. 2016).

98 main vector. The infection risk of ToMV, CMV and TSWV, estimated as the probability of a plant being
99 infected by at least one of the three viruses or by each virus separately, was evaluated in tomato fields
100 cultivated under conventional or organic management in Eastern Spain by using a Bayesian logistic
101 regression model.

102 **Material and methods**

103 Sample and data collection

104 Several surveys were conducted in tomato (*Solanum lycopersicum*) crops cultivated in open fields during
105 summer of 2012 and 2014 in small farms (less than 1 ha) scattered in a coastal stretch of about 50 km
106 width and 200 km length (about 7000 km²) in the provinces of Valencia and Alicante, Eastern Spain (Fig.
107 1). To minimize possible bias, organic and conventional farms were selected to be of similar size, as
108 nearby as possible and were surveyed in the same day. In June of 2012, 20 farms were sampled: 15 based
109 on organic management and 5 on conventional management. Although farms varied broadly in
110 agronomical practices and histories, they were classified as conventional when synthetic fertilizers and/or
111 pesticides were used and as organic when they followed the European Union Regulation for Organic
112 Food and Farming: (EC) N. 834/2007, 889/2008 and 1325/2008 at least for four years. In June and
113 September of 2014, other 20 farms were selected: 12 organic and 8 conventional. Sampling the same
114 farms in 2012 and 2014 was not possible since this geographical area comprises small-scale farms with
115 a heterogeneous and dynamic horticulture, so crops can change in different years.

116 Eight plants were chosen for each farm following a W pattern, without considering the symptoms,
117 and were used to analyze the presence of ToMV, CMV and TSWV. Only a local or traditional tomato
118 cultivar (Valenciano) was sampled because: I) it lacks resistance to these viruses, and II) seeds are
119 produced and distributed by both organic and conventional farmers so transmission of ToMV by seed
120 would have the same probability for both organic and conventional management. Chemical and physical
121 soil characteristics and plant diversity were also evaluated in the farms sampled in 2012. Four soil
122 samples were randomly collected and analyzed according to the official methods of the Spanish Ministry
123 of Agriculture, Food and Fisheries (MAPA 1994). The following soil variables were determined: pH in
124 water extract 1:2.5 (p/v); electrical conductivity in saturation extract; oxidizable organic carbon by the
125 Walkley-Black titration method; nitrogen content by using the Kjeldahl digestion procedure; organic
126 matter, Olsen phosphorus; extractable cations by using ammonium acetate (calcium, magnesium,
127 potassium and sodium), carbonates and active lime. Plant diversity within farms was evaluated as the
128 number of simultaneous crop species (D_c) and wild plant species (D_w) per farm. Plant diversity in the
129 farm surroundings (D_s) was evaluated by visual inspection with three categorical values: low, medium

130 and high, being low when no plant or only one predominant species was observed (e.g. pine forests or
131 citrus crops), and high when many wild species were observed.

132 Virus detection

133 Each sample corresponded to a pool of several leaflets obtained from an individual tomato plant which
134 was analyzed to detect the presence of ToMV, CMV and TSWV. Viral infection in each plant was
135 determined by detection of the viral protein component by double antibody sandwich enzyme-linked
136 immunosorbent assay (DAS-ELISA) and the nucleic acid component by molecular hybridization. DAS-
137 ELISA was performed by incubating crude plant extracts with polyclonal antibodies specific for ToMV,
138 CMV and TSWV (Loewe Biochemica GmbH, Sauerlach, Germany) following the standard protocol
139 (Clark and Adams 1977). Total RNAs were purified by a standard phenol-chloroform method
140 (Debreczeni et al. 2011). Molecular hybridization was performed by incubating total RNA extracts
141 spotted onto positively charged nylon membranes (Roche Diagnostics) in ULTRAhyb ultrasensitive
142 hybridization buffer (Ambion, Thermo Fisher Scientific) at 68 °C with 20 ng of RNA probes per ml of
143 hybridization buffer (Ferriol et al. 2015). Digoxigenin RNA probes specific for ToMV, CMV and
144 TSWV were synthesized by *in vitro* transcription of cDNA templates obtained previously by RT-PCR
145 from ToMV, CMV and TSWV total RNAs with primer pairs specific for each virus (Table 1). PCR
146 conditions were: 2 min at 94°C, 40 cycles of 30 s at 94°C, 30 s at 52°C for ToMV or CMV or 55°C for
147 TSWV, and 30 s at 72°C, and finally 5 min at 72°C.

148 Statistical analysis

149 First, comparison of soil between organic and conventional farms was performed by evaluating
150 independently each soil variable through a Bayesian Normal model,

$$\begin{aligned} 151 & (Y_{oi}|\mu_o, \sigma_o) \sim N(\mu_o, \sigma_o), \\ 152 & (Y_{ci}|\mu_c, \sigma_c) \sim N(\mu_c, \sigma_c), \end{aligned} \quad (1)$$

153 where Y_{oi} (Y_{ci}) is the soil normal variable in organic (conventional) farm i . The assumption of
154 homoscedasticity between both standard deviations (σ_o and σ_c) was tested by the Levene's test (Levene
155 1960) and residual analysis. In case of a homoscedastic analysis, the Bayesian normal model for the
156 corresponding soil variable is

$$\begin{aligned} 157 & (Y_{oi}|\mu_o, \sigma) \sim N(\mu_o, \sigma), \\ 158 & (Y_{ci}|\mu_c, \sigma) \sim N(\mu_c, \sigma), \end{aligned} \quad (2)$$

159 Differences between organic and conventional farms for each soil variable were assessed with the direct
160 posterior probability $P(\mu_o \geq \mu_c | Data)$ computed from the posterior distribution of all relevant
161 parameters in the non-homoscedastic models, $\pi(\mu_o, \mu_c, \sigma_o, \sigma_c | Data)$, or $\pi(\mu_o, \mu_c, \sigma | Data)$ in the

162 homoscedastic models. Differences were considered relevant when $P(\mu_o \geq \mu_c | Data) \geq 0.95$ (higher
 163 in organic farms) or $P(\mu_o \geq \mu_c | Data) \leq 0.05$ (higher in conventional farms).

164 Second, comparison of plant diversity within farms between organic and conventional
 165 management was analyzed for the diversity variables D_c and D_w through independent Bayesian Poisson
 166 models formulated generically as

$$\begin{aligned}
 167 \quad & (D_{co,i} | \lambda_{co}) \sim \text{Poisson}(\lambda_{co}), \\
 168 \quad & (D_{cc,i} | \lambda_{cc}) \sim \text{Poisson}(\lambda_{cc}),
 \end{aligned} \tag{3.1}$$

$$\begin{aligned}
 170 \quad & (D_{wo,i} | \lambda_{wo}) \sim \text{Poisson}(\lambda_{wo}), \\
 171 \quad & (D_{wc,i} | \lambda_{wc}) \sim \text{Poisson}(\lambda_{wc}),
 \end{aligned} \tag{3.2}$$

172 where $D_{co,i}$ ($D_{cc,i}$) is the count variable that quantifies the number of simultaneous crops per organic
 173 (conventional) farm i with mean λ_{co} (λ_{cc}). $D_{wo,i}$ ($D_{wc,i}$) is the number of wild plant species in organic
 174 (conventional) farm i with mean λ_{wo} (λ_{wc}). Differences for each D_c and D_w between organic and
 175 conventional farms were assessed with the direct posterior probability $P(\lambda_{co} \geq \lambda_{cc} | Data)$ and
 176 $P(\lambda_{wo} \geq \lambda_{wc} | Data)$ computed from the posterior distribution of all relevant parameters
 177 $\pi(\lambda_{co}, \lambda_{cc} | Data)$ and $\pi(\lambda_{wo}, \lambda_{wc} | Data)$, respectively.

178 Plant diversity in the farm surroundings (D_s) between organic and conventional farms was
 179 compared by an inferential model based on a Bayesian Dirichlet-multinomial conjugated process
 180 (Alvares 2016) formulated for organic and conventional farms, respectively, as

$$\begin{aligned}
 181 \quad & (D_{so}^{(L)}, D_{so}^{(M)}, D_{so}^{(H)} | n_o, \theta_{so}) \sim \text{Multinomial}(n_o, \theta_{so}^{(L)}, \theta_{so}^{(M)}, \theta_{so}^{(H)}), \\
 182 \quad & (D_{sc}^{(L)}, D_{sc}^{(M)}, D_{sc}^{(H)} | n_c, \theta_{sc}) \sim \text{Multinomial}(n_c, \theta_{sc}^{(L)}, \theta_{sc}^{(M)}, \theta_{sc}^{(H)}),
 \end{aligned}$$

183 where the number of organic (conventional) farms with low, medium and high diversity surroundings
 184 $D_{so}^{(L)}, D_{so}^{(M)}, D_{so}^{(H)}$ ($D_{sc}^{(L)}, D_{sc}^{(M)}, D_{sc}^{(H)}$) were assumed to follow a Multinomial distribution with
 185 sizes n_o (n_c) and unknown probabilities $\theta_{so}^{(L)}, \theta_{so}^{(M)}, \theta_{so}^{(H)}$, ($\theta_{sc}^{(L)}, \theta_{sc}^{(M)}, \theta_{sc}^{(H)}$) for categories low,
 186 medium and high, respectively.

187 The conjugated Dirichlet-multinomial process start with a Dirichlet prior distribution, a
 188 multivariate generalization of the Beta distribution. We worked within a non-informative scenario, in
 189 particular, we selected the Perk's distribution (Alvares, 2015) (among a wide number of proposals)
 190 which assigns the same value, $\frac{1}{K}$, being K the number of categories, for all the hyperparameters of the
 191 distribution as stated as

$$\begin{aligned}
 192 \quad & \pi(\theta_{so}^{(L)}, \theta_{so}^{(M)}, \theta_{so}^{(H)}) = \text{Dirichlet}\left(\frac{1}{3}, \frac{1}{3}, \frac{1}{3}\right), \\
 193 \quad & \pi(\theta_{sc}^{(L)}, \theta_{sc}^{(M)}, \theta_{sc}^{(H)}) = \text{Dirichlet}\left(\frac{1}{3}, \frac{1}{3}, \frac{1}{3}\right).
 \end{aligned}$$

194 The posterior distributions are

$$195 \quad \pi(\theta_{so}^{(L)}, \theta_{so}^{(M)}, \theta_{so}^{(H)} | Data) = \text{Dirichlet}\left(d_{so}^{(L)} + \frac{1}{3}, d_{so}^{(M)} + \frac{1}{3}, d_{so}^{(H)} + \frac{1}{3}\right),$$

$$196 \quad \pi(\theta_{sc}^{(L)}, \theta_{sc}^{(M)}, \theta_{sc}^{(H)} | Data) = \text{Dirichlet}\left(d_{sc}^{(L)} + \frac{1}{3}, d_{sc}^{(M)} + \frac{1}{3}, d_{sc}^{(H)} + \frac{1}{3}\right).$$

197 where $d_{so}^{(L)}, d_{so}^{(M)}, d_{so}^{(H)}, (d_{sc}^{(L)}, d_{sc}^{(M)}, d_{sc}^{(H)})$ are the observed data of $D_{so}^{(L)}, D_{so}^{(M)}, D_{so}^{(H)}$
198 $(D_{sc}^{(L)}, D_{sc}^{(M)}, D_{sc}^{(H)})$.

199 Finally, the viral infection risk was estimated as the probability of a plant being infected by at
200 least one of the three viruses, ToMV, CMV and/or TSWV (overall), or by each virus separately. Data
201 from the samples collected all years and seasons were independently evaluated according to a Bayesian
202 logistic regression model (Christensen et al. 2011; Lázaro et al. 2017) defined as

$$203 \quad (Y_i | \theta_i) \sim \text{Binomial}(n_i, \theta_i),$$
$$204 \quad \text{logit}(\theta_i | x_i, \boldsymbol{\beta}) = x_i' \boldsymbol{\beta}, \quad (4)$$

205 where the random variable Y_i , which describes the number of plants infected in farm i from a total of n_i
206 plants analyzed, is assumed to follow a Binomial distribution (likelihood function) with unknown
207 probability of infection θ_i (parameter of interest), interpreted as infection risk; x_i is the vector of
208 covariates containing information on farm management: organic or conventional; and $\boldsymbol{\beta}$ is the
209 corresponding vector of the regression coefficients (parameters of interest).

210 The viral infection risk, θ_i , for a generic plant i with covariates x_i , can computed from (4) as

$$211 \quad (\theta_i | x_i, \boldsymbol{\beta}) = \frac{\exp(x_i' \boldsymbol{\beta})}{1 + \exp(x_i' \boldsymbol{\beta})}$$

212 The posterior distributions of the quantities of interest in all models proposed (normal, Poisson,
213 multinomial and logistic) were approximated using the Integrated Nested Laplace Approximation
214 (INLA) methodology (Rue et al. 2009) by means the R-INLA software. As a general rule prior
215 distributions for the regression coefficients of the logistic regression model (4), means in the normal
216 models (1,2) and mean (in logarithmic scale) of the Poisson models (3.1, 3.2) were elicited by means of
217 normal distributions centered at zero and a wide variance (100). Prior for the standard deviations (in
218 terms of precision) were defined through a log Gamma distribution ($\text{logGamma}(1,0.01)$) which is a
219 default distribution in the INLA software.

220 Results

221 Soil and plant diversity

222 Soil analysis showed that the most relevant differences were in the organic carbon and nitrogen, which
223 were higher in organic than in conventional farms, with a posterior probability of at least 0.95 (Table 2).

224 Plant diversity measured as the number of crops (D_c) and the number of wild plants (D_w) per farm was
225 higher in organic than in conventional farms with posterior probabilities of 1.00 for both D_c and D_w (Table
226 3A), indicating that these differences are relevant with respect to the agricultural system. Also, the plant
227 diversity of the farm surroundings was much higher in organic than in conventional farms (Table 3B),
228 with posterior probability 1.00.

229 Early viral infection risk in organic and conventional farms

230 When comparing farms in June (early crop stages) of 2012 and 2014, the overall infection risk (risk
231 infection by any of the three viruses analyzed) was lower in the organic farms compared with the
232 conventional ones (Fig. 2). In 2012 the difference was small (0.24 and 0.33 for organic and conventional,
233 respectively), with probability 0.85, whereas in 2014 the conventional farms showed a much higher
234 infection risk (0.58) with respect to the organic farms (0.24), with probability 1.00.

235 ToMV was the main contributor to the overall viral infection and followed a similar pattern, with
236 lower infection risk in organic than in conventional farms. In 2012 the difference was small with
237 probability 0.69 and in 2014 the infection risk was more than twice in conventional than in organic farms
238 (Fig. 2), with probability 1.00. CMV infection risk was a little lower in organic (0.11) than conventional
239 farms (0.13) in 2012, with probability 0.65, but it dropped to 0.03 for both organic and conventional
240 farms in 2014. No single tomato plant was found to be infected with TSWV in all surveys performed.

241 Late viral infection risk in organic and conventional farms.

242 To test the viral infection risk in a later developmental stage, the same farms sampled in June of 2014
243 were analyzed in September, using other randomly selected plants. In June, the overall infection risk was
244 lower in organic (0.26) than in conventional (0.66) farms, with probability 1.0. In September the organic
245 farms showed also lower infection risk than conventional farms with probability 0.87, although the
246 difference between both agricultural systems decreased (Fig. 3). ToMV showed the same trend since
247 CMV infection risk was scant (≤ 0.03) and TSWV was not detected in any plant in 2014 (Fig. 3).

248 **Discussion**

249 Understanding how organic management affects virus diseases to develop disease control strategies
250 under the agroecological paradigm is challenging and remains underexplored given the diversity of
251 agronomical practices and the complex and dynamical interplays of numerous factors affecting virus
252 epidemiology, such as wild and crop host populations, local climate, topography, insect vector
253 populations, etc. The first step would be to evaluate the incidence of different plant viruses in different
254 crops and geographical locations comparing organic management with other agronomic systems, but

255 this subject was never addressed. Our analysis of ToMV, CMV and TSWV in crops of tomato, lacking
256 resistance to these viruses, in Eastern Spain in two nonconsecutive years showed that organic farms had
257 a lower viral infection risk than in those under conventional management. ToMV contributed mainly to
258 the infection risk since CMV incidence was very low and TSWV did not infect any plant. It seems
259 reasonable that the transmission risk of ToMV by seed and contact were similar for organic and
260 conventional management since there were not differences on the seed source and plant handling.

261 These organic farms also had higher organic matter in soil and plant diversity as described for
262 other organic agrosystems (Mäder et al. 2002, Tuck et al. 2004, Bengtsson et al. 2005, Pimentel et al.
263 2005). Organic matter in soil might promote microbial diversity and beneficial bacteria and fungi
264 associated to plant roots inducing systemic resistance (Entz et al. 2004, Pieterse et al. 2014).
265 Accumulation of *Tomato yellow leaf curl Sardinia virus* was reduced in tomato plants when roots were
266 colonized by mycorrhiza (Maffei et al. 2014). Empirical evidence of the effect of plant diversity on viral
267 diseases is limited. A study of *Pepper golden mosaic virus* and *Pepper huasteco yellow virus* in
268 populations of wild pepper under different levels of human management showed that infection risk
269 increased with lower plant species diversity (Pagán et al. 2012). This negative correlation could be due
270 the presence of wild species acting as reservoirs of natural enemies of insect vectors of plant viruses.
271 Unfortunately, the low incidence of the aphid-transmitted CMV and absence of the thrips-transmitted
272 TSWV in our surveys precluded any interpretation on the dynamics of these vectors. No important
273 populations of aphids or thrips were observed during crop development. Also, high plant diversity might
274 harbor a more complex microflora and insect population which would enhance or trigger systemic
275 acquired resistance (Fu and Dong 2013).

276 Under our knowledge, this is the first study evaluating viral infection risk in organic crops. More
277 studies with different viruses, crops, cultivars, farming systems and geographic locations with the
278 adequate analytical and conceptual tools are necessary to gain a full picture of how organic management
279 affects viral disease. Also, multidisciplinary approaches, integrating different disciplines such as
280 agronomy, botany, virology, soil bacteriology, entomology, plant physiology, molecular biology,
281 system biology and statistics are necessary to gain insight on the underlying mechanisms and ecological
282 interactions in soil and plants, aimed to improve disease control strategies compatible with an
283 environmentally sustainable agriculture.

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288 **Compliance with ethical standards**

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403

404 **Figures and Tables**

405 **Figure 1.** Areas surveyed in Eastern Spain, corresponding to the provinces of Valencia and Alicante.
406 Red or green circles represent farms under conventional or organic management, respectively.

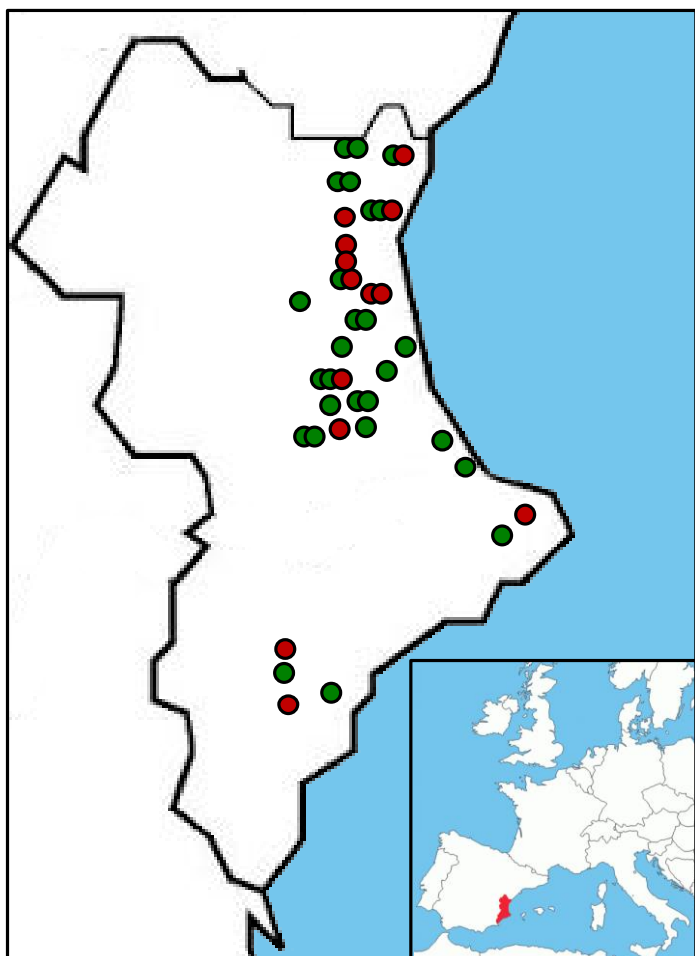
407 **Figure 2.** Viral infection risk by any of the three viruses analyzed (Overall) and by ToMV and CMV,
408 separately in organic and conventional farms in June of 2012 and 2014. No plant resulted infected by
409 TSWV. Dots represent posterior means and vertical segments are 95% credible intervals.

410 **Figure 3.** Viral infection risk by any of the three viruses analyzed (Overall) and by ToMV, and CMV
411 separately in organic and conventional farms in June and September of 2014. No plant resulted infected
412 by TSWV. Dots represent posterior means and vertical segments are 95% credible intervals.

413

414 **Figure 1**

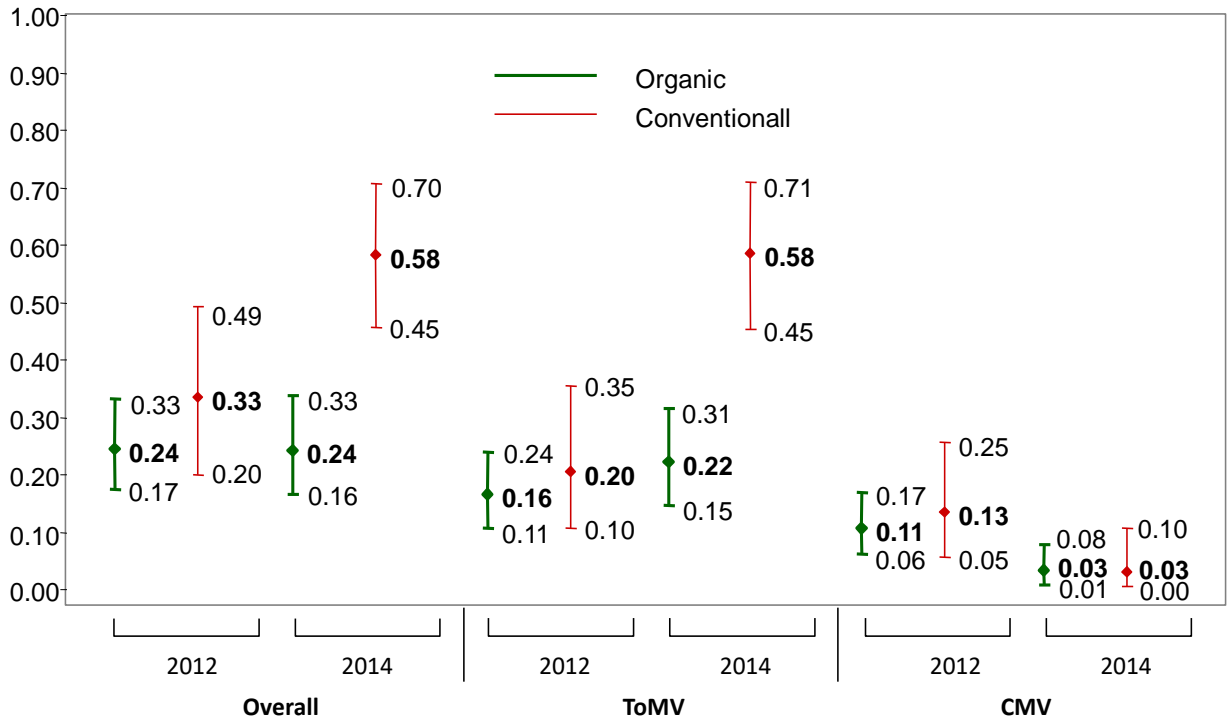
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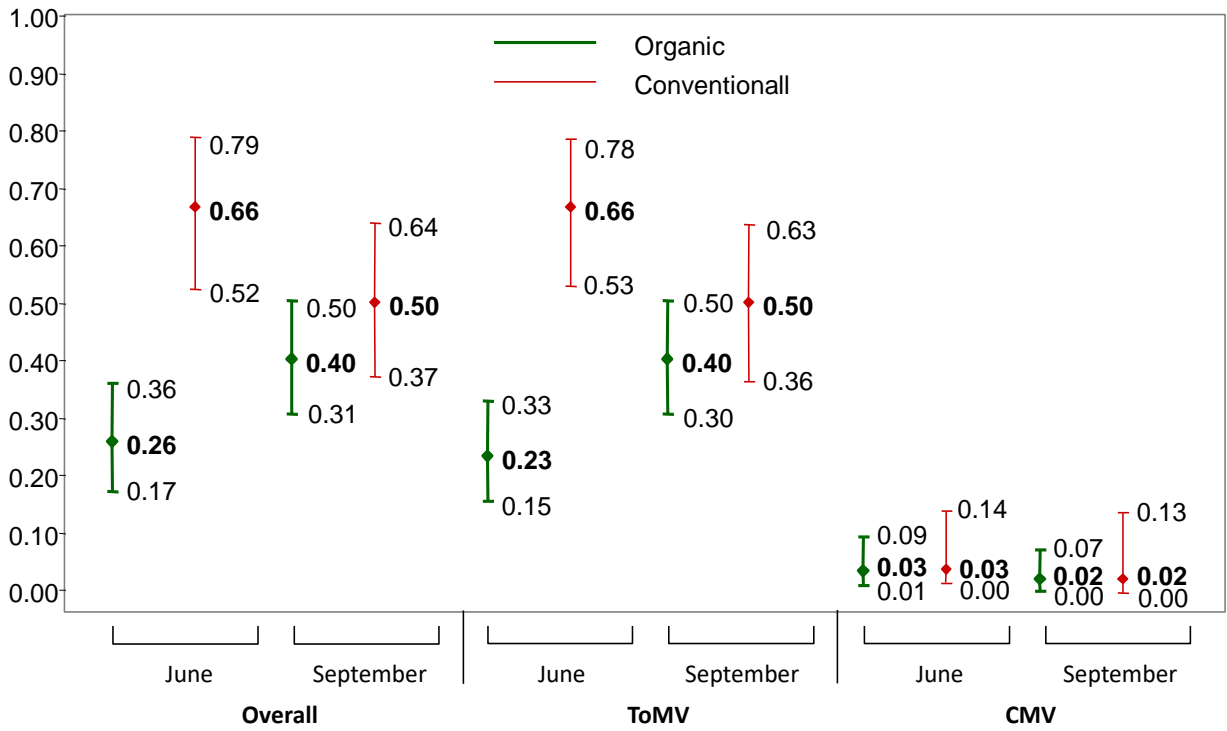
418 **Figure 2**



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421 **Figure 3**



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Table 1. Synthetic oligonucleotide primers for RT-PCR

Virus	Primer^a	Sequence 5'-3'	Position^b	Size^c
ToMV	ToMV-1F	TGCAGCAAAGGTAATAGTAG	1841-1860	338
	ToMV-1R	CCGAACTTTTGACGAGTTTC	2280-2293	
CMV	CMV-1F	CTAACTTTAGAGTCTTGTCGG	1343-1363	448
	CMV-1R	ACCATAGCAGAGATGGCGG	1622-1680	
TSWV	TSWV-S2	GAACCTGTGCAAAAGATGTGTGAG	1122-1145	544
	TSWV-S8	GATCGAGATGTGCTATAATCAAGC	601-624	

426

^aToMV and CMV primers (designed here), and TSWV primers (Debreczeni et al. 2015).

427

^b Nucleotide positions of the primers in the genomic RNA of ToMV (GenBank AJ417701), RNA 3 of CMV (GenBank KP033526) and S segment of TSWV (GenBank AY74479).

428

429

^c RT-PCR product size

430

431 **Table 2.** Soil characteristics (mean \pm standard deviation) in organic and conventional farms

Soil characteristic	Organic	Conventional	Prob (organic > conventional)
Electrical conductivity (dS/m)	0.45 \pm 0.24	0.54 \pm 0.16	0.30
pH	8.32 \pm 0.11	8.31 \pm 0.10	0.57
Organic carbon (%)	1.83 \pm 0.47	1.21 \pm 0.31	0.96
Organic nitrogen (%)	0.18 \pm 0.05	0.12 \pm 0.03	0.95
Carbon/nitrogen ratio	10.15 \pm 0.59	10.47 \pm 0.39	0.23
Carbonates (%)	28.90 \pm 12.41	39.81 \pm 8.17	0.11
Active lime (%)	6.69 \pm 2.42	8.83 \pm 1.58	0.12
Phosphorous (mg/kg)	96.07 \pm 32.54	103.71 \pm 22.9	0.37
Sodium ions (me/100g)	1.03 \pm 1.00	1.53 \pm 0.29	0.29
Potassium ions (me/100g)	1.60 \pm 0.71	1.54 \pm 0.46	0.55
Calcium ions (me/100g)	24.73 \pm 2.04	25.70 \pm 1.34	0.26
Magnesium ions (me/100g)	3.68 \pm 1.06	3.92 \pm 0.69	0.38

432 *Data from 20 farms (15 organic and 5 conventional)

433

434 **Table 3.** Plant diversity

435 **A)** Plant diversity within farms (mean \pm standard deviation)

Diversity	Organic	Conventional	Prob (organic > conventional)
Number of crop species (Dc) ^a	7.43 \pm 0.71	1.69 \pm 0.58	1.00
Number of wild species (Dw) ^a	12.89 \pm 0.93	7.90 \pm 1.25	1.00

436 ^aData from 20 farms (15 organic and 5 conventional)

437 **B)** Plant diversity in the farm surroundings (*Ds*)

Diversity (<i>Ds</i>)^a			
Management	Low^b	Medium^b	High^b
Organic	0.14	0.40	0.46
Conventional	0.72	0.22	0.06

438 ^{a*}Data from 20 farms (15 organic and 5 conventional)

439 ^bProportion of farms for the three categorical values of *Ds*: low, medium and high