



Factors affecting the occurrence of *Escherichia coli* O157 contamination in irrigation ponds on produce farms in the Suwannee River Watershed

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3 **Suwannee River Watershed**

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23

24 **Abstract** Outbreaks of enteritis caused by *Escherichia coli* O157 associated with fresh produce
25 have resulted in questions about the safety of irrigation water; however, associated risks have not
26 been systematically evaluated. In this study, the occurrence and distribution of the human
27 pathogen *E. coli* O157 from vegetable irrigation ponds within the Suwannee River Watershed in
28 Georgia were investigated and the relationship to environmental factors was analyzed. Surface
29 and subsurface water samples were collected monthly from 10 vegetable irrigation ponds from
30 March, 2011 to February, 2012. *E. coli* O157 was isolated from enriched filtrates on
31 CHROMagar™ and Sorbitol MacConkey agar media and confirmed by an agglutination test.
32 Presence of virulence genes *stx1*, *stx2* and *eae* was tested by PCR. In addition, 27 environmental
33 variables of the sampled ponds were measured. Denaturing gradient gel electrophoresis was
34 conducted for the analysis of bacterial communities in the water samples. Biserial correlation
35 coefficients were calculated to evaluate the correlations between the environmental factors and
36 the occurrence of *E. coli* O157. Stepwise and canonical discriminant analyses were used to
37 determine the factors that were associated with the presence and absence of *E. coli* O157 in
38 water samples. All 10 ponds were positive for *E. coli* O157 some of the time, mainly in summer
39 and fall of 2011. The temporal distribution of this bacterium differed among the 10 ponds.
40 Temperature, rainfall, populations of fecal coliform, and culturable bacteria were positively
41 correlated with the occurrence of *E. coli* O157 ($P < 0.05$), while the total nitrogen concentration,
42 oxidation-reduction potential and dissolved oxygen concentration were negatively correlated
43 with the occurrence of this pathogen ($P < 0.05$). Temperature and rainfall were the most
44 important factors contributing to the discrimination between samples with and without *E. coli*
45 O157, followed by bacterial diversity and culturable bacteria population density. Bacterial
46 numbers and diversity, including fecal coliforms and *E. coli* O157, increased after rainfall (and

47 possibly run-off from pond margins) in periods with relatively high temperatures, suggesting that
48 prevention of run-off may be important to minimize the risk of enteric pathogens in irrigation
49 ponds.

50

51 *Key words:* *Escherichia coli* O157, irrigation ponds, fecal indicators, biserial correlation,
52 discriminant analysis

For Review Only

53 **Introduction**

54 Enterohemorrhagic *Escherichia coli* (EHEC), an important zoonotic pathogen, is attracting
55 global attention. *E. coli* O157 is typically responsible for most infections (80%) among the Shiga
56 toxin producing bacteria in the United States and in some European countries (Muniesa et al.
57 2006; Paton and Paton 1998). The pathogenicity of *E. coli* O157 is associated with a number of
58 virulence factors, in particular Shiga toxins 1 and 2 (encoded by *stx1* and *stx2* genes), and intimin
59 (encoded by the *eae* gene).

60 Contamination of water bodies with fecal matter or inadequately treated water bodies
61 have led to many outbreaks of *E. coli* O157 in the past, which showed that water contamination
62 with *E. coli* O157 is a major issue of concern and needs more attention and research to control
63 the outbreaks occurring worldwide (Bruneau et al. 2004; Hruday et al. 2003; Olsen et al. 2002).
64 In addition, irrigation water may play an important role in contaminating soils and vegetables
65 with *E. coli* O157 (Solomon et al. 2002). *E. coli* O157:H7 from irrigation sources can adhere to
66 plants, enter into plants, and survive for long periods of time (Franz and van Bruggen 2008;
67 Franz et al. 2007; Semenov et al. 2009; Solomon et al. 2002). The 2006 multistate *E. coli* O157
68 outbreak associated with spinach was reported to be related to contaminated irrigation water
69 (Gelting et al. 2011). However, associated risks of irrigation water for the contamination of
70 *Escherichia coli* O157 have not been systematically evaluated.

71
72 Fecal pollution, including *E. coli* O157, is traditionally evaluated by detecting fecal
73 indicator bacteria like fecal coliforms and generic *E. coli* (USEPA 2002). However, some studies
74 provided evidence that these indicators may not be adequate to assess the health risks of surface
75 water (Ahmed et al. 2009). Chigor et al. (2010) reported that some environmental factors,

76 including water turbidity, and concentrations of nitrate, phosphate and chloride were positively
77 correlated to the population of fecal coliforms in a river used for fresh produce irrigation in
78 Nigeria (Chigor et al. 2010). Rain events may promote pathogen transport from forested and
79 grassed buffer zones into farm ponds (Gaertner et al. 2009). Survival of *E. coli* O157 strains in
80 the environment depends on physiological differences in terms of the ability to use carbon
81 compounds under aerobic versus semi-anaerobic conditions (Franz et al. 2011). Thus, the risk of
82 survival of this pathogen is related to the availability of organic carbon and nitrogen sources as
83 affected by microbial competition (Franz et al. 2008b; Franz et al. 2011), as well as average
84 temperatures and their daily amplitudes (Semenov et al. 2007) and moisture conditions
85 (Semenov et al. 2010). In addition a negative correlation between enteropathogen populations
86 and microbial diversity has been reported for manure, soil and plants (Klerks et al., 2007; van
87 Elsas et al., 2012; van overBeek et al., 2010).

88 The Suwannee Watershed, including all the creeks, streams, rivers and springs that feed
89 the Suwannee River, is an ideal location to investigate the risk of transmission of *E. coli* to
90 vegetables, because waterways and irrigation ponds are interspersed with irrigated vegetable
91 production areas. This watershed extends from South Central Georgia to Northwest Central
92 Florida and drains 9,950 square miles
93 (<http://www.epa.gov/owow/showcase/suwaneeriver/location.html>). Fruit and vegetable crops in
94 this region are mainly irrigated via drip systems, overhead sprinklers, or pivots that are used
95 daily during periods of high evapotranspiration (May-October). The water source is primarily
96 from surface water captured in small man-made reservoirs. Many ponds are supplemented with
97 ground water, pumped from the Floridian Aquifer, to maintain volumes during periods without
98 stream flow. Many growers are testing their water sources for generic *E. coli*, depending on the

99 requirements of the buyers of their produce. These requirements vary from being very lax to a
100 strict requirement for a 5-day geometric mean of *E. coli* for each irrigation source. However, the
101 relationship between these test results and the presence of virulent *E. coli* has not been
102 established (Shelton et al. 2011).

103 The objectives of this study are to assess the prevalence of *E. coli* O157 in the irrigation
104 ponds located in the Suwannee river watershed, evaluate the relationship between *E. coli* O157
105 occurrence and environmental factors, and investigate if current fecal indicators are adequate for
106 the prediction of the presence and virulence of *E. coli* isolates.

107

108 **Materials and Methods**

109 **Irrigation ponds and water sampling**

110 The study was conducted from March 2011 to February 2012 within the Suwannee River
111 watershed. The study area lies in the heart of a principal agricultural production area in the state
112 Georgia, where vegetable acreage with supplemental irrigation is increasing rapidly. Ten
113 irrigation ponds that serve as water sources for vegetable and field crops spread throughout this
114 area were selected for the detection of *E. coli* O157 and measurement of environmental factors.
115 The sizes and depths of the 10 ponds varied from 12,000 to 93,000 m², and 3 to more than 10
116 meters deep, respectively. The distances among the ponds range from 30 km to 200 km. In this
117 study, two water samples (10 L) were collected monthly from each pond close to the pumps at
118 two depths: near the irrigation water intake level and at 50 cm below the surface. Collected water
119 samples were stored on ice in the field and transported to lab refrigerators for analysis. Totally
120 240 water samples were collected from these 10 irrigation ponds during the 12 months for *E. coli*
121 O157 detection and measurement of environmental factors.

122 Isolation and identification of *E. coli* O157

123 Three 500 mL aliquots of each water sample were vacuum filtered through a 0.8 µm sterile
124 isopore membrane and then a 0.45 µm sterile nitrocellulose membrane (Millipore Corporation,
125 Billerica, MA). Both membranes were incubated without shaking at 37°C in 50 mL tubes
126 containing 20 mL of Luria Bertani (LB) broth. After incubation for 18-20h, 1 mL enriched
127 culture was transferred to 19 mL modified trypticase soy broth (TSB) containing 20 mg/L
128 novobiocin (Jokinen et al. 2010) and incubated at 42 °C overnight. A bacterial suspension from
129 each tube was first streaked on CHROMagar™ O157 with 2.5 mg/L potassium tellurite
130 (CHROMagar, Paris, France) and incubated at 37°C for 24 h. CHROMagar™ O157 is a
131 selective culture medium for isolation and enumeration of *E. coli* O157. Suspect colonies (color
132 mauve) were then streaked on sorbitol MacConkey agar plates containing 50 mg/L cefixime and
133 2.5 mg/L tellurite and incubated at 37°C for 24 h. Because of the pathogen's inability to ferment
134 sorbitol, *E. coli* O157 colonies are colorless in sorbitol MacConkey agar. Three colonies were
135 randomly selected on each plate if more colonies that looked like *E. coli* O157 were present per
136 plate. Positive colonies on sorbitol MacConkey agar plates were stored at -80 °C and tested for
137 agglutination using O157 BD Difco™ *E. coli* Antisera (Difco, Detroit, MI) for confirmation.
138 Streaking of colonies and agglutination tests were conducted in triplicate.

139 Virulence gene assays

140 Genomic DNA was extracted from *E. coli* O157 isolates using illustra™ bacteria genomicPrep
141 Mini Spin Kit (GE Healthcare, Buckinghamshire, UK). The presence of virulence genes *stx*₁,
142 *stx*₂ and *eae* were determined by PCR as reported before (Sanchez et al. 2010). *E. coli* O157
143 strains ATCC 43895 and ATCC 43888 were used as positive and negative controls, respectively.

144 The presence of these genes in *E. coli* O157 isolates serves as an indication of the potential
145 virulence of the strains obtained.

146 **Fecal indicator analysis**

147 Water samples were screened for presence and absence of *E. coli* in Quanty-Tray cells and
148 positive samples enumerated as MPN cells per 100 mL (Edberg et al. 1990). Two dilutions of
149 each sample were assayed for MPN of generic *E. coli* (IDEXX Laboratories, Inc., Westbrook,
150 ME). Fecal coliform bacteria (CFU/100 mL) analysis of two dilutions prepared from each
151 sample were performed using membrane filtration techniques as described before (Stuart et al.
152 1977).

153 **Chemical and physical parameters of irrigation water**

154 During sampling from irrigation ponds, pond water was tested for temperature (Temp, °C), pH,
155 specific conductance (SpCond, mS/cm), dissolved oxygen percentage (DO, %), dissolved
156 oxygen concentration (DO Conc, mg/L), dissolved oxygen charge (DO Charge), turbidity
157 (nephelometric turbidity units, NTU), and oxidation reduction potential (ORP, mV) with an YSI®
158 6600 Multiparameter Sonde (Yellow Springs, OH). All water samples were analyzed for the
159 concentrations of nitrate (mg/L) and the soluble reactive portion of total phosphorus (Ortho-P,
160 mg/L) and total suspended solids (TSS, mg/L) using standard analytical techniques in the lab
161 (APHA 1998). Samples were also analyzed for dissolved organic carbon (DOC, mg/L) and total
162 nitrogen (TN, mg/L) contents using TOC-VCPH/CPN and TNM-1 analyzers, respectively
163 (Shimadzu Scientific Instruments, Kyoto, Japan). All tests were performed in duplicate.

164 **Weather information collection and analysis**

165 Temperature ($^{\circ}\text{C}$) and rainfall data (mm) of the closest weather stations to the 10 irrigation ponds
166 were collected from the Georgia automated environmental monitoring network
167 (<http://www.georgiaweather.net/>). The distance from irrigation ponds to their closest weather
168 stations ranged from 10-40 km. Average temperature and total rainfall from weather stations
169 nearby the ponds in the second but last week (L2 avg Tm and L2 tot rain) and last week before
170 sampling (L avg Tm and L tot rain) and between samplings (Average Tm and Total rainfall)
171 were calculated based on the daily weather information.

172 **Copiotrophic and culturable bacterial populations**

173 Water samples were dilution-plated on carbon-rich and carbon-poor media (Senechkin et al.,
174 2010) in triplicate and incubated for 2 or 15 days, respectively, to enumerate the populations of
175 copiotrophic (Copio, CFU/100 mL on carbon-rich media) and culturable (Culturable, CFU/100
176 mL on carbon-poor media) bacteria, respectively, as reported elsewhere (Franz et al. 2008a).

177 **DNA extraction of water samples**

178 200 mL of each water sample was vacuum filtered through a 0.22 μm sterile nitrocellulose
179 membrane (Millipore Corporation, Billerica, MA). In case of membrane clogging during
180 filtration, multiple membranes were used. DNA of bacteria captured by the membranes was
181 extracted using a PowerWater[®] DNA Isolation Kit (MOBIO Laboratories, Inc., Carlsbad, CA)
182 and stored at -80°C until use.

183 **Polymerase chain reaction (PCR) and denaturing gradient gel electrophoresis (DGGE)**

184 To investigate a possible relationship between the occurrence of *E. coli* O157 and bacterial
185 communities in the irrigation water, the Shannon-Wiener diversity index (Shannon diversity),
186 Simpson diversity index (Simpson diversity), the species richness and evenness of bacterial

187 communities were determined as described before (Klerks et al. 2007). Briefly, extracted DNA
188 was amplified by PCR using primers for 16S rDNA genes of eubacteria with primers R1378 and
189 U968 (Klerks et al. 2007) and DGGE was performed using a gradient maker and a Manostat[®]
190 Carter Pumpdrive (Thermo Fisher Scientific Inc., Barrington, IL) and electrophoresis in 0.5x
191 Tris-acetate-EDTA buffer for 16 h at 100 V at a constant temperature of 60°C. After
192 electrophoresis, the gels were stained for 30 min with SYBR Gold nucleic acid gel stain (Life
193 Technologies, Inc., Carlsbad, CA) and bands were visualized by the Molecular Imager[®] Gel
194 Doc[™] XR System (Bio-Rad Laboratories, Inc.) and standardized by referring to the DGGE
195 marker. The DGGE banding patterns were analyzed using Gelcompar II software (version 1.61;
196 Applied Maths, Woluwe, Belgium) for gel comparison. Each gel contained four marker lanes as
197 standards and background corrections were performed before identification of bands with 5%
198 significance threshold. Correspondence of operational taxonomic units (OTUs or bands) between
199 different samples was performed with 1% dynamic range settings. DGGE analysis was done in
200 duplicate on separate gels. The Shannon diversity, Simpson diversity, species richness and
201 evenness of bacterial communities were calculated as the means of the two replicas.

202 **Statistical analysis**

203 The Chi square (χ^2) test was conducted to compare the occurrence of *E. coli* O157 in surface and
204 subsurface water samples. Space (pond) and time (season) effects on the occurrence of *E. coli*
205 O157 were assessed by logistic regression analysis. Unpaired t-tests were performed to compare
206 log-transformed population densities of generic *E. coli* and fecal coliform bacteria in the water
207 samples with those of *E. coli* O157 carrying virulence genes and the samples without *E. coli*
208 O157 collected in the same months. Data were tested for normality after log-transformation.
209 Biserial correlation coefficients were calculated to evaluate the correlations between the 27

210 environmental factors (Table 1) and the occurrence of *E. coli* O157 isolated from irrigation
211 ponds (Portney and Watkins 1993). Biserial analysis is recommended for assessing the
212 correlation between a continuous variable and a binomial (dichotomous) one (Portney and
213 Watkins 1993). In this case the presence/absence of *E. coli* O157 was the dichotomous variable,
214 and the values of the parameters tested were continuous variables.

215 For discriminant analysis, the factors to be considered should be normally distributed and
216 not be strongly correlated with each other (Afifi and Clark 1984). Moreover, the number of
217 factors should be considerably smaller than the number of observations. Therefore, all data were
218 first standardized and normalized and all normalized factors were subjected to Pearson's
219 correlation analysis, so that groups of factors could be distinguished that 'belonged together'
220 (were correlated). Grouping was based on relatively high Pearson's correlation coefficient values
221 ($r > 0.7$) between factors, and one factor in each group was selected to be included in the
222 discriminant analyses (to avoid highly correlated factors in the analyses). Stepwise discriminant
223 and canonical discriminant analyses were performed based on the measurements of 18 selected
224 environmental factors after standardization and normalization in SAS. The inclusion criterion for
225 discriminant analysis was $P = 0.15$ (Afifi and Clark 1984). Classification values were assigned to
226 all *E. coli* O157 positive water samples and the same number of randomly selected negative
227 samples (because the number of samples in the different classes should be about equal for the
228 analysis). Stepwise discriminant analysis was used to identify variables that contributed most to
229 the classification. Canonical discriminant analysis was used to determine the magnitude and
230 direction of the association of individual variables with the classification variable. The same
231 discriminant analyses were performed based on the relative intensities of 65 OTUs of DGGE

232 data to group the 240 water samples according to the predicted presence or absence of *E. coli*
233 O157.

234 Chi square tests were conducted in Microsoft Excel. All other statistical analyses (logistic
235 regression, t-tests, correlation and discriminant analyses) were performed using SAS (SAS
236 release 9.2, SAS Institute Inc., Cary, NC).

237

238 **Results**

239 **Spatial and seasonal distribution of *E. coli* O157 in irrigation water**

240 All ten irrigation ponds assessed in the southern Georgia region of the Suwannee River
241 Watershed were positive for *E. coli* O157 in water samples at some time point during this survey
242 (Fig. 1A). The overall percentages of positive samples for surface (11.7%) and subsurface
243 (17.5%) water samples were not significantly different ($\chi^2 = 1.639$, $P = 1$), so the data for the
244 prevalence of *E. coli* O157 in both water samples from each pond per month were lumped in this
245 study with an overall prevalence of 14.6%. Although there were no statistically significant
246 spatial (pond) differences within the watershed with respect to the occurrence of *E. coli* O157 (P
247 = 0.1025), pond 6 was most frequently positive (50% of the sampling times), while ponds 2, 4, 5,
248 7 and 8 were most frequently negative (83.3%) for *E. coli* O157.

249 There were significant seasonal differences in the detection of *E. coli* O157 ($P < 0.001$,
250 Fig. 1A). The pathogen was isolated every month from May to December of 2011 from some
251 irrigation ponds. The overall percentages of *E. coli* O157 occurrence in summer (June to August,
252 51.7%) and fall (September to November, 31.1%) were significantly higher than those in spring
253 (March to May, 10.3%) and winter (December to February, 6.9%).

254 Out of all colonies isolated from the water samples during this study, only 44 were
255 positive in CHROMagarTM O157 and sorbitol MacConkey, as well as for the agglutination tests.
256 From the 44 isolated *E. coli* O157 colonies, three isolates (from pond 10 in August and pond 10
257 in June and August) were positive for *stx*₂ gene, one isolate (from pond 4 in November) was
258 positive for *stx*₁ gene, and one isolate (from pond 2 in July) carried all three *stx*₁, *stx*₂ and *eae*
259 virulence genes as indicated by conventional PCR. Pond 2 was adjacent to a tomato field, and
260 discarded tomato fruits were noticed floating in the pond when sampling in July. The populations
261 of generic *E. coli* and fecal coliform bacteria in the water samples with or without *E. coli* O157
262 carrying virulence genes were not significantly different (generic *E. coli*, $P = 0.569$; fecal
263 coliforms, $P = 0.311$).

264 **Relationships among environmental factors and their correlations to the occurrence of *E.***
265 ***coli* O157 in irrigation ponds**

266 Overall, 27 environmental factors were evaluated as potential indicators for the risk of *E. coli*
267 O157 contamination (Table 1, Table S1). Based on biserial correlation analysis, Average Tm,
268 Total rainfall, culturable bacteria, copio bacteria and fecal coliforms were positively correlated to
269 *E. coli* O157 occurrence in samples from the ten irrigation ponds. However, ORP, TN, Nitrate
270 and DO concentration were negatively correlated with the occurrence. The positive correlation
271 between Simpson diversity and *E. coli* O157 occurrence was almost significant ($P = 0.0891$).
272 The temporal variation in the average values of the main environmental factors that correlated
273 with *E. coli* O157 was similar or opposite to the temporal variation in *E. coli* O157 occurrence
274 (Fig. 1 B-D, Table S2).

275 Environmental factors, which were highly positively correlated to each other ($r > 0.7$),
276 were assigned to one factor group (Table S3). The factors in the first column of the table, which

277 had the highest correlation to *E. coli* O157 occurrence in each factor group, as well as
278 independent factors (that were not correlated to other environmental factors) were selected for
279 further discriminant analysis.

280 **Correlations between OTUs of DGGE and the occurrence of *E. coli* O157 in irrigation** 281 **ponds**

282 In total, 65 OTUs (bands) were generated through DGGE analysis of the bacterial communities
283 in the 240 water samples. Based on biserial correlation analysis, the intensities of 12 bands were
284 significantly correlated to *E. coli* O157 occurrence ($P < 0.05$), and the correlations of another 6
285 bands were possibly significant ($0.1 > P > 0.05$) (Table S4). None of these bands were highly
286 correlated ($r > 0.7$) to each other.

287 **Environmental factors and bacterial OTUs affecting the distinction between the presence** 288 **and absence of *E. coli* O157 in irrigation ponds**

289 Discriminant analysis on 58 water samples positive for *E. coli* O157 (surface and subsurface
290 water samples were considered as replicate samples from the same pond because averages of
291 both samples were statistically indistinguishable) and the same number of randomly selected
292 negative water samples resulted in significant separation of water samples with and without *E.*
293 *coli* O157. The separation of samples into two *E. coli* O157 occurrence classes, based on the
294 environmental factors (Fig. 2) or OTUs of DGGE (Fig. 3), are illustrated in a plot of canonical
295 variable one versus the variable with the highest correlation to occurrence of the pathogen.
296 Canonical variable one is the linear combination that maximized the correlation with *E. coli*
297 O157 occurrence.

298 Stepwise discriminant analysis for the presence or absence of *E. coli* O157 in each water
299 sample identified six environmental factors (Table 2) and 26 DGGE OTUs (data not shown) that
300 contributed to the classification ($P < 0.05$). The selected OTUs by stepwise discriminant analysis
301 that affected the classification of *E. coli* O157 presence included all 12 significantly correlated
302 bands (Table S4) and other bands with relatively high correlation coefficients. The selected
303 environmental factors and OTUs did not change when different sets of random negative samples
304 were used for the analysis. Because the use of 12 microbial species for estimating the presence of
305 *E. coli* O157 is not practical, no attempt to sequence the bands with significant correlations was
306 made.

307

308 Discussion

309 *E. coli* O157 was detected in the irrigation ponds located in the Suwannee River Watershed with
310 an overall prevalence of 14.6%, which indicated that irrigation water could be a contamination
311 source of this pathogen for fresh vegetables and fruits in the field. Although there are no records
312 linking *E. coli* O157 infections to contaminated vegetables or fruits in this region, there were
313 several outbreaks of *E. coli* O157 due to contaminated water sources like swimming pools. Since
314 the studied pond water serves as irrigation for vegetable crops like tomatoes and lettuce that are
315 likely eaten raw, the epidemiological importance of *E. coli* O157 in this water source cannot be
316 overlooked. The concern here is heightened by recent studies about the internalization of
317 foodborne pathogens into the edible parts of plants (Franz et al. 2007; Gu et al. 2011). Enteric
318 pathogens coming from feces of wild animals could have reached the irrigation ponds,
319 potentially exposing the plants to *E. coli* O157.

320 The virulence of *E. coli* O157 has mainly been associated with the production of Shiga
321 toxin genes (*stx1* and *stx2*) and the intimin gene (*eae*), although the presence of *stx1* and/or *stx2*
322 does not by itself prove that the strains are pathogenic. In this study, five isolates were positive
323 for at least one of these virulence genes, but only one isolate from pond 2 with discarded tomato
324 fruits carried all three virulence genes. These isolates may pose serious threats for human health
325 when the virulent genes are expressed in sufficient quantities. However, it should be realized that
326 there are many different genotypes of *E. coli* O157, including small differences in the toxin
327 genes with several *stx2* subtypes, that may differ in their pathogenicity towards humans (Franz et
328 al. 2012). Conversely, other serotypes not screened in this study might be associated with EHEC
329 disease; therefore, the presence of potential pathogens may be underestimated.

330 The significantly higher occurrence of *E. coli* O157 during the summer and fall could be
331 partly attributable to run-off of soil by rain into the irrigation ponds and also to the higher
332 multiplication rates at the higher temperatures during those seasons (Semenov et al. 2007;
333 Semenov et al. 2009). Irrigation of the fruit and vegetable crops in this region were mainly
334 applied from May to October to compensate for the high evapotranspiration, which is the period
335 with high risks of contamination. If this period cannot be avoided for the planting of vegetable
336 crops, like fall tomato crops, more intensive monitoring of the pathogen should be conducted.

337 Populations of fecal coliforms, but not of generic *E. coli*, were correlated to the
338 occurrence of *E. coli* O157, and might be a suitable indicator for the prediction of this pathogen
339 in irrigation ponds. However, there was a poor correlation between fecal indicators and
340 potentially virulent *E. coli* O157 isolated in this study as well as in previous studies (Ahmed et
341 al. 2009). Therefore, testing for fecal indicators alone may not be adequate to assess the
342 microbiological quality of surface water and potential health risks. In addition, the presence of

343 virulence genes in *E. coli* O157 isolates was not related to the occurrence of *E. coli* O157. For
344 example, pond 6 was most frequently positive (50%) for *E. coli* O157 occurrence, but no
345 virulence genes were amplified from the bacterial colonies isolated from this pond. Thus, the use
346 of the tested indicators alone might not be appropriate for estimating the occurrence of virulent
347 *E. coli* O157.

348 Correlation and discriminant analyses indicated that the presence of *E. coli* O157 in water
349 samples from irrigation ponds was positively associated with average temperature, total rainfall,
350 populations of culturable, copiotrophic and fecal coliform bacteria, which were higher in *E. coli*
351 O157 positive water samples, while the TN, ORP and DO concentration were negatively
352 correlated to the occurrence of this pathogen. Higher temperatures correlated with higher
353 presence of the pathogen. This might be due to a combination of factors including the closer-to-
354 optimal temperatures for growth of the pathogen as well as populations of culturable,
355 copiotrophic and fecal coliform bacteria; and an increase in wildlife (and their droppings) during
356 warmer seasons. Temperature, total rainfall, Simpson diversity and evenness of bacterial
357 communities, culturable bacterial population and phosphorous concentration were consistently
358 selected by stepwise discriminant analysis for the classification of the presence of *E. coli* O157
359 (Table 2). The negative correlation between TN and the presence of *E. coli* O157 could be
360 explained by the relative infrequent samplings (once a month), while microbial dynamics have a
361 time constant of less than a day. Eutrophication by run-off from the first rainfall event and
362 discarded produce in early Spring probably led to a temporary increase in TN, immediately
363 followed by an increase in copiotrophic bacteria and a decline in TN; the increase in coliforms
364 and *E. coli* O157 occurred in early and midsummer, after TN had already declined. The
365 difference in the speed of microbial dynamics and the sampling interval could have been the

366 reason why TN was not selected by stepwise discriminant analysis to explain the occurrence of
367 *E. coli* O157. Nevertheless, the significant positive correlation between culturable bacterial
368 populations and the pathogen and the selection of phosphorus concentration as a classification
369 factor indicate a potential relation between *E. coli* O157 occurrence and eutrophication.

370 To minimize the risk of contamination of irrigation water with *E. coli* O157, it is
371 therefore important to prevent eutrophication by adding waste materials into the ponds. Under
372 eutrophied conditions, the predictability of the survival of *E. coli* O157 proved to be worse than
373 in more oligotrophic conditions (Semenov et al. 2011). In addition, electrolyzed oxidizing water
374 with higher oxidation-reduction potential values could be used for the inactivation of *E. coli*
375 O157 (Kim et al. 2000; Stevenson et al. 2004), because this pathogen survives better in anaerobic
376 conditions (Semenov et al. 2011). Therefore, increasing the pond water ORP by enhancing the
377 flow rate and biofiltration capacity, or pumping air into irrigation ponds to increase dissolved
378 oxygen concentration, especially in the seasons with higher temperature and rainfall, would be
379 suggested to reduce the risks of the contamination with *E. coli* O157 during irrigation.

380 The presence and absence of *E. coli* O157 was clearly distinguished by discriminant
381 analysis based on 26 selected OTUs generated from DGGE analysis. Among these 26 OTUs,
382 there were 18 OTUs for which the relative band intensities were correlated to the occurrence of
383 *E. coli*. The diversity and evenness of bacterial communities were selected as classification
384 factors by stepwise discriminant analysis. In addition, the presence or absence of *E. coli* O157
385 was also related to the composition of the bacterial communities in these irrigation ponds.
386 Further studies will be conducted to sequence the selected OTUs that were significantly
387 correlated to the presence or absence of *E. coli* O157 to identify potential biomarkers or
388 biocontrol agents for the pathogen. In addition, other methods, like microbial source tracking,

389 could be conducted in the future using extracted genomic DNAs to identify the sources of fecal
390 contamination of the pond water (Dorai-Raj et al., 2012). There were no fences around the 10
391 irrigation ponds sampled in this study, and natural vegetation around the ponds varies in different
392 planting seasons. Wild animals could be the main source of contamination with *E. coli* O157 in
393 these ponds. Various wild animals live in this watershed, including deer, hogs, raccoons,
394 squirrels, marsh rabbits, opossums, birds, armadillos, as well as various reptile and amphibian
395 species. All of these animals except armadillos were reported to be carriers of *E. coli* (Jokinen et
396 al. 2011; Leotta et al. 2006; Mohapatra et al. 2007). The seasonality of *E. coli* O157 in irrigation
397 ponds with high frequency in summer and fall is similar to the prevalence of this pathogen on the
398 hides and in the feces of cattle (Berry and Wells 2010), which may indicate that the
399 contamination source is likely to be animals that fed on plants, like ruminants.

400 Results obtained in this study may lead to hypotheses about the factors that promote or
401 suppress *E. coli* O157 in irrigation ponds. Further studies will be conducted for more detailed
402 genotyping of the *E. coli* O157 isolates. In this project, real-time PCR based on the extracted
403 genomic DNAs using the specific primers (Ahmed et al., 2009) were conducted to test the
404 prevalence and population of *E. coli* O157 in pond water samples in addition to the enrichment
405 method. However, no positive results were detected for any of the 10 ponds during the whole
406 year (data not presented) probably due to the low population density of this bacterium in the
407 pond water. Further studies using a more sensitive method would be useful to quantify the
408 populations of STEC in irrigation ponds.

409

410 **Supplementary Materials**

411 **Table S1.** Measured variables (means and standard deviations of ten irrigation ponds over a
412 period of 12 months) for water samples that were positive or negative for *E. coli* O157.

413 **Table S2.** Mean values and standard deviations of highly correlated environmental factors from
414 March, 2011 to February, 2012 in 10 irrigation ponds.

415 **Table S3.** Groups of environmental factors with high positive correlations to each other ($r > 0.7$).

416 **Table S4.** Operational taxonomic units (OTUs) of DGGE data with significant correlations to the
417 occurrence of *E. coli* O157 isolated from irrigation ponds ($P < 0.1$).

418

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604

605 **Figure Legends**

606

607 **Fig. 1.** Occurrence of *E. coli* O157 and dynamic changes in environmental factors. A,
608 Occurrence of *E. coli* O157 from March, 2011 to February, 2012 in 10 irrigation ponds; B,
609 dynamic changes in total rainfall and average temperature nearby the ponds between samplings;
610 C, dynamic changes in total nitrogen and dissolved oxygen concentration of ponds at the time of
611 sampling for *E. coli* O157; D, dynamic changes in oxidation reduction potential and fecal
612 coliform populations of ponds at the time of sampling for *E. coli* O157. P1 - P10 are the 10
613 irrigation ponds located in the Suwannee River watershed.

614 **Fig. 2.** Grouping of *E. coli* O157 occurrence in water samples from 10 irrigation ponds located in
615 the Suwannee River watershed by discriminant analysis of environmental factors based on
616 canonical function one and standardized values of temperature. Small circles represent water
617 samples without *E. coli* O157, and stars represent *E. coli* O157 positive water samples. *E. coli*
618 O157 positive samples were mainly grouped in a big circle.

619 **Fig. 3.** Grouping of *E. coli* O157 occurrence in water samples from 10 irrigation ponds located in
620 the Suwannee River watershed by discriminant analysis of DGGE data based on canonical
621 function one and standardized values of band 5. Small circles represent water samples without *E.*
622 *coli* O157, and stars represent *E. coli* O157 positive water samples. *E. coli* O157 positive
623 samples were mainly grouped in a big rectangle.

624 **Table 1.** Correlation coefficients between environmental factors and the occurrence of *E. coli*
 625 O157 isolated from irrigation ponds.

626

Environment factors	Biserial correlation coefficients to <i>E. coli</i> O157 occurrence	P value
L2 avg Tm¹	0.424	0
Average Tm²	0.416	0
L avg Tm³	0.348	0
Temp⁴	0.324	0
Total rainfall⁵	0.249	0.0001
ORP⁶	-0.245	0.0001
TN⁷	-0.232	0.0003
Culturable⁸	0.223	0.0005
Fecal coliforms⁹	0.222	0.0005
L2 tot rain¹⁰	0.212	0.0009
Nitrate¹¹	-0.161	0.0127
DO Conc¹²	-0.142	0.0282
Copio¹³	0.131	0.0432
DO Charge¹⁴	0.118	0.0682
Simpson diversity^{15*}	0.110	0.0891
Ortho-P¹⁶	-0.104	0.1086
pH¹⁷	-0.104	0.1160
L tot rain¹⁸	0.081	0.2142
Shannon diversity¹⁹	-0.078	0.2303
Species richness²⁰	0.055	0.3936
TSS²¹	0.055	0.3965
Generic <i>E. coli</i>²²	0.054	0.4021
SpCond²³	-0.033	0.6097
Evenness²⁴	0.027	0.6798
Turbidity²⁵	-0.018	0.7780
DOC²⁶	0.014	0.8314
DO%²⁷	-0.001	0.9897

627

628 ¹ Average temperature in the pond region in the second to last week before sampling (°C); ²
629 average temperature in the pond region between samplings (°C); ³ average temperature in the
630 pond region in the last week before sampling (°C); ⁴ temperature of the pond water during
631 sampling (°C); ⁵ total rainfall of the pond region between samplings (mm); ⁶ oxidation reduction
632 potential (mV); ⁷ total nitrogen (mg/L); ⁸ population of culturable bacteria (CFU/100ml); ⁹
633 population of fecal coliform bacteria (CFU/100ml); ¹⁰ total rainfall in the pond region in the
634 second but last week before sampling (mm); ¹¹ nitrate concentration (mg/L); ¹² dissolved oxygen
635 concentration (mg/L); ¹³ population of copiotrophic bacteria (CFU/100ml); ¹⁴ dissolved oxygen
636 charge (mV); ¹⁵ Simpson diversity index of bacterial community; ¹⁶ soluble reactive portion of
637 total phosphorus (mg/L); ¹⁷ pH value of water samples; ¹⁸ total rainfall in the pond region in the
638 last week before sampling (mm); ¹⁹ Shannon-Wiener diversity index of bacterial community; ²⁰
639 species richness of bacterial community; ²¹ total suspended solids (mg/L); ²² population of
640 generic *E. coli* (CFU/100ml); ²³ specific conductance (mS/cm); ²⁴ evenness of bacterial
641 community; ²⁵ turbidity of water samples (NTU); ²⁶ total organic carbon (mg/L); ²⁷ dissolved
642 oxygen percentage (%); * Simpson index is negatively correlated to the diversity of bacterial
643 communities. Environment factors with significant correlations ($P < 0.05$) to *E. coli* O157
644 occurrence are shown in bold font.

645

646 **Table 2.** Environmental factors that contributed significantly to classification of the occurrence
 647 of *E. coli* O157 in irrigation ponds by stepwise and canonical discriminant analyses. All data
 648 presented originate from canonical discriminant analysis; the order of the factors comes from the
 649 stepwise discriminant analysis.

650

Factors ²	Canonical function 1 ¹		<i>E. coli</i> O157 occurrence/ Mean values of factors	
	Standardized Coefficients ³	Pooled within- class correlation ⁴	Negative	Positive
L2 avg Tm (°C)	0.869	0.789	18.65	25.05
Total rainfall (mm)	0.289	0.281	61.2	85.87
Simpson diversity (-)	0.463	0.461	0.0653	0.071
Evenness (-)	0.417	0.414	0.9444	0.9457
Culturable (CFU/100ml)	0.216	0.211	5759.6	11989
Ortho-P (mg/L)	0.224	0.223	0.0443	0.0677

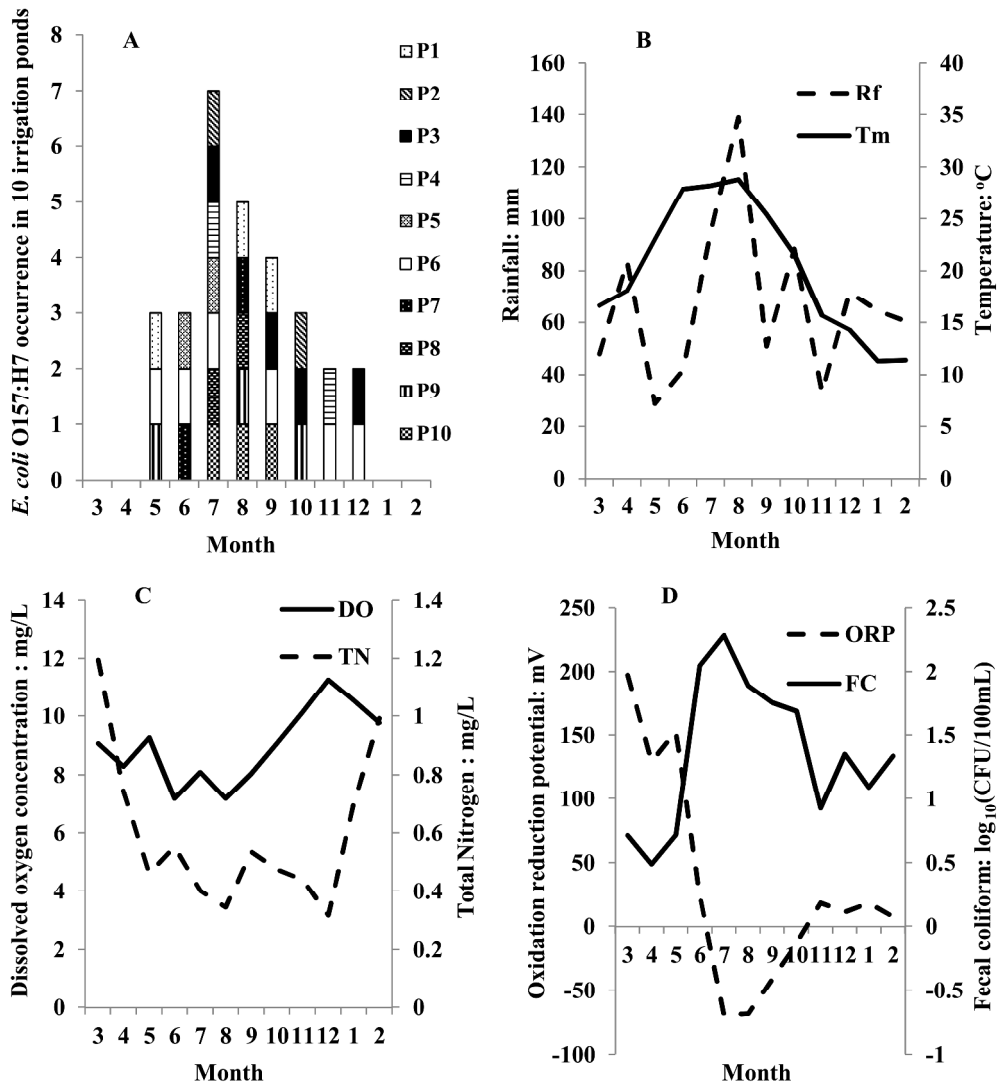
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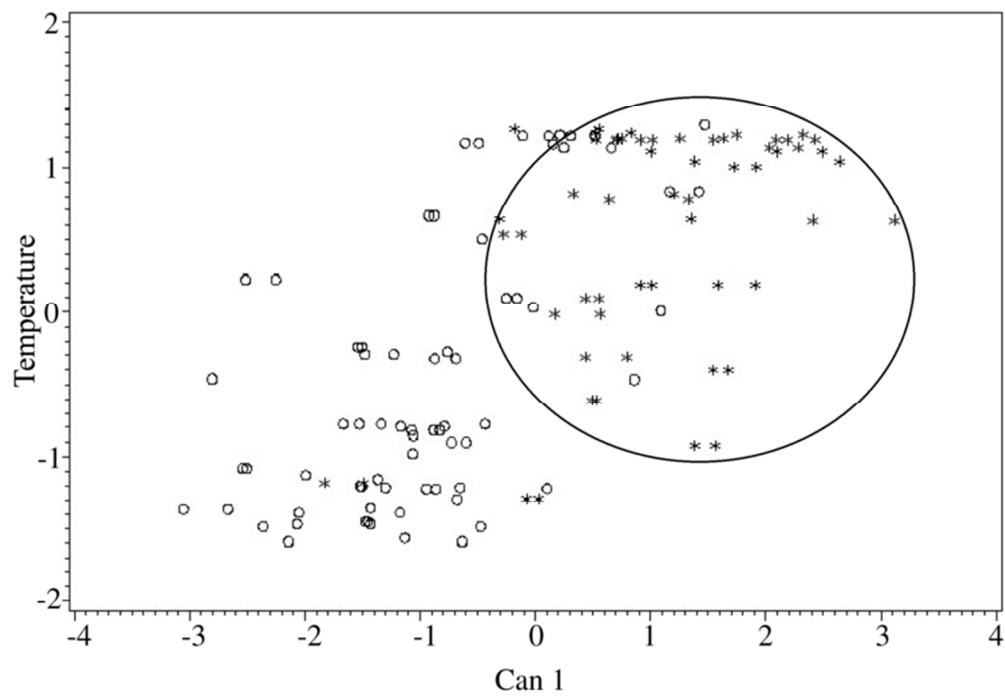
652 ¹ Canonical function 1 is the linear combination of selected factors that best explain the
 653 presence/absence grouping of *E. coli* O157; if there are only two groups, there is only one
 654 canonical function.

655 ² Environmental factors are listed in order of selection by stepwise discriminant analysis. All
 656 variables listed contributed significantly to the discrimination.

657 ³ Standardized coefficients indicate the direction (positive or negative) and the degree to which
 658 each variable contributes to the classification.

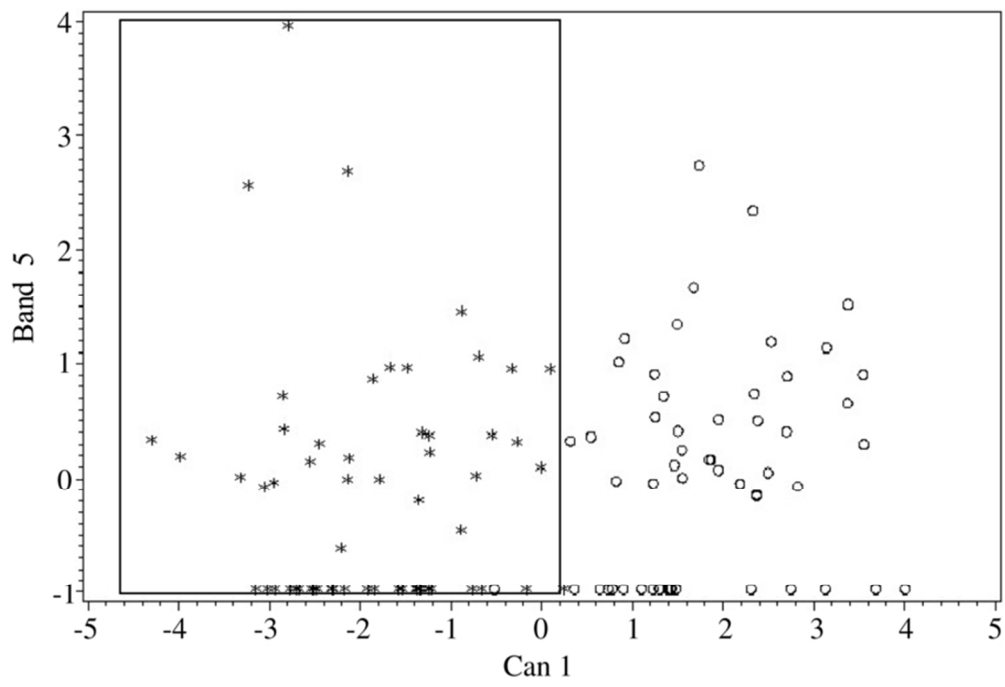
659 ⁴ Pooled within-class correlations between each selected variable and the canonical function;
 660 variables with a correlation of 0.2 or more were considered important.





72x49mm (300 x 300 DPI)

Pre-proof Only



72x48mm (300 x 300 DPI)

Pre-proof Only

Table S1 Measured variables (means and standard deviations of ten irrigation ponds over a period of 12 months) for water samples that were positive or negative for *E. coli* O157:H7.

Measured variables			<i>E. coli</i> O157:H7 positive samples		<i>E. coli</i> O157:H7 negative samples		
			mean	standard deviation *	mean	standard deviation *	
Bacterial data	<i>E. coli</i>	MPN/100 mL	13.97	28.01	17.77	35.46	
	Fecal coliforms	CFU/100mL	33.05	81.03	91.95	175.40	
	Copiotrophic bacteria on C-rich agar	CFU/100mL	2572.20	4327.40	3931.00	4719.60	
	Culturable bacteria on C-poor agar	CFU/100mL	5759.60	8975.90	11989.00	17713.00	
	Shannon- Wiener Diversity Index	-	2.90	0.24	2.85	0.33	
	Simpson Diversity Index	-	0.07	0.02	0.07	0.03	
	Species Richness (S)	-	22.07	5.17	21.38	5.88	
	Species evenness	-	0.94	0.02	0.95	0.02	
	Chemical characteristics	Total soluble solids (TSS)	mg/L	9.00	9.04	7.85	8.70
		Nitrate concentration	mg/L	0.16	0.26	0.07	0.17
Ortho-phosphate concentration		mg/L	0.04	0.09	0.07	0.12	
Dissolved oxygen (DO)		%	104.90	55.70	104.80	32.80	
DO Concentration		mg/L	9.20	2.32	8.36	2.97	
DO Charge		mV	59.96	13.30	63.27	5.94	
Dissolved organic carbon (DOC)		mg/L	9.21	7.96	9.45	5.54	
Dissolved organic Nitrogen (DON)		mg/L	0.67	0.59	0.37	0.18	
pH		-	8.02	0.76	7.84	0.74	
Oxidative-reductive potential (ORP)		mV	43.45	91.10	-9.35	85.40	
Physical characteristics	Temperature (water) at sampling	°C	21.79	6.28	26.75	6.00	
	Average air temperature (1 month)	°C	18.98	5.25	24.41	4.52	
	Lag (one week before sampling) of average temperature (L Avg Tm)	°C	18.67	6.02	23.82	5.71	
	Lag (two weeks) of average temperature (L2 avg Tm)	°C	18.65	6.16	25.05	4.77	
	Total rainfall (1 month)	mm	61.20	37.00	85.87	52.10	
	Lag (one week) of total rainfall (L tot rain)	mm	21.59	23.18	26.06	25.48	
	Lag (two weeks) of total rainfall (L2 tot rain)	mm	16.14	20.22	27.04	25.18	
	Specific conductivity	mS/cm	0.21	0.24	0.19	0.23	
	Turbidity	NTU	14.64	15.21	13.98	16.28	

* The standard deviations reflect the variation over time rather than the variation due to sampling error.

Table S2 Mean values and standard deviations of highly correlated environmental factors from March, 2011 to February, 2012 in 10 irrigation ponds

month	DO concentration (mg/L)		Total nitrogen concentration (mg/L)		Oxidative-reductive potential (mV)		Fecal coliform bacteria ($\text{Log}_{10}(\text{CFU}/100 \text{ mL})$)	
	Mean	Stand. dev.	Mean	Stand. dev.	Mean	Stand. dev.	Mean	Stand. dev.
Mar-11	9.08	1.46	1.19	1.03	197.41	75.37	0.72	0.82
Apr-11	8.28	0.72	0.74	0.45	129.16	14.29	0.49	0.68
May-11	9.28	1.45	0.46	0.18	152.94	31.11	0.72	0.95
Jun-11	7.17	1.40	0.55	0.41	24.48	114.13	2.05	2.19
Jul-11	8.09	1.99	0.40	0.16	-69.73	8.12	2.29	2.38
Aug-11	7.17	2.35	0.34	0.17	-68.16	20.12	1.89	2.16
Sep-11	8.05	3.52	0.54	0.56	-41.11	11.77	1.75	2.05
Oct-11	9.09	3.45	0.48	0.45	-12.59	14.10	1.69	1.87
Nov-11	10.14	10.14	0.44	0.44	18.39	18.39	0.93	0.93
Dec-11	11.28	1.91	0.32	0.32	11.37	20.89	1.35	1.32
Jan-12	10.54	1.14	0.70	0.54	18.36	17.42	1.09	1.43
Feb-12	9.77	2.15	0.99	0.57	7.56	18.68	1.34	1.62

Table S3. Groups of environmental factors with high positive correlations to each other ($r > 0.7$).

Group	Environmental factors			
1	TSS*	Turbidity		
2	DO Conc	DO%		
3	L2 avg Tm	Temp	Average Tm	L avg Tm
4	TN	Nitrate		
5	Simpson index	Shannon index	Species richness	
6	Culturable	Copio		

* Factors in the first column have the highest correlations to *E. coli* O157 occurrence in each factor group, and are shown in bold.

Table S4. Operational taxonomic units (OTUs) of DGGE data with significant correlations to the occurrence of *E. coli* O157 isolated from irrigation ponds (P<0.1).

Relative band position (%)	Band No.	Biserial correlation coefficient to <i>E. coli</i> O157 occurrence	P-value
4.5	b5	0.183	0.005
46.2	b36	-0.182	0.005
57.1	b43	0.169	0.009
22.5	b18	-0.162	0.012
21.5	b17	-0.149	0.020
41.4	b33	0.145	0.025
10.7	b10	0.144	0.025
43	b34	0.142	0.028
64.7	b48	-0.137	0.035
60	b45	0.131	0.043
17.1	b14	-0.131	0.043
49.1	b38	0.127	0.050
0.2	b1	-0.122	0.059
1	b2	-0.121	0.062
79.8	b56	0.117	0.072
61.7	b46	0.112	0.083
50.5	b39	-0.109	0.089
37	b29	-0.108	0.094

DGGE OTUs (bands) with significant correlations (P < 0.05) to *E. coli* O157 occurrence are shown in bold font.