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Waselkov and Olsen, Population genetics of waterhemp invasion

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**Population Genetics and Origin of the Native North American Agricultural Weed
Waterhemp (*Amaranthus tuberculatus*)¹**

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48 **ABSTRACT**

49 **Premise of the study**—The evolution of invasiveness has been extensively studied in
50 natural ecosystems; however, far less is known about the evolution of agricultural
51 invasiveness, despite the major economic impact of weeds on crop
52 productivity. Examining the population structure of recently arisen weeds can provide
53 insights into evolutionary avenues to invasion of agroecosystems. Weeds that originate
54 from wild plants are the most common yet least frequently studied type of agricultural
55 invasive. Here we address several questions about the origin of the native North
56 American agricultural weed waterhemp (*Amaranthus tuberculatus*), which invaded corn
57 and soy fields in the Midwestern U.S. in the 20th century.

58 **Methods**—We genotyped 38 populations from across the species range with 10
59 microsatellite markers, and used these data to assess genetic diversity and population
60 structure within and outside the geographical region where waterhemp is agriculturally
61 problematic.

62 **Key Results**—We found evidence for two ancestral genetic lineages in our data,
63 supporting the hypothesis that *A. tuberculatus* was diverging into two evolutionary
64 lineages prior to the 20th century. However, we found no support for the hypothesis that
65 agricultural weed populations arose from admixture of these two lineages after secondary
66 contact. Our data suggest that eastward movement of the western genetic lineage,
67 facilitated by changing agricultural practices, is the source of the agricultural invasion of
68 waterhemp.

69 **Conclusions**—This research demonstrates that agricultural invasion by native, wild plant

70 species can proceed via different evolutionary trajectories from weeds related to
71 domesticated plants, which has implications for evolutionary biology and weed control.

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73 **Key Words:** agricultural weed; *Amaranthus tuberculatus*; hybridization; invasive;
74 population admixture; waterhemp

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93 The evolution of invasiveness, broadly defined as the ability of an organism to
94 establish, persist, and proliferate in a new habitat or range (Mack et al., 2000), has been
95 extensively studied in natural ecosystems (Lambrinos, 2004; Ward et al., 2008).
96 However, far less is known about the evolution of invasiveness in heavily human-
97 modified, anthropogenic habitats such as agricultural ecosystems. Agricultural weeds,
98 plants that invade crop fields and range lands, are the single greatest threat to agricultural
99 productivity worldwide, costing an estimated \$33 billion per year in the US alone
100 (Pimentel et al., 2005). Examining the population structure and genetic composition of
101 these weeds can potentially provide insights into the evolutionary avenues to invasion in
102 agricultural habitats; this approach has been successful in natural ecosystem invasions
103 (Sakai et al., 2001). Despite the economic importance of agricultural weeds, population
104 genetics has been used to study the origin of very few weed species, aside from weedy
105 relatives of crops (Vigueira et al., 2013).

106 Agricultural weeds are often presumed to have evolved along with plant
107 domestication and the beginnings of agriculture roughly 12,000 years ago (De Wet and
108 Harlan, 1975). In such cases, the weed's origin in the distant past and long association
109 with highly mobile human populations can limit the ability to draw inferences about the
110 population-level processes underlying the evolution of weediness. However, agricultural
111 weeds may also evolve on a more contemporary timescale. The 20th century saw
112 enormous changes in agricultural practices in the U.S., including the introduction of
113 herbicides and the widespread adoption of conservation tillage (Owen, 2008), and these
114 changes have allowed species that were formerly confined to natural habitats to find a
115 new niche in an agricultural environment (Buhler et al., 1997). Unlike weeds whose

116 origins date to the beginnings of agriculture, recently arisen weeds may retain a clear
117 genetic signature of the events that led to their agricultural invasion.

118 Three main hypotheses about the origin of agricultural weeds are prevalent in the
119 literature (reviewed in Vigueira et al., 2013, following De Wet and Harlan, 1975). Weed
120 species that are related to domesticated species may arise either through “de-
121 domestication” (domesticated species becoming feral), or by hybridization between
122 related domesticated and wild species. Support for these two hypotheses has been found
123 in many systems, including beets, rye, rice, and sunflowers (Burger et al. 2006; Londo
124 and Schaal, 2007; Olsen et al., 2007; Fénart et al., 2008; Muller et al., 2010). A close
125 phylogenetic relationship between a crop species and a sympatric weed leads to
126 interesting evolutionary dynamics, as ongoing gene flow between the two can shape
127 adaptive evolution of the weed (possibly even through transgene escape), and many
128 evolutionary studies have focused on these related crop-weed systems (eg., Warwick et
129 al., 2003; Morrell et al., 2005; Aono et al., 2006; Campbell et al., 2006).

130 The third hypothesized mode of weed origination, the niche expansion of wild
131 plants into agroecosystems through plasticity, adaptation, or exaptation, has received less
132 attention by evolutionary biologists (but see Barrett et al., 1983; Menchari et al., 2007;
133 Welsh and Mohamed, 2011), even though all weeds without close crop relatives must
134 have followed this pathway to agricultural invasion, and even though this type of weed
135 species is the most common (De Wet and Harlan, 1975). Of the few studies of this mode
136 of agricultural invasion in the literature, the origin of weedy sunflower populations
137 (*Helianthus annuus*) from wild populations is the best documented (Kane and Rieseberg,
138 2008; Lai et al., 2008). Due to the scarcity of studies on wild-to-weed evolutionary

139 transitions, many fundamental questions about these systems remain unaddressed,
140 including: whether evolutionary changes in the plant and/or changes in agricultural
141 management practices are required for the invasion; whether such invasions usually have
142 a single or multiple wild sources; and what morphological, physiological, and ecological
143 traits predispose a wild species to expand into agricultural habitats.

144 Among agricultural weeds that have evolved directly from wild species, a
145 distinction can be drawn between those that are introduced in the region where they are
146 invasive and those that are native. While agricultural weeds in North America are often
147 assumed to be mostly introduced from elsewhere, approximately 50% of U.S. cropland
148 weeds are in fact native (Clements et al., 2004). In many cases, wild populations of these
149 native agricultural weeds still exist in the same geographic area, which opens up the
150 potential for gene flow between populations in agricultural and natural habitats. This
151 study focuses on one such native plant species that became agriculturally invasive over a
152 very short, recent time scale.

153 Our study species, waterhemp (*Amaranthus tuberculatus* (Moq.) Sauer), is an
154 herbaceous, outcrossing annual plant native to the Midwestern U.S., where it occurs
155 naturally along riverbanks and in floodplains. Domesticated species of *Amaranthus* are
156 largely absent from its range (Mosyakin and Robertson, 2003). Waterhemp has invaded
157 Midwestern agricultural ecosystems since the 1950s and has become a major problem for
158 corn and soybean farmers in Missouri, Iowa, and Illinois since the 1990s (Sauer, 1957;
159 Tranel and Trucco, 2009). In Illinois alone, waterhemp accounts for about 10% of weed
160 control costs for corn and soybean fields, costing farmers an additional \$65 million per
161 year (Patrick Tranel, Univ. of IL, pers. comm.). If uncontrolled, it can reduce corn yields

162 by up to 74%, and soybean yields by as much as 56% (Steckel, 2007). As a small-seeded
163 annual with sporadic or discontinuous germination, waterhemp is a prime example of the
164 class of agricultural weeds that benefited from the widespread adoption of conservation
165 tillage in the late 20th century (Hager et al., 2000; Owen, 2008; Refsell and Hartzler,
166 2009). Other aspects of the species' biology have contributed to another factor in
167 waterhemp's success: the rapid evolution and spread of herbicide resistance. A dioecious
168 mating system and wind pollination are expected to promote extensive gene flow,
169 potentially leading to genetic admixture and homogenization across large geographical
170 areas. To date, resistance to five different chemical classes of herbicides has been
171 detected in *A. tuberculatus* populations, and resistance to one of the older classes (ALS-
172 inhibitors) is very widespread (Hausman et al., 2011; Tranel and Trucco, 2009).

173 Furthermore, there is some morphological evidence that the species may have
174 been diverging into two species, one on either side of the Mississippi River, until human
175 disturbance brought the taxa back into contact, and possibly gave rise to the agriculturally
176 invasive strain through admixture (Sauer, 1957). Sauer studied herbarium specimens
177 from 1856-1955, and noted that what he considered the "western species" had invaded
178 the range of the "eastern species," with specimens appearing as far east as Indiana by the
179 1950s. He also found that hybrids between the two taxa were more likely to be collected
180 in "artificial" habitats, including agricultural fields, than in natural habitats (Sauer, 1957).

181 In this study, we used population genetic techniques to address several questions
182 about the origin and evolution of the agricultural weed form of this native Midwestern
183 U.S. weed, to add to the small body of research on wild, native plants that have expanded
184 their niche to encompass cropland. We extensively sampled populations of waterhemp

185 across the species' range, both within and outside of the region where waterhemp is
186 agriculturally problematic, and genotyped these populations using polymorphic
187 microsatellite markers. These population genetic data were used to test the following
188 hypotheses. First, we hypothesized (following Sauer, 1957) that *A. tuberculatus* was
189 diverging into two evolutionary lineages on opposite sides of the Mississippi River prior
190 to the 20th century, and that the present-day species would retain some genetic and
191 geographical signature of past subdivision into two evolutionary units.

192 The second hypothesis, contingent on the first, was that the agricultural weed
193 originated through hybridization between the two diverged lineages. Based on this latter
194 hypothesis, we predicted that populations of waterhemp collected from agricultural fields
195 would show strong evidence of admixture between western and eastern genetic
196 subpopulations. In order to test this prediction, we examined the genetics of agricultural
197 and non-agricultural waterhemp populations across the species' range and also in a
198 smaller geographical region at the range edge of weedy waterhemp in Ohio. Our data
199 support the first hypothesis but not the second, and suggest that eastward movement of
200 the western genetic lineage, facilitated by changing agricultural practices, is the source of
201 the agricultural invasion of waterhemp.

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MATERIALS AND METHODS

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Study system—*Amaranthus tuberculatus* sensu lato (including *A. rudis* sensu
Sauer, 1972), is an annual herb native to North America. The species' range is centered
around the Mississippi Valley region, from the Great Plains (roughly as far west as the
100th meridian) eastward to Ohio, and from Louisiana northward to Minnesota, with a

208 northern range boundary in southern Ontario (Fig. 1). The region of agricultural invasion
209 is more restricted: waterhemp is most problematic in the central Mississippi Valley
210 region (MO, IL, IA, IN), but also occurs agriculturally in the eastern Great Plains and in
211 parts of Kentucky and Ohio (Tranel and Trucco, 2009). Waterhemp is dioecious (and
212 thus obligately outcrossing) and wind-pollinated, with small one-seeded utricle fruits that
213 may be dehiscent or indehiscent. Natural populations of *A. tuberculatus* are almost
214 always found in wet habitats, especially seasonally inundated riverbanks in the Midwest,
215 but also banks of creeks and drainage ditches, lakeshores, and marshy floodplains
216 (Mosyakin and Robertson, 2003).

217 Until Pratt and Clark's 2001 taxonomic study of populations across the species'
218 range, waterhemp was considered two species, distinguished primarily by utricle
219 dehiscence, tepal number, and geographic range: *A. tuberculatus*, the entity with
220 indehiscent utricles and no pistillate tepals found to the east of the Mississippi River; and
221 *A. rudis* (earlier misapplied name = *A. tamariscinus*; see Sauer, 1972), the dehiscent-
222 fruited taxon with one pistillate tepal found natively west of the Mississippi River (Sauer,
223 1955; 1957; 1972; Fig. 1). Pratt and Clark discovered a continuum of morphological and
224 isozyme characters across the range of both species and lumped them into the more
225 broadly defined *A. tuberculatus*, but some authors still distinguish the two former species
226 as varieties: *A. tuberculatus* var. *tuberculatus* and var. *rudis* (Costea and Tardif, 2003).
227 The varietal taxonomy is used here, with Pratt and Clark's species called *A. tuberculatus*
228 sensu lato (s.l.) or simply *A. tuberculatus*.

229 **Sample collection**—We collected plant samples from 38 populations of *A.*
230 *tuberculatus* s.l. across the entire species range in 2009 and 2010 (Table 1 and Fig. 1;

231 Supporting information, Table S1). Populations were sampled in Nebraska, Kansas,
232 Oklahoma, Arkansas, Missouri, Illinois, Indiana, Ohio, Michigan, and Ontario. Ohio was
233 intensively surveyed because it is the edge of the range of agricultural waterhemp, with
234 agricultural populations in ~10 counties west of Columbus but only non-crop populations
235 in the remainder of the state (J. Stachler, NDSU, pers. comm.; Fig. S1). Gene flow
236 between the weed and non-weed populations, which could obscure the genetic signature
237 of the weed's origin, should be lowest in this area.

238 We located populations using a combination of herbarium record data and new
239 surveys of typical *A. tuberculatus* habitat along riverbanks, lakeshores, and in crop fields.
240 For the areas with agricultural waterhemp populations, both crop field and non-
241 agricultural populations were included in the study. We recorded latitude and longitude
242 coordinates for each population using a Garmin eTrex H handheld GPS unit (Garmin,
243 Olathe, Kansas, USA), and collected voucher specimens (both male and female plants if
244 possible). For each population, either 10 dried leaf samples in silica gel were collected,
245 or 10 fresh leaf samples were collected and kept in a cooler until they could be frozen at -
246 80°C. Fruit dehiscence (considered an important taxonomic character for distinguishing
247 the two varieties) was recorded for each female voucher specimen (Table 1).

248 ***DNA extraction and genotyping***—DNA was extracted from each sample with
249 Qiagen DNeasy Plant Mini Kits (Qiagen Inc., Valencia, California, USA). Ten
250 microsatellite loci were amplified and genotyped. Primers, repeat motifs, and sizes of
251 products are listed in Table S2. Multiple primer pairs from Lee et al. (2009), originally
252 designed from *A. tuberculatus* genomic sequence data, were tested for consistent
253 amplification and polymorphism, and three primer pairs were selected. The other seven

254 primer pairs were selected from a set of 14 mined from *A. tuberculatus* transcriptomic
255 data using the program SSR Finder (Schroeder, 2003). The transcriptome contigs were
256 provided by the Tranel lab (Univ. IL). In order to multiplex products from different
257 primers in a cost-effective manner, we designed the forward primers with an M13(-21)
258 sequence (TGTAACGACGGCCAGT) at the 5' end, to allow the attachment of a
259 universal fluorescent-dye labeled M13(-21) tag (Schuelke, 2000). The universal tags
260 were labeled with the fluorescent dyes HEX, 6FAM, and NED (Applied Biosystems,
261 Carlsbad, California, USA). In addition, we designed the reverse primers to incorporate a
262 PIG-tail, the sequence "GTTTCTT" at the 5' end of the reverse primer, to facilitate
263 consistent non-template adenylation of the 3' end of the PCR product and to reduce
264 stutter (Brownstein et al., 1996).

265 PCR was performed on ABI GeneAmp 9700 thermocyclers (Applied
266 Biosystems), in 10 μ L reactions containing: 1X GoTaq Flexi Buffer (Promega, Madison,
267 Wisconsin, USA), 2.5 mM MgCl₂, 0.05 mM each dNTPs, 0.15 μ M M13(-21) dye-
268 labeled tag, 0.04 μ M forward primer, 0.16 μ M reverse primer, 0.075 μ L GoTaq
269 (Promega), 3.875 μ L nanowater, and 1.25 μ L genomic DNA. Amplification conditions
270 were: 94°C for 5 minutes; then 30 cycles of 94°C (30 seconds), 51°C (45 seconds), 68 °C
271 (45 seconds) to amplify the product; followed by 8 cycles of 94°C (30 seconds), 48°C (45
272 seconds), 68°C (45 seconds) to attach the labeled tag; and 72°C (30 minutes) final
273 extension. PCR products were diluted 1:10 and multiplexed (combining PCR products
274 from up to three loci with different dye labels and different sizes in the same well) with
275 0.1 μ L GeneScan 400HD ROX size standard (Applied Biosystems), denatured for 5

276 minutes at 95°C, and genotyped on an ABI Prism 3130x Genetic Analyzer (Applied
277 Biosystems).

278 Microsatellite data were visualized using GeneMapper v3.7 software (Applied
279 Biosystems). The alleles at each locus for each individual were recorded by hand and
280 double-checked by repeated amplification and genotyping if more than two peaks
281 appeared (since *A. tuberculatus* is diploid) or unusual allele size classes were observed.
282 If these anomalies were observed twice (which happened very rarely for any particular
283 locus), the data for that marker for that particular individual were coded as missing.
284 Additionally, if genotyping failed for an individual for a particular locus, several
285 subsequent attempts were made to obtain these data before they were coded as missing.
286 Microsatellite data for all populations and loci is available from Dryad (XXX).

287 ***Microsatellite data analysis***—Microsatellite markers were checked for null
288 alleles using MICRO-CHECKER 2.2.3 (Van Oosterhout et al., 2004). The program
289 Genepop 4.2 (Rousset, 2008) was used to test the probability of Hardy-Weinberg
290 equilibrium for each population (with the Markov chain method to estimate exact p-
291 values), to test for linkage disequilibrium between loci (with Fisher’s method), and to
292 detect private alleles for each population. Popgene 1.31 (Yeh et al. 1997) was used to
293 estimate the average number of observed alleles and effective alleles and average
294 observed and expected heterozygosity over all loci for each population, and per-locus for
295 all populations combined. Weir and Cockerhams’s theta (an estimate of F_{ST}) was
296 calculated over all loci and all populations using the program FSTAT 2.9.3.2 (Goudet,
297 1995).

298 To test for isolation by distance (IBD), we calculated the geographic great circle
299 distance in kilometers between each pair of populations using the Geographic Distance
300 Matrix Generator (Ersts, 2013). We then generated a matrix of pairwise F_{st} values
301 between populations, and compared the two matrices in a Mantel test for isolation by
302 distance (with 1000 permutations) using Genepop. This procedure was used to test for
303 IBD across the entire species range, and across subsets of the species range: the Plains
304 states (TR, CHE, TCL, and SaltR populations); Missouri and Illinois; Ohio; and Northern
305 Ohio (OTT, MAU, and PTC populations), Michigan, and Ontario.

306 To identify the highest-likelihood number of genetic subpopulations (K) in the
307 data, we employed the program STRUCTURE 2.3.1 (Pritchard et al., 2000). We used the
308 correlated allele frequencies model with sampling locations (population assignment) as a
309 prior, which facilitates clustering for data with weak genetic structure. We ran separate
310 analyses for the admixture and no-admixture ancestry models for both datasets. For the
311 total species range dataset, we ran the analysis for $K=1-20$; and for the Ohio dataset, from
312 $K=1-7$, with five runs per K , 100,000 Markov Chain Monte Carlo (MCMC) burnin steps,
313 and 500,000 MCMC steps after the burnin for both datasets. The separate analysis of the
314 Ohio dataset was conducted to examine fine-scale structure in this intensively sampled
315 part of the range. To estimate the number of genetic clusters from the \ln Probability
316 $(X|K)$ values output by STRUCTURE, we used STRUCTURE HARVESTER v0.6.93
317 (Earl and vonHoldt, 2012) to implement the ΔK method of Evanno et al. (2005). We
318 combined the results of multiple runs for each K , using the *FullSearch* algorithm, with
319 the program CLUMPP v1.1.2 (Jakobsson and Rosenberg, 2007) and visualized the
320 combined results as bar graphs with *distruct* v1.1 (Rosenberg, 2004).

321 The program BAPS v5.3 (Bayesian Analysis of Population Structure; Corander et
322 al., 2003) was used to incorporate spatial information into the estimation of genetic
323 clusters for the total species range dataset, using an admixture model rather than a no-
324 admixture model, as recommended by François and Durand (2010). Unlike
325 STRUCTURE, BAPS does not use MCMC to infer K. Instead, BAPS uses a stochastic
326 search algorithm that considers multiple K values simultaneously to directly estimate the
327 number of genetic clusters and assign individuals to those clusters using mixture analysis.
328 Geographic localities of populations were employed as priors, using the “spatial
329 clustering of groups” option (Corander et al., 2008). We set $K_{\max} = 2, 5, 10,$ and 20, with
330 three runs per K. For admixture analysis based on the mixture analysis results from the
331 highest-probability K-value, we used a minimum population size of five, 200 iterations,
332 100 reference individuals for each population, and 20 iterations of reference individuals
333 (as suggested in the manual). The graphical output from BAPS is an “admixture
334 partition” bar graph showing genetic assignment of individuals, and a Voroni tessellation
335 diagram showing the spatial genetic assignment of populations.

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RESULTS

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Genetic diversity—Populations largely conformed to Hardy-Weinberg
expectations. MICRO-CHECKER revealed that none of the loci were consistently more
homozygous than expected, indicating no evidence for null alleles in the dataset.
Likewise, no single population showed a deviation from Hardy-Weinberg equilibrium
(HWE) at more than one locus. Hardy-Weinberg probability tests yielded slightly
different results, showing that the locus *AACI* deviated from HWE in five populations,

344 and that one population, MAU, deviated from HWE when all loci were taken into
345 account ($P = 0.024$). Population structure analyses were therefore run with and without
346 this locus and population; however, exclusion of these data had negligible effect on the
347 results (data not shown). No significant linkage disequilibrium was detected between any
348 pair of loci.

349 Genetic diversity data for each population are presented in Table 2, with per-locus
350 values shown in Table S3. Gene diversity (H_e) ranged between 0.42 and 0.68 for
351 individual populations, with a mean of 0.56 over all populations, indicating high within-
352 population genetic diversity. Populations in the western half of the species range tended
353 to have higher average observed and effective numbers of alleles than populations in the
354 eastern half of the species range. Several populations in Indiana (VIGO, KANK) and
355 Ohio (NEV, CAN, SCIO, MC, PTC) and one population in Illinois (PEK) had higher
356 average observed than expected heterozygosity, potentially suggesting recent admixture
357 (Table 2). These populations include only two of the ten populations from crop fields
358 (see Table 1), and agricultural waterhemp populations did not have higher average
359 observed than expected heterozygosity on average (results not shown). The number of
360 alleles per locus ranged from 6 to 20, and in general both observed and expected
361 heterozygosity per locus were high, with the exception of the locus *ATC9*, which had
362 approximately one effective allele (Table S3).

363 Genetic differentiation among populations was low overall. Weir and
364 Cockerham's theta (analogous to F_{st}) was 0.075 averaged across loci, with a range of
365 0.029-0.186 for individual loci. Nonetheless, Mantel tests revealed significant isolation
366 by distance across the species range ($P < 0.00001$, Fig. 2), with pairwise F_{st} values

367 between populations ranging from 0.0013 to 0.2681. For geographical subsets of the
368 species range, there was no isolation by distance at the state or bi-state level, or across the
369 three Plains states. However, the dataset composed of populations from northern Ohio,
370 Michigan, and Ontario did show weak isolation by distance ($P = 0.037$).

371 ***Population structure—***

372 *Whole species range dataset—*STRUCTURE output and the ΔK statistic indicated
373 two genetic clusters within *A. tuberculatus*, one characteristic of the western part of the
374 geographic range and one characteristic of the eastern part, with greater than 25%
375 admixture inferred for the populations PEK and KNK (IL), KANK, IND, and WAB (IN),
376 SCF (ON), and the OH agricultural waterhemp region populations (Fig. 3; Supporting
377 information, Fig. S2). Overall for $K=2$, the ten crop field populations had an average of
378 23.9% admixture, while the 28 non-agricultural populations had an average of 15.0%
379 admixture (calculated from STRUCTURE output). Analyzing the dataset with the no-
380 admixture model yielded the same inferred numbers of clusters (results not shown).

381 The analysis of population structure that explicitly incorporated information on
382 the geographical locations of populations yielded generally similar results to the
383 STRUCTURE analysis. BAPS identified the highest K value as $K=3$ (for $K_{\max} = 5, 10,$
384 and 20). Population and individual assignments to these three clusters are shown in the
385 admixture partition bar graph (resulting from a mixture analysis, followed by admixture
386 analysis) (Fig. 4a). The population assignments largely correspond to the same
387 western/eastern divide seen in the STRUCTURE analysis, with the switch from primarily
388 western to eastern genetics between VIGO (IN) and KANK (IN), PEK having a strong
389 affinity for the eastern genetic cluster, and IND, RT29, GTB, and STW primarily

390 assigned to the western cluster. The MC population (OH) was the only population
391 assigned to the third cluster. BAPS identified only eight individuals as exhibiting
392 admixture, but these individuals were in the central populations (PEK, KNK, KANK,
393 IND) and agricultural waterhemp region of Ohio (STW, SCIO), which correspond to
394 populations with high admixture in STRUCTURE. The Voroni tessellation diagram
395 shows the same population genetic assignments spatially (without admixture) (Fig. 4b).
396 The agreement between the STRUCTURE and BAPS results suggests that a genetic
397 signature of the two previously-diverging lineages in the species still remains in the
398 present-day species.

399 *Ohio dataset*—For the dataset composed of only Ohio population genetic data, the
400 ΔK method of Evanno et al. (2005) (implemented in STRUCTURE HARVESTER)
401 weakly supported two genetic clusters, one in the agricultural waterhemp region of Ohio
402 and the other in the Ohio River region, with strong admixture between the two clusters
403 inferred for populations in northern Ohio and in the southern Ohio population BTL (Figs.
404 5, S3). In contrast to the whole range dataset results, three of the four agricultural
405 populations in the Ohio dataset (GTB, MC, and RT29) have less than 25% admixture in
406 the STRUCTURE bar graphs for $K=2$: instead, most individuals in these populations
407 were assigned almost entirely to the western genetic cluster (Fig. 5). Overall for $K=2$,
408 populations in the agricultural waterhemp region had an average of 12.6% admixture,
409 while the Ohio populations outside of this region had an average of 31.8% admixture.
410 There was a second peak in ΔK at $K=5$ for the Ohio dataset (Figs. S3, S4).

411

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DISCUSSION

413 *Support for two ancestral evolutionary units*— The combined results from
414 isolation by distance tests, STRUCTURE, and BAPS analyses are largely congruent and
415 paint an interesting picture of the recent origin and evolution of the agricultural weed
416 form of *Amaranthus tuberculatus*. The hypothesis that the species was formerly diverging
417 into two evolutionary units prior to the 20th century is supported by our data.
418 STRUCTURE recovered two genetic clusters from the total species range dataset, and at
419 the range edges, the geographical structure of these clusters corresponds closely to the
420 hypothesized eastern/western divide between the two former taxonomic units (Sauer,
421 1957) (Figs. 1, 3). BAPS identified an additional cluster consisting of one Ohio
422 agricultural population, which might have distinctive multigene allele frequencies due to
423 admixture. It appears from our data as though the Mississippi River is no longer the
424 geographical divide between the two genetic clusters; instead, the western genetic cluster
425 extends into Indiana. Interestingly, this boundary shift was documented more than half a
426 century ago by Sauer (1957), who observed from herbarium specimen records that the
427 western taxon, now called *A. tuberculatus* var. *rudis*, had been moving steadily northward
428 and eastward across the Mississippi River since the 1850s, into the range of *A.*
429 *tuberculatus* var. *tuberculatus*. Furthermore, he noted that this movement was associated
430 with agricultural invasion: the earliest records of *A. tuberculatus* var. *rudis* in Illinois
431 (1940s) and Indiana (1950s) are reports from agricultural fields (Sauer, 1957).

432 Spatial genetic clustering allows the use of information beyond genotype data
433 (such as spatial autocorrelation and geographical trends) for inferring population
434 structure, and can be especially useful when closely-related taxa come into secondary
435 contact at regional geographic scales (François and Durand, 2010). The differences in

436 clustering between STRUCTURE and BAPS are probably due to differences in the
437 assumptions of the underlying Bayesian clustering methods, as well as the inclusion of
438 geographical information. While STRUCTURE uses Markov methods to find the highest
439 likelihood for each K value independently, BAPS uses a stochastic search algorithm that
440 directly estimates the most likely K value. Furthermore, BAPS estimates admixture after
441 partitioning the data into clusters with a mixture model, while STRUCTURE estimates
442 admixture and the likelihood of each K value simultaneously. Because of these
443 differences, the discovery by both programs of two major genetic clusters in our dataset
444 provides strong support for this inference.

445 Pratt and Clark's (2001) analysis of 27 morphological characters and 14 isozyme
446 loci across the range of *A. tuberculatus* s.l. revealed a continuum of morphological
447 character states and isozyme alleles across the entire range. On the basis of no clear
448 clustering in a PCA of these characters, they concluded that the two previously described
449 taxa are one variable species. The observed continuum is not surprising, given the
450 geographical overlap between the two varieties that occurred in the middle of the range as
451 *A. tuberculatus* var. *rudis* pushed eastward. In our own voucher specimens, the
452 morphological character of utricle dehiscence is nearly constant at the western and
453 eastern ends of the range (the Plains states and Ontario), and variable among populations
454 in the range center (Table 1). Both Sauer and Pratt and Clark were primarily focused on
455 taxonomy, and tended not to focus on population-level patterns. Our application of a
456 relatively recently-developed genetic tool, microsatellite genotyping, has largely
457 confirmed their broad-scale observations and has also shed more light on the origins of
458 the agricultural weed form.

459 ***Intraspecific hybridization did not create the agricultural form***—Our second
460 hypothesis, that weedy waterhemp was created through hybridization between the two
461 evolutionary units in *A. tuberculatus* s.l., was not supported by our data. If this were the
462 case, one would expect that the agricultural populations of waterhemp would show strong
463 evidence of admixture between the two genetic clusters. Instead, four out of the six
464 Missouri, Illinois, and Indiana agricultural populations show a strong affinity with the
465 western (red) genetic cluster in STRUCTURE, with the two remaining populations, KNK
466 (IL) and VIGO (IN), showing around 25% contribution from the eastern genetic cluster
467 (Fig. 3). Over the whole range, average admixture is about 9% higher in agricultural
468 populations than in non-agricultural populations: however, the average admixture of
469 weedy populations is still less than 25%. Additionally, many individual non-weed
470 populations, especially those in Indiana, have levels of admixture equal to or greater than
471 those observed in agricultural habitats in STRUCTURE; the result is also seen in the
472 heterozygosity comparisons in Table 2. The geographical component of the observed
473 admixture suggests that it was simply an inevitable consequence of *A. tuberculatus* var.
474 *rudis* migrating eastward.

475 We intensively sampled the edge of the range of agricultural waterhemp in Ohio,
476 in order to examine evidence for weedy admixture at a finer geographic scale in this
477 region with recent contact between varieties and presumably, little historical gene flow.
478 According to STRUCTURE analysis of the total range dataset, admixture is prevalent in
479 10 out of the 12 sampled Ohio populations (including six of the eight non-agricultural
480 populations) (Fig. 3). However, when only the Ohio populations are analyzed in
481 STRUCTURE, admixture was 25% or less in the four agricultural populations (CAN,

482 GTB, MC, and RT29), which were mainly assigned to the western genetic cluster (Fig.
483 5). In fact, average admixture was almost 20% lower within the 10 counties that
484 constitute the “agricultural waterhemp region” of the state than in the remainder of Ohio.
485 Together with the whole range results, this suggests that admixture is not a prerequisite
486 for weediness in *A. tuberculatus*.

487 The population structure data suggest that the movement of *A. tuberculatus* var.
488 *rudis* eastward almost completely replaced *A. tuberculatus* var. *tuberculatus* populations
489 in natural environments in central Illinois (e.g., the natural populations RIP and KEY
490 have very little signature of the eastern genetic cluster). Interestingly, the central part of
491 Indiana (IND) is genetically more "eastern" than the western part of Ohio, potentially
492 indicating that *A. tuberculatus* var. *rudis* might have been secondarily introduced to Ohio
493 from farther west. The populations in the “agricultural waterhemp region” of Ohio are
494 either strongly admixed or primarily western genetically in the STRUCTURE analyses
495 (Figs. 3, 5), and three of these populations are genetically western according to the BAPS
496 Voroni diagram (Fig. 4b). The range boundary of agricultural waterhemp is around
497 Columbus, Ohio (J. Stachler, NDSU, pers. comm.), and natural populations were not
498 sampled in the eastern half of the state. The inclusion of additional eastern populations
499 could confirm the inference that *A. tuberculatus* var. *rudis* genetic material hits a range
500 boundary in central Ohio.

501 The western variety of waterhemp may also have northern and southern
502 geographic boundaries in the areas it has invaded: the northern Illinois populations PEK
503 and KNK and the northern Indiana populations KANK and WAB show more evidence of
504 eastern genetic ancestry than populations in the middle of those states. The southern

505 populations along the Ohio River in Indiana and Ohio are almost entirely composed of
506 the eastern genetic cluster, and the southern population BTL and the northern populations
507 OTT, MAU, and PTC are eastern according to BAPS or admixed according to
508 STRUCTURE.

509 Altogether, these patterns of genetic clustering point to a geographical invasion of
510 *A. tuberculatus* var. *rudis* almost directly eastward through the primary agricultural
511 regions of the eastern states, facilitated by introduction first in crop fields (as observed by
512 Sauer, 1957). Waterhemp weed seeds are extensively moved around by farm equipment,
513 which is often shared between farms and transported long distances (Patrick Tranel,
514 University of IL, pers. comm.). With the evolution of resistance to multiple herbicide
515 classes in the species, the spread of *A. tuberculatus* var. *rudis* throughout the Midwest
516 became highly probable. The reasons for the possible northern, southern, and eastern
517 geographical boundaries to the invasion deserve further study: the Ohio boundary may
518 involve soil substrate (which changes abruptly in the middle of the state, in Licking
519 County, east of Columbus (ODNR, 2014)), and the northern and southern boundaries are
520 more likely to involve differences in climate and topography.

521 ***The origin of weedy waterhemp***—Returning to the major question of the study —
522 how the weedy form of *A. tuberculatus* arose — introgression between the two varieties
523 is not supported as a causative factor in this study. The most likely scenario based on our
524 results is that the weed form is simply *A. tuberculatus* var. *rudis*, which was already
525 genetically and phenotypically suited to agricultural environments. When Mississippi
526 Valley environments became increasingly dominated by agriculture in the 20th century,
527 due to large-scale mechanized farming and the channeling of rivers for the greater

528 agricultural availability of floodplain habitats (Ghersa et al., 1994), *A. tuberculatus* var.
529 *rudis* was already well-suited to coexist and compete with crops in these new
530 environments. Later in the 20th century, the further expansion of waterhemp as a weed
531 was facilitated by the widespread adoption of no-till agriculture and herbicide-based
532 weed control (Costea et al., 2005). The idea that *A. tuberculatus* var. *rudis* was already
533 “weedy” and might not have required genetic changes to be successful in agricultural
534 ecosystems is supported by Sauer’s description of the taxon, in which he states that in
535 contrast to *A. tuberculatus* var. *tuberculatus*, var. *rudis* has “very definite weedy
536 tendencies,” and one-third of the herbarium collections of the species are from artificial,
537 anthropogenically-disturbed habitats (Sauer, 1955). Further evidence for the agricultural
538 inclinations of the western variety of *A. tuberculatus* was discovered in a separate
539 common garden experiment (K. Waselkov, unpublished data).

540 In the few other population genetic studies of agricultural invasion by wild plants,
541 where gene flow from cultivated plants is unlikely, a key conclusion is often exaptation
542 or “preadaptation” of these species to agricultural environments (Vigueira et al., 2013).
543 For example, weedy *Helianthus annuus* populations appear to have arisen multiple times
544 without genetic bottlenecks (Kane and Rieseberg, 2008), and an important parasite of
545 cereal crops, *Striga hermonthica*, shows no evidence of host specificity across Ethiopia,
546 with genetic structure influenced instead by geography (Welsh and Mohamed, 2011).
547 Exceptions to this trend include crop mimicry, in which weeds are strongly selected to
548 resemble the co-occurring crop during one or more life history stages (Barrett, 1983),
549 and also herbicide avoidance and/or resistance, although these adaptive changes would

550 require enough preliminary tolerance to agricultural practices to enable the wild plants to
551 occur in crop fields, before selection could act.

552 Our interest in *Amaranthus tuberculatus* stemmed not only from its “wild-to-
553 weed” path to agricultural invasion, but also from the opportunity to trace this
554 evolutionary transition in a native plant. Given the often close proximity of agricultural
555 fields and natural riverbank habitats, it is perhaps surprising that any genetic signature of
556 the two varieties, let alone a genetic signature of the eastward invasion of *A. tuberculatus*
557 var. *rudis*, still exists. Indeed, our genetic diversity results support the idea that gene
558 flow homogenizes neutral genetic variation over large areas of the species range
559 (Thinglum, 2010). This is evident in the isolation by distance analyses, which show no
560 isolation by distance at scales smaller than groupings of three states or provinces, and the
561 low overall F_{st} in the total range dataset. These results are also consistent with the
562 species’ biology, as it is locally abundant, obligately outcrossing, and wind pollinated,
563 and thus probably has very large effective population sizes and very high effective
564 recombination across the genome (Thinglum et al., 2011).

565 The lack of complete genetic homogenization of waterhemp after secondary
566 contact between the two varieties might suggest some degree of reproductive isolation
567 between them: however, greenhouse experiments have found no evidence for pre- or
568 postzygotic reproductive barriers between the two varieties (Murray 1940). Furthermore,
569 pollen of *A. tuberculatus* is viable for up to 120 hours, allowing for long-distance
570 dispersal, although most pollen fertilizes plants within 50 meters in field trials (Liu et al.,
571 2012). There is some anecdotal evidence that prezygotic isolation may be occurring in
572 the wild: the timing of reproduction appears to differ between riverbanks and crop fields,

573 with agricultural waterhemp senescing while nearby riverbank waterhemp is just
574 beginning to flower (K. Waselkov, pers. obs.). Further studies of observed dispersal and
575 realized gene flow between the different varieties and habitats in this species could shed
576 light on the apparent contradiction between our results and the species' biology.

577 Our results also suggest that finer-scale geographic sampling as well as more
578 genetic markers and/or candidate genes would be needed for studies attempting to detect
579 the genetic basis of agricultural adaptation in *A. tuberculatus*. Various herbicide
580 resistance genes are already known to be strongly favored in agricultural populations of
581 *A. tuberculatus* (Tranel and Trucco, 2009); population genetic studies with denser
582 genomic coverage could reveal other specific genomic regions showing adaptive
583 differentiation between agricultural and natural environments (e.g., Loh et al., 2008;
584 Bouchet et al., 2012). Gene expression differences were detected using a cDNA
585 microarray between nearby wild and weedy populations of sunflowers, suggesting both
586 agricultural and local adaptation (Lai et al, 2008); however, a European study of the
587 rapidly expanding, wind-pollinated weed blackgrass (*Alopecurus myosuroides*) found
588 that even though agricultural populations experienced strong selection from herbicide
589 application, this did not modify their genetic structure at 116 AFLPs distributed across
590 the genome (Menchari et al., 2007).

591 **Conclusions**—In this study, we have built on the observations of Sauer (1957)
592 and Pratt and Clark (2001) to present a new hypothesis about the origin of the agricultural
593 weed form of *A. tuberculatus*. Weedy *A. tuberculatus* var. *rudis* appears to have blazed a
594 path from west to east through the central Midwestern states without significant genetic
595 change at neutral markers. Its surprisingly limited admixture with the native conspecific

596 eastern variety is intriguing, and should be investigated further. Evolution in response to
597 agricultural management practices is ongoing in this species, as exemplified by its
598 continual adaptation to new herbicides (e.g., Hausman et al., 2011), and current range
599 boundaries may shift in response to evolution or land use changes.

600 This research shows that the most common mode of weed origination, the
601 expansion of the niches of wild plants to include agricultural environments, can proceed
602 via quite different evolutionary trajectories from weeds related to domesticated plants.
603 Future evolutionary investigations of the understudied wild-to-weed category of weed
604 origins have the potential to show how general or specific the patterns found in this paper
605 are. Generalizations from these studies would be interesting from the perspective of both
606 basic evolutionary biology and weed control.

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TABLES

Table 1. Genotyped populations of *Amaranthus tuberculatus*: name, U.S. state/Canadian province, geographical region of population (from Figure 1: west = historical range of *A. tuberculatus* var. *rudis*, east = historical range of *A. tuberculatus* var. *tuberculatus*, overlap = historical range of both varieties), habitat of population (agricultural or natural), number of individuals genotyped (N), and voucher specimen fruit dehiscence (whether the ripe utricle opens or not).

Name	State/ Province	Geographical region	Habitat	N	Voucher fruit dehiscence
SaltR	OK	west	riverbank	10	dehiscent
CHE	KS	west	lake shore	10	too young to tell
TCL	KS	west	lake shore	10	dehiscent
TR	NE	west	riverbank	9	dehiscent
MSH	MO	west	soy field	10	dehiscent
GASC	MO	west	riverbank	10	too young to tell
JCK	AR	west	riverbank	9	dehiscent
WSS	MO	west	sunflower field	7	dehiscent
WSR	MO	west	riverbank	10	indehiscent
AAF	MO	west	soy field	10	dehiscent
RIP	IL	west	riverbank	10	indehiscent
GTP	MO	west	riverbank	10	dehiscent
EMN	MO	west	riverbank	8	dehiscent
PEK	IL	overlap	riverbank	10	indehiscent
KEY	IL	overlap	lake shore	10	too young to tell
KEYC	IL	overlap	soy field	10	dehiscent
KNK	IL	overlap	soy field	10	indehiscent
VIGO	IN	overlap	soy field	10	indehiscent
KANK	IN	east	riverbank	10	indehiscent
IND	IN	east	riverbank	10	indehiscent
WAB	IN	east	riverbank	10	indehiscent
AUR	IN	east	riverbank	10	too young to tell
DMD	MI	east	riverbank	9	indehiscent
RT29	OH	east	corn field	10	dehiscent
BTL	OH	east	riverbank	9	dehiscent
GTB	OH	east	soy field	10	indehiscent
STW	OH	east	riverbank	10	indehiscent
NEV	OH	east	riverbank	10	indehiscent
OTT	OH	east	riverbank	10	indehiscent
MAU	OH	east	riverbank	10	indehiscent
MC	OH	east	soy field	10	indehiscent
PCL	OH	east	lake shore	10	indehiscent
CAN	OH	east	soy field	10	indehiscent
SCIO	OH	east	lake shore	10	dehiscent
PTC	OH	east	lake shore	9	indehiscent
SCF	ON	east	lake shore	10	too young to tell
DEL	ON	east	riverbank	9	indehiscent
YORK	ON	east	riverbank	10	indehiscent

856 Table 2. Population genetic statistics for each population summarized over all loci.
 857 Na = number of alleles, Ne = effective number of alleles (estimated reciprocal of
 858 homozygosity), Ho = observed heterozygosity, He = expected heterozygosity.
 859 Populations with higher observed than expected heterozygosity (potentially reflecting
 860 admixture) are in bold font.
 861

Population	Mean Na	Mean Ne	Mean Ho	Mean He
TR	5.1	3.22	0.57	0.65
CHE	4.9	3.48	0.57	0.60
TCL	5.2	3.05	0.58	0.59
SaltR	5.2	3.50	0.65	0.68
GASC	4.9	3.09	0.54	0.54
MSH	4.8	3.07	0.50	0.55
AAF	4.7	3.39	0.60	0.61
WSR	4.9	3.39	0.57	0.61
GTP	5.1	3.52	0.59	0.62
WSS	4.4	3.44	0.63	0.64
EMN	4.6	3.21	0.49	0.55
JCK	5.2	3.70	0.51	0.62
PEK	4.8	3.31	0.59	0.58
RIP	5.1	3.12	0.54	0.57
KEY	5.0	3.27	0.55	0.60
KEYC	4.7	3.17	0.51	0.56
KNK	5.3	3.18	0.55	0.60
VIGO	4.3	2.56	0.69	0.55
KANK	4.8	3.22	0.61	0.60
WAB	5.3	3.44	0.63	0.64
IND	5.6	4.05	0.59	0.66
AUR	4.4	3.01	0.46	0.54
BTL	4.7	3.00	0.51	0.58
PCL	3.9	2.86	0.49	0.50
NEV	3.8	2.64	0.52	0.49
STW	5.0	3.55	0.57	0.60
CAN	3.3	2.34	0.58	0.55
SCIO	4.5	3.27	0.64	0.63
GTB	4.5	2.74	0.47	0.53
MC	3.7	2.44	0.62	0.58
RT29	5.0	3.64	0.60	0.64
OTT	4.2	2.83	0.49	0.59
MAU	4.5	3.08	0.54	0.60
PTC	4.6	2.96	0.59	0.58
DMD	4.2	2.91	0.50	0.55
DEL	3.0	2.01	0.46	0.46
SCF	4.7	3.47	0.60	0.63
YORK	3.5	2.01	0.38	0.42
All Populations	4.6	3.11	0.56	0.58

FIGURE LEGENDS

862

863

864 Figure 1. Locations of 38 genotyped populations of *A. tuberculatus* from across the
865 species range. Geographic coordinates were plotted in ArcGIS, and each population is
866 shown as an orange circle, with the population name in orange text (corresponding to
867 Table 1). The green line outlines the geographical region corresponding to the historical
868 range of *A. tuberculatus* var. *rudis*, and the purple line outlines the historical range of *A.*
869 *tuberculatus* var. *tuberculatus* (adapted from Sauer, 1957). The red dashed trapezoid
870 outlines the "agricultural waterhemp region" of Ohio. Map sources: ESRI, DeLorme,
871 USGS, NOAA.

872

873 Figure 2. Plot of pairwise genetic distances ($F_{st}/(1-F_{st})$) versus pairwise geographic
874 distances ($\ln(\text{kilometers})$) for the 38 *A. tuberculatus* populations genotyped over the
875 entire species range, showing isolation by distance. The regression has been constrained
876 to go through the origin.

877

878 Figure 3. STRUCTURE population assignment of individuals for $K=2$, for the 38
879 genotyped populations from across the species range. The "western" genetic cluster is in
880 green and the "eastern" genetic cluster is in purple. Population names are shown below
881 the bar graph, and the arrow below the graph shows the geographical organization of the
882 populations. A red asterisk above a population indicates it was found in an agricultural
883 habitat.

884

885 Figure 4. BAPS graphical output for K=3, for the 38-population species' range dataset.
886 The "western" genetic cluster is in green and the "eastern" genetic cluster is in blue,
887 while the third cluster (the MC population) is in red. A. The admixture bar graph for
888 K=3. Population names are shown below the population clusters, and the organization of
889 populations geographically is the same as in Figure 3. B. The Voroni tessellation
890 diagram for K=3, labeled with population names.

891

892 Figure 5. STRUCTURE population assignment of individuals for K=2, for the 12-
893 population Ohio dataset. The "western" genetic cluster is in green and the "eastern"
894 genetic cluster is in purple. Population names are shown below the bar graph, a red
895 asterisk above a population indicates it was found in an agricultural habitat, and a black
896 asterisk indicates a population found in the "agricultural waterhemp region" but in a non-
897 agricultural habitat.

898

899

900 SUPPORTING INFORMATION

901 Table S1. Genotyped populations of *Amaranthus tuberculatus*, with name, U.S.

902 state/Canadian province, voucher information, and geographical coordinates.

903

904 Table S2. Microsatellite loci forward (F) and reverse (R) primers, repeat motif, dye label

905 (used in multiplexed reactions), size range, and primer source. Sources are Lee et al.

906 (2009) and the Tranel lab at the University of Illinois-Urbana/Champaign.

907

908 Table S3. Population genetic statistics for each locus summarized over all populations.

909 N_a = number of alleles, N_e = effective number of alleles (estimated reciprocal of

910 homozygosity), H_o = observed heterozygosity, H_e = expected heterozygosity.

911

912 Figure S1. Locations of 12 genotyped populations of *A. tuberculatus* from Ohio.

913 Geographic coordinates were plotted in ArcGIS, and each population is shown as an

914 orange circle, with the population name in orange text (corresponding to Table 1). The

915 red dashed trapezoid outlines the “agricultural waterhemp region” of the state (J.

916 Stachler, NDSU, pers. comm.). Map sources: ESRI, DeLorme, USGS, NOAA.

917

918 Figure S2. Plots of (A) mean $\ln P(D)$ (the natural log of the probability of the data from

919 STRUCTURE output) with vertical lines showing standard deviation, and (B) ΔK (the

920 second-order rate of change of K) versus K , for the 38 genotyped populations from across

921 the species range, showing a highest ΔK of 2. Plots are from the STRUCTURE

922 HARVESTER output.

923

924 Figure S3. Plots of (A) mean $\ln P(D)$ (the natural log of the probability of the data from

925 STRUCTURE output) with vertical lines showing standard deviation, and (B) ΔK (the

926 second-order rate of change of K) versus K , for the 12 genotyped populations from Ohio,

927 showing a highest ΔK of 2, and a second peak at $K=5$. Plots are from the STRUCTURE

928 HARVESTER output.

929

930 Figure S4. STRUCTURE population assignment of individuals for K=5 for the 12-
931 population Ohio dataset. Population names are shown below the bar graph, a red asterisk
932 above a population indicates it was found in an agricultural habitat, and a black asterisk
933 indicates a population found in the "agricultural waterhemp region" but in a non-
934 agricultural habitat.

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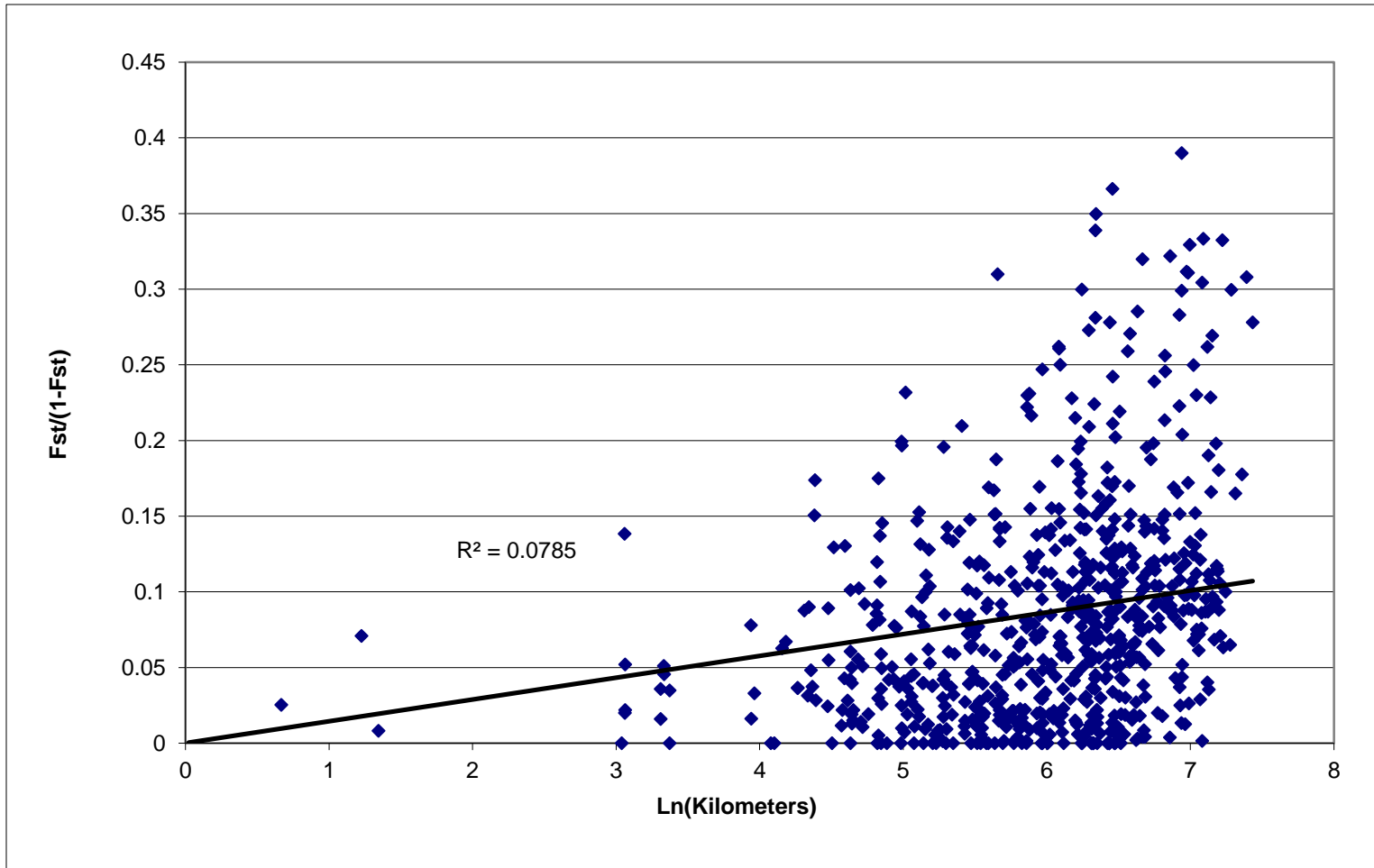


Figure 2.

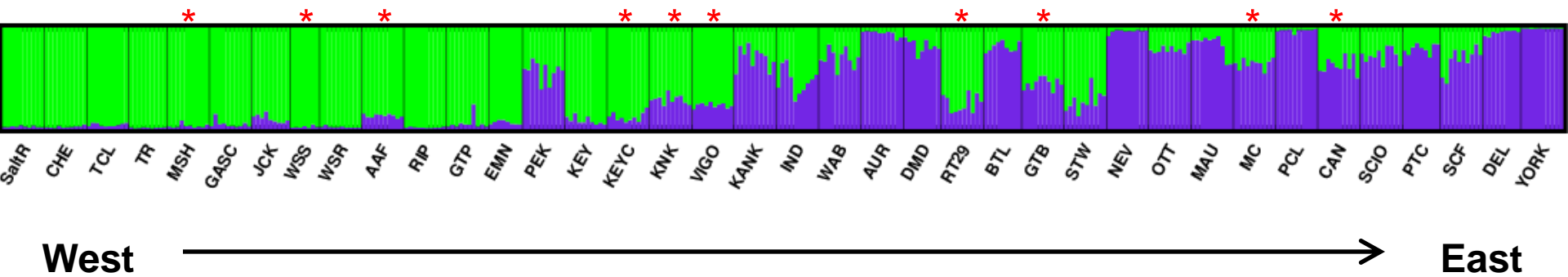


Figure 3.

A.

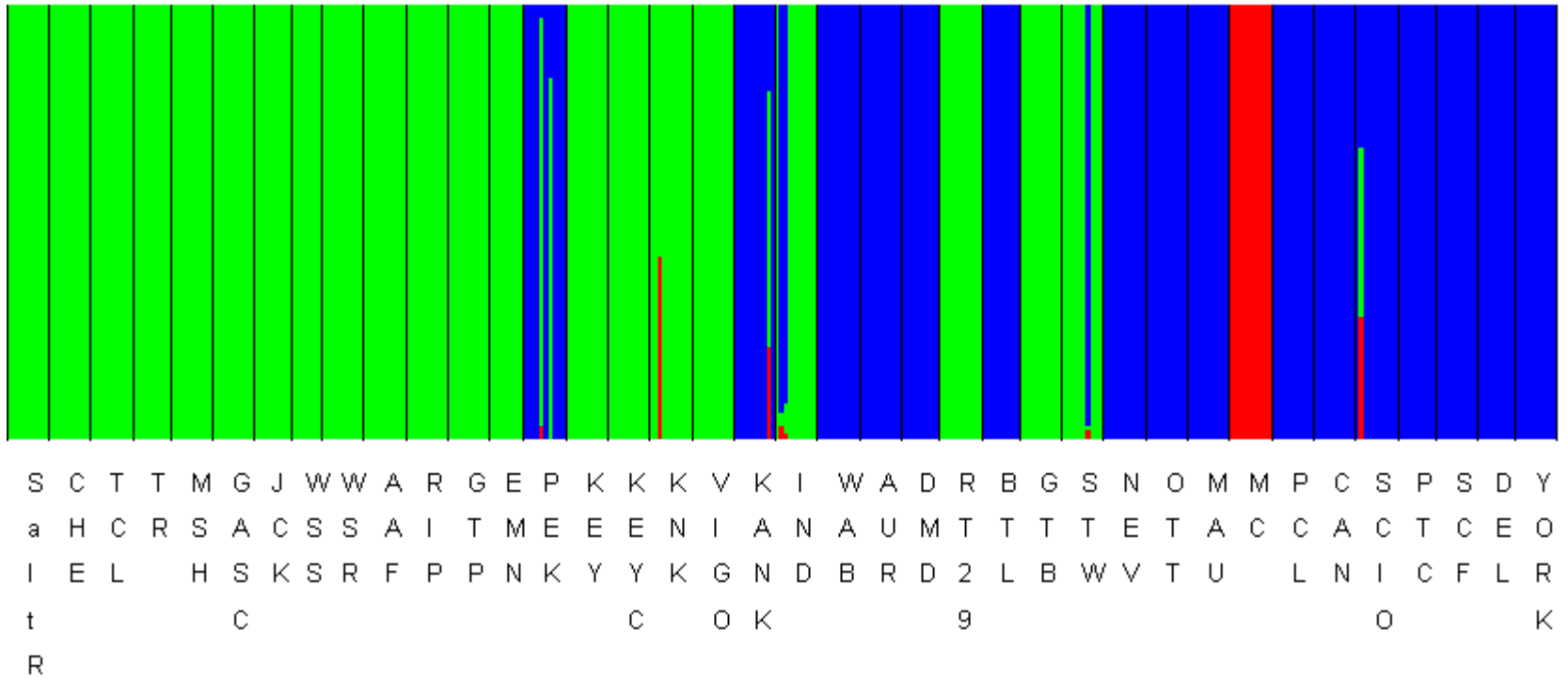


Figure 4a.

B.

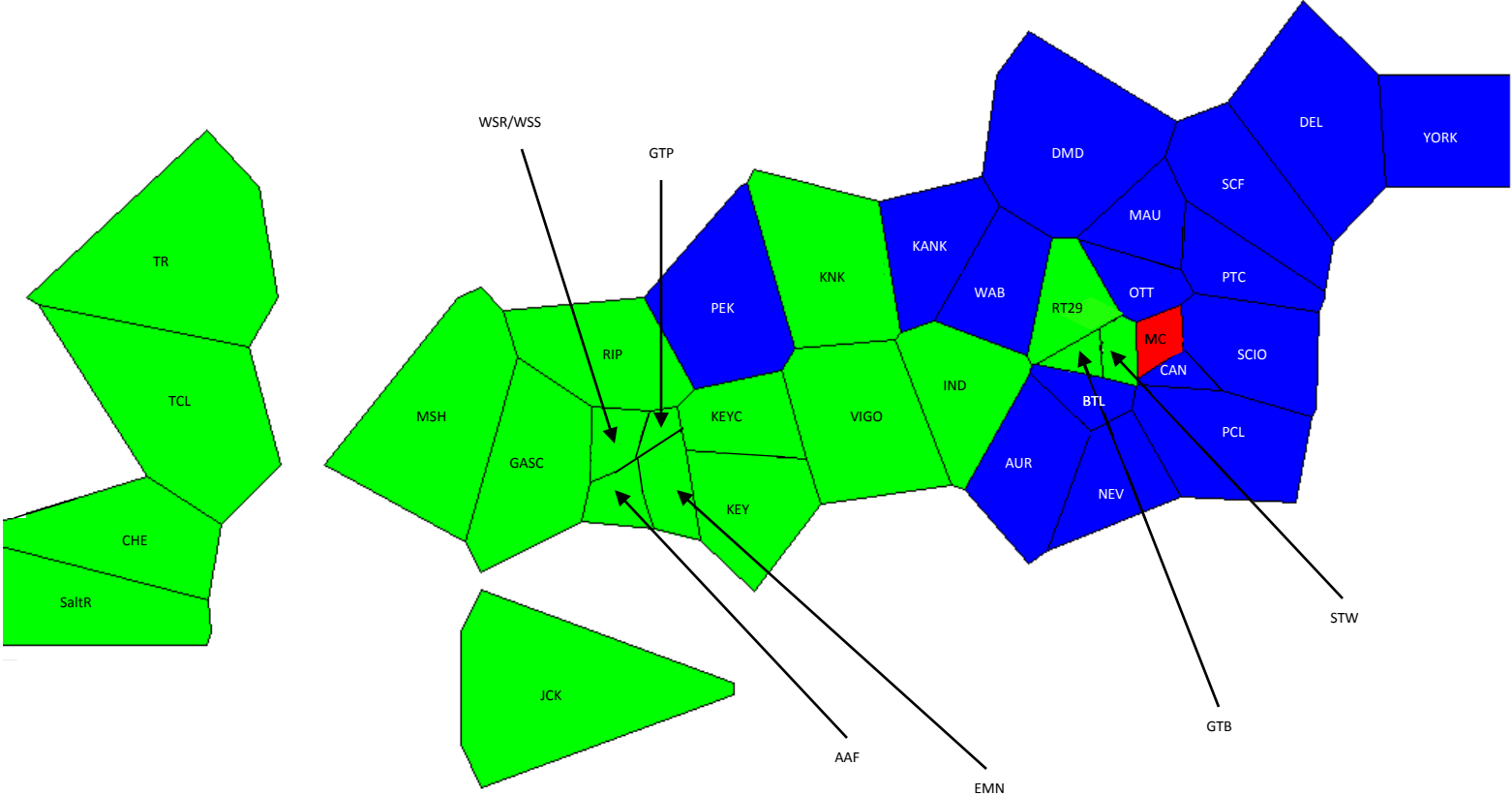


Figure 4b.

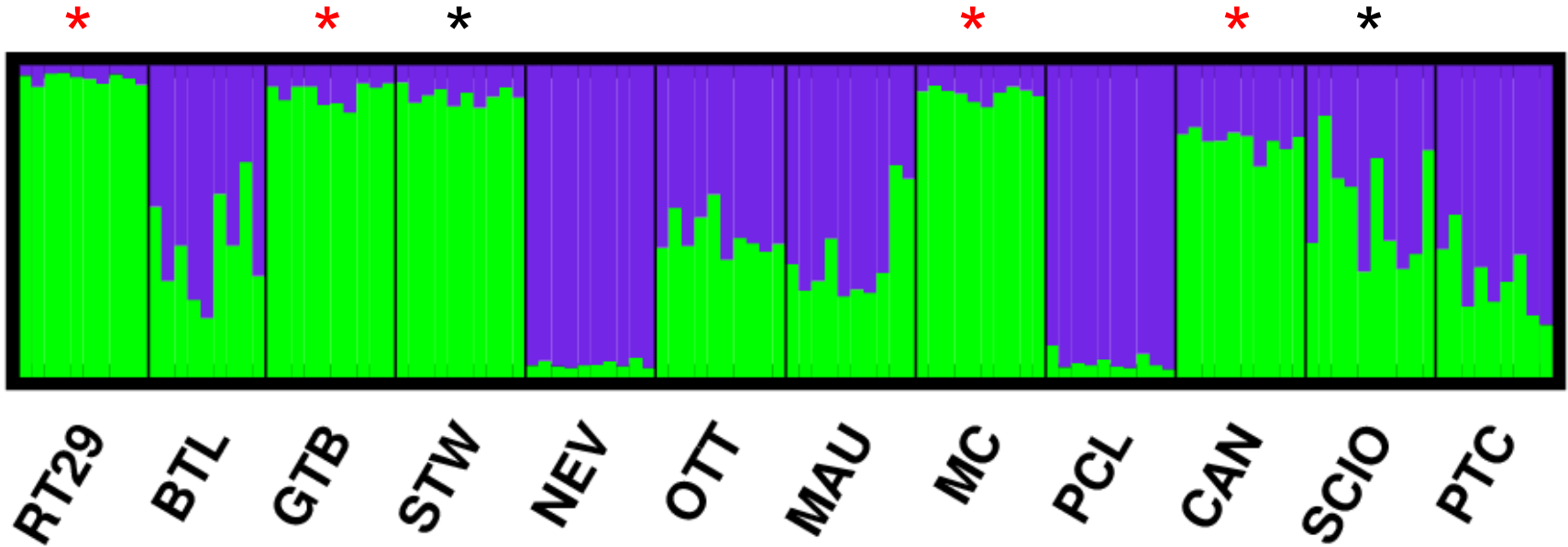


Figure 5.

Table S1. Genotyped populations of *Amaranthus tuberculatus*, with name, U.S. state/Canadian province, voucher information, and geographical coordinates.

Name	State/ Province	Voucher Information:		Latitude	Longitude
		Collector, Collection #:	Herbarium		
SaltR	OK	K. Waselkov, #75: MO		36.771660	-98.038000
CHE	KS	K. Waselkov, #74: MO		37.744750	-97.783860
TCL	KS	K. Waselkov, #72: MO		39.439230	-96.710250
TR	NE	K. Waselkov, #68: MO		41.223310	-96.357610
MSH	MO	K. Waselkov, #138: KSC		39.168783	-93.289057
GASC	MO	K. Waselkov, #137: MO		38.668122	-91.556135
JCK	AR	K. Waselkov, #133: MO		35.642113	-91.319192
WSS	MO	K. Waselkov, #31: MO		38.656280	-90.736955
WSR	MO	K. Waselkov, #32: MO		38.656280	-90.736950
AAF	MO	K. Waselkov, #25: KSC		38.473250	-90.661016
RIP	IL	K. Waselkov, #58: MO		40.027434	-90.631546
GTP	MO	K. Waselkov, #24: MO		38.558930	-90.447360
EMN	MO	K. Waselkov, #26: KSC		38.545160	-90.433450
PEK	IL	K. Waselkov, #56: MO		40.574410	-89.655980
KEY	IL	K. Waselkov, #53: MO		38.733710	-89.275850
KEYC	IL	K. Waselkov, #142: KSC		38.768113	-89.273209
KNK	IL	K. Waselkov, #64: MO		41.160983	-87.627515
VIGO	IN	K. Waselkov, #119: MO		39.273930	-87.470000
KANK	IN	K. Waselkov, #115: MO		41.314810	-86.737550
IND	IN	K. Waselkov, #109: MO		39.783310	-86.189750
WAB	IN	K. Waselkov, #111: MO		40.790980	-85.820860
AUR	IN	K. Waselkov, #106: MO		39.056110	-84.898350
DMD	MI	K. Waselkov, #82: MO		42.645000	-84.649700
RT29	OH	K. Waselkov, #101: MO		40.545911	-84.634131
BTL	OH	K. Waselkov, #95: MO		39.427430	-84.540710
GTB	OH	K. Waselkov, #97: MO		40.120100	-84.398680
STW	OH	K. Waselkov, #98: MO		40.121630	-84.358660
NEV	OH	K. Waselkov, #92: MO		38.807630	-84.211710
OTT	OH	K. Waselkov, #91: MO		41.037830	-83.813490
MAU	OH	K. Waselkov, #90: MO		41.556350	-83.662410
MC	OH	K. Waselkov, #102: MO		40.155580	-83.455330
PCL	OH	K. Waselkov, #94: MO		39.268010	-83.388610
CAN	OH	K. Waselkov, #104: MO		39.985850	-83.339630
SCIO	OH	K. Waselkov, #103: MO		40.177450	-83.126400
PTC	OH	K. Waselkov, #89: MO		41.514500	-82.938430
SCF	ON	K. Waselkov, #84: MO		42.030950	-82.603850
DEL	ON	K. Waselkov, #86: MO		42.933750	-81.421060
YORK	ON	K. Waselkov, #88: MO		43.020700	-79.891050

Table S2. Microsatellite loci forward (F) and reverse (R) primers, repeat motif, dye label (used in multiplexed reactions), size range, and primer source. Sources are Lee et al. (2009) and the Tranel lab at the University of Illinois-Urbana/Champaign.

Locus name	Primer	Repeat	Dye label	Size range	Source
C1140	F: 5'-TTGAAGACGACGATCTTTCTGGAT R: 5'-CCCCTCTGTACACCATAATCGAAC	(GAT) ₁₀	6FAM	113-181 bp	Tranel lab <i>A. tuberculatus</i> transcriptome data
C4097	F: 5'-ATCATCTTCTGCTAAGGCTGTGG R: 5'-ATATCTTCCCAATTGGACTCCTC	(ACC) ₈	NED	164-179 bp	Tranel lab <i>A. tuberculatus</i> transcriptome data
C0745	F: 5'-TAGGAAGTTCATCCATAAGCTCGG R: 5'-CAATTCCAAGGAATCATCCTCATC	(TGA) ₁₀	NED	130-164 bp	Tranel lab <i>A. tuberculatus</i> transcriptome data
C3561	F: 5'-CCATAAACCATTTTCCAGACC R: 5'-ACTTCTGGCCCAATTAGGAAGTC	(CCA) ₈	HEX	123-141 bp	Tranel lab <i>A. tuberculatus</i> transcriptome data
C4999	F: 5'-CCACCAATGACCCATACCTACTA R: 5'-GATGAGGTTGATAATTGGGGTTCA	(ACC) ₈	NED	120-141 bp	Tranel lab <i>A. tuberculatus</i> transcriptome data
AAC1	F: 5'-CCCACCAAGGATGATCATTTAGAC R: 5'-TCATCATTATTTGTTGGCGTTGAC	AAC	6FAM	112-130 bp	Lee et al. 2009
TAG5	F: 5'-GTCGCTGAATTGTTTGTAGCTGGT R: 5'-TGGGAATTCTCTCTGTGACACAGT	TAG	HEX	132-163 bp	Lee et al. 2009
ATC9	F: 5'-TAGCCATTTCAACCTTACGAGGAA R: 5'-ACCGTTGATTGATTTATGGCATC	ATC	NED	142-160 bp	Lee et al. 2009
C3695	F: 5'-TCAACTTCTTATTCTTGGGTGCTTC R: 5'-CCTTACCTTCTCTCAAAGCACCA	(TGA) ₈	6FAM	127-174 bp	Tranel lab <i>A. tuberculatus</i> transcriptome data
C9333	F: 5'-AACTAAACGCATTTGCCATTGAA R: 5'-TGTTTCATCTAACCCATCATAATGGAA	(GAT) ₈	HEX	165-199 bp	Tranel lab <i>A. tuberculatus</i> transcriptome data

Table S3. Population genetic statistics for each locus summarized over all populations. Na = number of alleles, Ne = effective number of alleles (estimated reciprocal of homozygosity), Ho = observed heterozygosity, He = expected heterozygosity.

Locus	Sample size	Na	Ne	Ho	He
C1140	722	20	8.86	0.82	0.89
C4097	720	6	2.04	0.49	0.51
C0745	702	14	5.87	0.76	0.83
C3561	722	7	1.55	0.35	0.35
C4999	716	9	3.02	0.58	0.67
AAC1	714	6	2.46	0.43	0.59
TAG5	710	10	2.55	0.46	0.61
ATC9	716	6	1.09	0.09	0.09
C3695	718	16	9.10	0.85	0.89
C9333	704	13	6.46	0.73	0.85

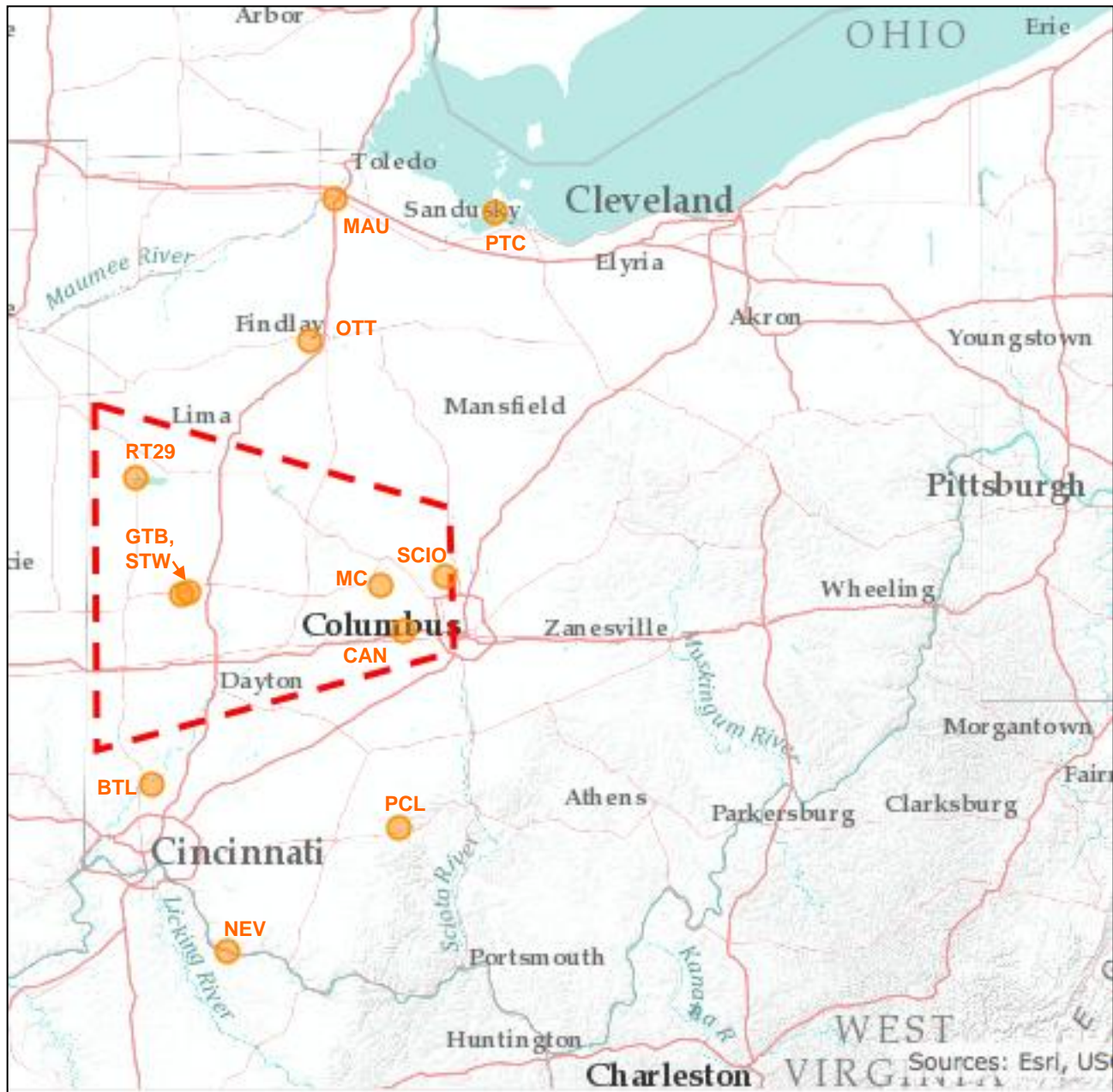


Figure S1.

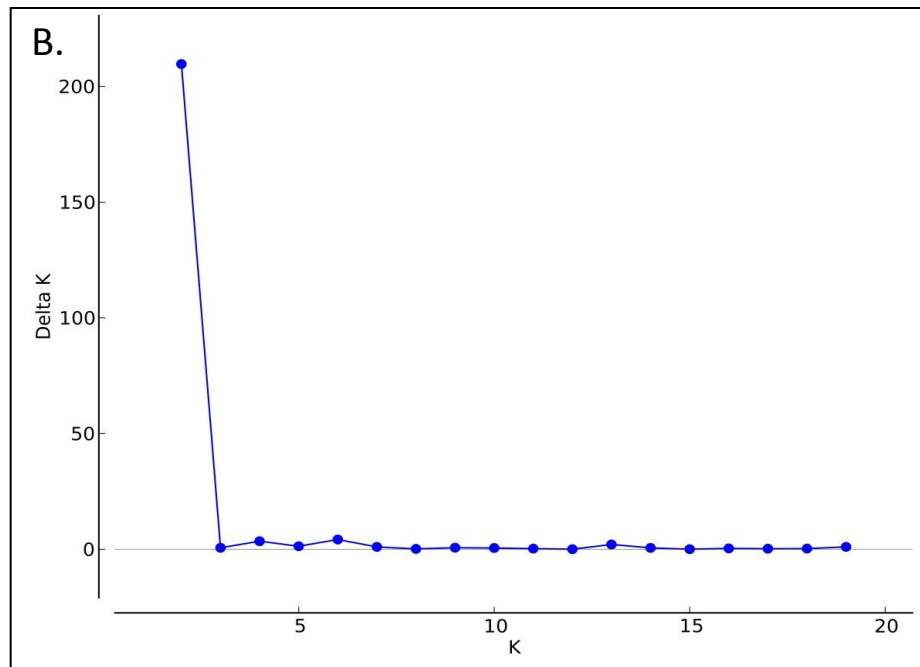
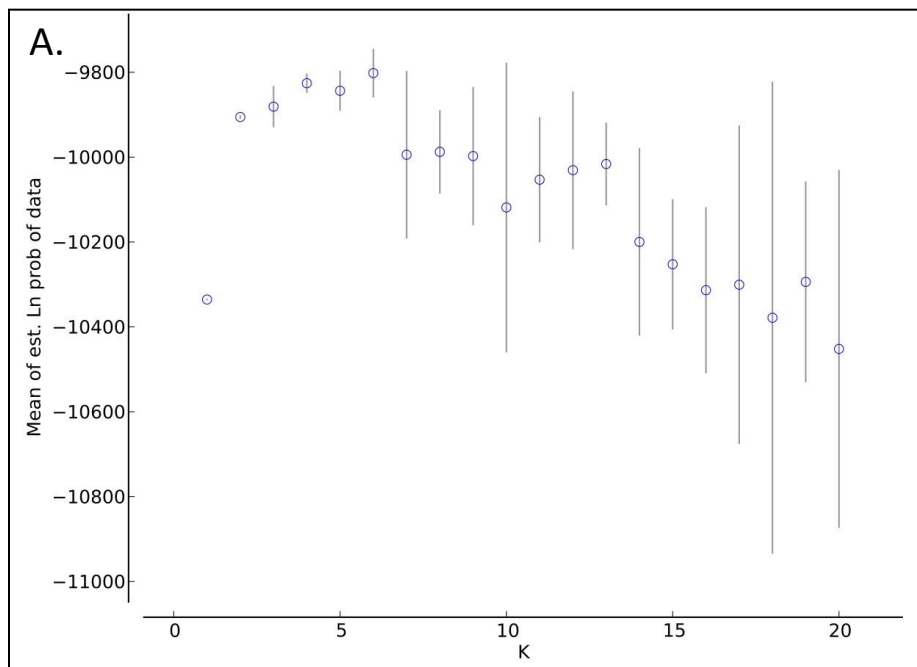


Figure S2.

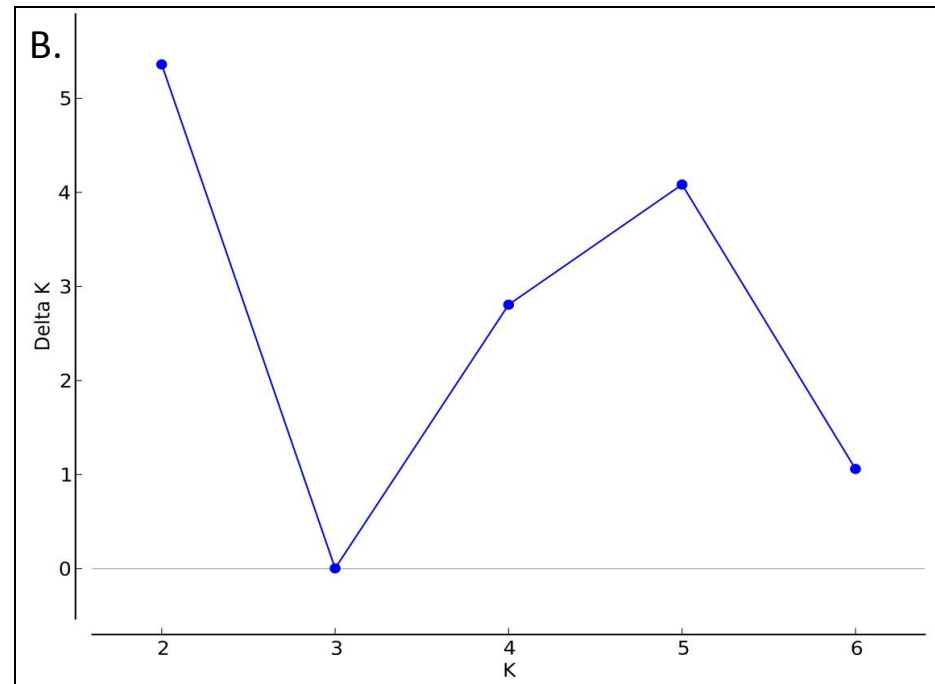
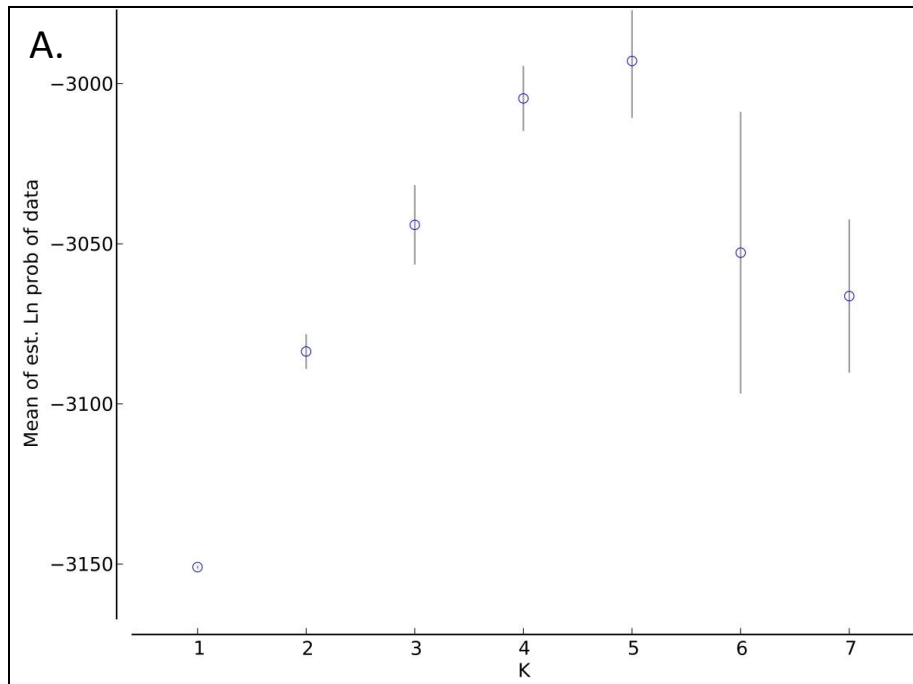


Figure S3.

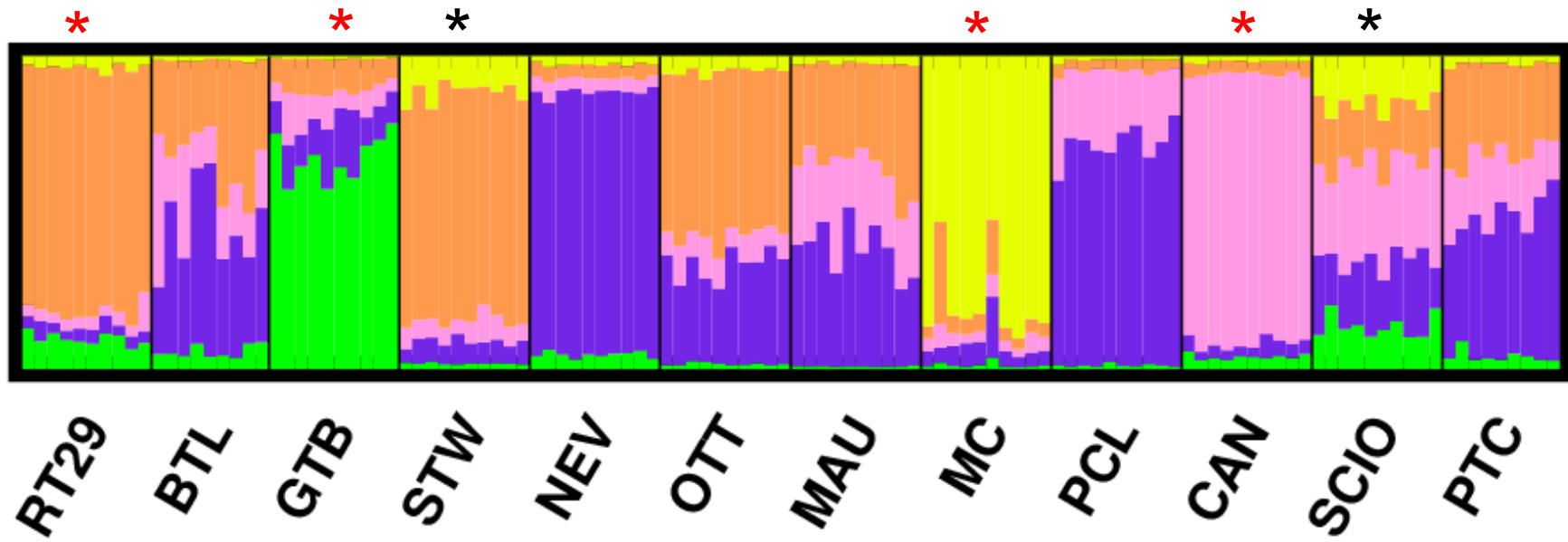


Figure S4.