**Methods**

*Overview of simulations*

To examine the formation of spatial clines in HCN, we created a series of spatially-explicit simulations in Python 2.7 (CITE?) to track the frequency of HCN within populations across space. We set up a one-dimensional, linear matrix with 40 cells, consistent with the number of populations sampled across cities by Thompson et al. (2016), where each cell (hereafter patch) represents a patch of suitable habitat that can support a population of *Trifolium repens*. These simulations allowed for fine scale, independent control of both stochastic and deterministic parameters important for varying and maintaining the frequency of *CYP79D15* and *Li*—and thus HCN—in patches distributed across the landscape (Table 2). The order of events in the simulations are as follows: (1) Local reproduction (i.e. population growth), (2) selection, (3) migration, (4) colonization (Figure 1C). We first explored two broad colonization scenarios, described below, which differ in how they manipulate the amount of genetic drift acting within populations. We then simulated a range of scenarios exploring the interactive effects of selection, migration, and drift, which we summarize in Table 2.

*Scenario 1:* *Gradient in carrying capacity across the matrix*

In the first scenario, we imposed a gradient in the carrying capacity (*K*) of populations across the matrix, thereby placing an upper-limit on the population size (*N,* Figure 1A). Drift is expected to be greatest in populations with the smallest carrying capacity and this method has been used in other agent-based simulations exploring the effects of drift, gene flow, and selection on patterns of local adaptation (Alleaume-Benharira et al. 2006). We first simulated a scenario where *N* is assumed to be greatest in rural populations (*N* = 1000) and decline linearly with increasing urbanization (*N* = 10 at urban end, Figure 1A). This scenario represents a case where clover populations were initially similar but increased fragmentation associated with urbanization reduced urban population sizes and increased the strength of drift. All 40 populations were initialized—and remained— at carrying capacity; thus, population growth is irrelevant in this first case. These simulations were run for 500 non-overlapping generations.

*Scenario 2:* *Colonization and founder events*

In the second scenario, the simulations begin with a single rural population at carrying capacity and adjacent patches are repeatedly colonized toward the urban end until all patches contain populations (Figure 1B and 1C). There is no gradient in carrying capacity in this scenario; rather, the strength of drift is manipulated by varying the strength of founder events, determined as the proportion of alleles sampled from the parent population (i.e. smaller proportion = stronger founder event). The probability that a population colonizes an adjacent patch depends on its size: this probability is 1.0 for populations at carrying capacity and decreases linearly with decreasing population size. Because founder events reduce the size of newly formed populations, serial founder events would result in populations becoming rapidly extinct (or exceedingly small), preventing the colonization of new patches. We therefore implemented a model of logistic population growth allowing populations to grow every generation until they reach carrying capacity. Under this model, a population of size 10 takes 27 generations to reach a carrying capacity of 1000 (growth rate [r] = 1.5). Simulations were run for 500 generations beginning when all patches on the landscape contained populations.

*Selection*

We used two-locus selection models to explore the effects of selection in generating and maintaining cyanogenesis clines (Kimura 1956; Lewontin and Kojima 1960; Felsenstein 1965). Selection acted either for or against cyanogenic genotypes, depending on the population’s position in the landscape matrix. For each simulation, we defined a maximum strength of selection, which favoured cyanogenic (HCN+) genotypes in the rural-most population and acyanogenic (HCN–) genotypes in the urban-most population. The selection coefficient varied linearly across the matrix such that HCN+ and HCN– genotypes had equal fitness in the central population of the landscape (i.e. population 20, Figure X).

When selection acts on two or more loci, linkage disequilibrium (LD) may accumulate as genotypes with particular allele combinations are favored, resulting in gamete frequencies that differ from their expectation based on allele frequencies (Lewontin and Kojima 1960). However, given that the *CYP79D15* and *Li* loci are unlinked (REF NEEDED), theory predicts that free recombination (recombination fraction = 0.5) between these loci would limit the accumulation of significant LD even under selection (Felsenstein 1965). Simulations exploring the build-up of LD under varying selection regimes acting for or against cyanogenic genotypes confirmed that even strong selection (*s* = 0.1) results in little accumulation of LD (see supplementary materials: “Effects of selection on linkage between *CYP79D15* and *Li*”). We therefore ignored the effects of LD in our simulations and gamete frequencies each generation were thus calculated directly from allele frequencies, with recombinant gametes being produced with equal frequency (0.25) from heterozygous genotypes.

*Migration*

In all simulations, we varied the amount of migration between populations across the matrix to explore the effects of gene flow on the formation of clines due to drift and selection. We modelled migration according to a modified version of Wright’s island model (Wright 1943). Specifically, the frequency of the dominant allele (e.g. *CYP79D15*)in population in the next generation ()is given as:

where is the frequency of the dominant *CYP79D15* in population in the current generation, is the weighted-mean immigration rate from all populations into population and is weighted-mean frequency of the dominant allele in the current generation for population ’s migrant pool, averaged across all other existing populations, respectively. Migration is assumed to decline linearly with increasing distance between populations such that there is effectively no migration between populations in patches 1 and 40 of the matrix. Migration rates and dominant allele frequencies were weighted by population size such that larger populations contributed more migrants to the migrant pool. Specifically, the weighted-mean immigration rate from all populations into population was calculated as:

where is the realized migration rate between populations and , based on the distance between them, is the size of population , and in this case is 39—the number of populations minus one—since populations do not exchange migrants with themselves. Similarly, the weighted-mean dominant allele frequency for population ’s migrant pool was calculated as:

where is the frequency of the dominant allele in population . We perfomed the above process separately for both dominant alleles (i.e. *CYP79D15* and *Li*). For scenario (1) described above, we simulated 13 migration rates (*m* = 0; 0.001; 0.0025; 0.005; 0.01; 0.02; 0.035; 0.05; 0.1; 0.2; 0.35; 0.5, 1.0) to explore the full range of migration rates that can influence the formation and maintenance of clines via drift. Note that these values represent the maximum proportion of alleles exchanged between populations, which occurs among adjacent populations. To minimize the number of simulations performed in scenario (2), we simulated three migration rates: *m* = 0, 0.01, and 0.05, representing no, low, and high migration, respectively, and corresponding to levels of gene flow that resulted in substantial decreases in the strength of clines in scenario (1).



**Figure 1:** Diagrammatic representation of simulations examining the effects of genetic drift, gene flow and selection on spatial clines in HCN. We manipulated the effects of drift in two ways: (A) By creating a spatial gradient in carrying capacity (*K*) across the linear matrix, thereby placing an upper limit on the population size (*N*) in each population. Population size was greatest in the rural-most population (*N* = 1000) and declined linearly to the urban-most population (*N* = 10). In this case, all patches (separated by solid vertical lines) started with populations at carrying capacity in generation 1 (represented by grey filling of patches). (B) Through serial founder events during the colonization of the urban environment, beginning with a single rural population at carrying capacity. Populations could only colonize adjacent patches and the proportion of founding alleles was varied to control the strength of drift (i.e. lower proportion = stronger drift). (C) Schematic of the order of events during simulations of case 2 (i.e. B). Boxes represent a single population as it proceeds through the simulations. Upon colonization, populations first grow according to a logistic growth model (growth rate [r] = 1.5). Populations are then subject to selection, followed by migration. The frequency of alleles within a population in the next generation is thus a function of that allele’s frequency in the current generation, its relative fitness in the current patch, and the mean frequency of migrant alleles arriving from all other populations in the matrix. Every generation, we track the frequency of dominant alleles at both loci underlying HCN production (i.e. *CYP79D15* and *Li*) and the frequency of HCN within each population in the matrix.