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Introduction

Host-parasite diversity can be described in two different ways. The first is simply the observed variability among the hosts and parasites in a particular population. For example, Burdon and Jarosz (1991) classified 67 wild flax plants into 10 distinct resistance genotypes when tested against six races of flax rust. One host genotype was completely resistant to all six pathogen races, whereas another genotype was susceptible to five of six races.

The second type of variability is the range of potential genotypes that can occur over space and time. For example, Parker (1985) used field transplant experiments to study the legume *Amphicarpaea bracteata* and its fungal pathogen *Synchytrium decipiens*. Fungal infection was heavy in each of three locations. However, a plant moved to a new location developed little or no infection, suggesting that the pathogen populations differ among sites. In a second experiment, host lines derived from different locations varied in their ability to resist a single pathogen isolate, indicating spatial differentiation among the host populations.

Parker's study suggests that the potential range of diversity over space and time is often greater than the variability observed in a single location. The potential diversity is limited by the biochemistry and morphology of host-parasite traits, whereas the observed diversity is controlled by the local dynamics of disease and the global processes of extinction and colonization in the metapopulation.

The first goal of this paper is to suggest that increasing potential diversity causes a qualitative shift in metapopulation dynamics. Local processes dominate when potential diversity is low. Colonization-extinction dynamics of alleles in the metapopulation become more important with an increase in the potential number of distinct genotypes. In the next section I present a simple model to illustrate the importance of potential diversity.

After briefly discussing the model, I review evidence that many host-parasite systems do in fact have high potential diversity. Examples include plant-pathogen

genetics and bacterial defense systems against viral parasites and conspecific competitors. I also discuss the antagonistic interaction between cytoplasmic and nuclear genes in cytoplasmic male sterility.

Data from these studies suggest that spatial variation and colonization-extinction dynamics are important in the observed patterns of diversity. However, the data are difficult to interpret because of limited sampling over space and time. This difficulty leads to my second goal: the emphasis of space-time scaling when interpreting host-parasite diversity. Spatial scales that are small relative to migration distance have well-mixed populations dominated by local interactions. Local processes also dominate on temporal scales that are short relative to the expected times to extinction and recolonization of genotypes. By contrast, observations aggregated over long spatial and temporal scales may obscure colonizations, extinctions and rapid changes in genetic composition that occur on finer scales. Thus the patterns of observed variability are strongly influenced by the space-time scaling of colonizations and extinctions in the metapopulation.

Dimensionality and Colonization-Extinction Dynamics

In this section I describe more precisely the relationship between potential variation and observed diversity. I define the potential number of genotypes as the *dimensionality* of the system. I begin with a verbal illustration of the link between dimensionality and colonization-extinction dynamics. I then turn to a simple model.

Verbal description

The observed diversity of host-parasite genetics depends on the range of possible variants and the processes that govern local extinction or success of each genotype. For example, suppose that the host has just two alternative genotypes, h_1 and h_2 , and the parasite has two genotypes, p_1 and p_2 . The host h_1 can recognize and resist the matching parasite, p_1 , but h_1 is susceptible to p_2 . Likewise, h_2 can resist p_2 but is susceptible to p_1 . In this case strong frequency dependence will favor rare genotypes, and genotype frequencies will fluctuate around 0.5. Thus diversity is controlled by the local dynamics of frequency dependence.

Now consider the same pattern of host-parasite interaction but with more genotypes. In particular, each of the n host genotypes $h_1 \dots h_n$ matches the single corresponding parasite genotype from the set of $p_1 \dots p_n$. Thus h_1 resists p_1 but is susceptible to all other parasite genotypes, h_2 resists p_2 , and so on. The same frequency dependence occurs, favoring equal abundance of all genotypes. But the frequencies

now fluctuate about $1/n$. As the dimensionality n increases, the average frequency declines, and small fluctuations are more likely to cause local extinction of a genotype.

An extinction leads to a sequence of events that changes the local dynamics. For example, suppose that host genotype h_i is locally extinct. Then the matching parasite p_i has an advantage over other parasite types because it can attack all hosts in the local population. The other parasites are resisted by their matching host genotypes. Thus p_i increases and the other parasites decline toward local extinction. The patch is now ripe for recolonization and rapid increase by h_i , which would drive p_i and the other host types toward local extinction. The point is that dynamics are now controlled by the times to extinction and recolonization. The observed variation in a particular population at particular time will be much lower than the potential diversity.

The model

I now turn to the formal model. The ideas are the same as in the verbal model just given, but the points are made more precisely. Some readers may prefer to skip ahead to the sections on natural history and return later to the details of the model.

I focus on a single-patch model with extrinsic colonizations rather than an explicit, multi-patch metapopulation analysis. In the next section I discuss single-patch and multi-patch models.

The model has a single haploid locus. Each of the n host alleles causes recognition and resistance to only one of the n parasite alleles. Thus each host is resistant to $1/n$ of the parasite genotypes, and each parasite can attack $(n-1)/n$ of the host genotypes (Frank 1991a, 1993a). I call this the ‘matching-allele’ model. In a population-genetic context the different alleles constitute a polymorphic locus of a single species. In an ecological context each allele is associated with a different species. I will use the population-genetics language of allelic polymorphism, but an ecological interpretation of species diversity is equivalent for these assumptions.

I use Lotka-Volterra equations to describe the system. These equations show the dynamics of genotype abundances rather than just the relative genotype frequencies. Thus the model tracks epidemic fluctuations in population sizes and disease intensity in addition to changes in genotype frequency. The model is

$$\begin{aligned}\Delta h_i &= h_i [r(1 - H/K) - m(P - p_i)] \Delta t \\ \Delta p_j &= p_j [-s + b(H - h_j)] \Delta t.\end{aligned}\tag{1}$$

The values of h_i and p_j are the abundances of hosts of genotype i and parasites of genotype j . The total abundance of hosts is $H = \sum_{k=1}^n h_k$, and the total abundance of parasites is $P = \sum_{k=1}^n p_k$.

The term r is the host's intrinsic rate of increase; H/K is the strength of density dependent competition among hosts with carrying capacity of K ; m is the morbidity and mortality per parasite attack; s is the parasite death rate; and b is the parasite's intrinsic birth rate per host-parasite contact. The Δt term is the size of the time step over which the interactions occur. For example, Δt may be the length of one host generation or one season in a discrete-time model. When birth, death and disease cause continuous change of the abundances of hosts and parasites, $\Delta t \rightarrow 0$.

The system in equation (1) is easier to analyze when rewritten in nondimensional form (Segel 1972; Murray 1989). Nondimensional analysis focuses attention on a minimal set of parameters and highlights relative magnitudes (scaling relations) among the processes that drive the dynamics. This is accomplished without altering the dynamics or interpretation because one can translate freely between the biologically motivated formulation and the nondimensional quantities.

The system can be rewritten with the following substitutions

$$\begin{aligned}\hat{h}_i &= h_i/K, & \hat{p}_j &= mp_j/r, & \tau &= r\Delta t, \\ \hat{s} &= s/r, & \hat{b} &= Kb/r.\end{aligned}\tag{2}$$

Dropping the hats yields the nondimensional system

$$\begin{aligned}\Delta h_i &= h_i [1 - H - (P - p_i)] \tau \\ \Delta p_j &= p_j [-s + b(H - h_j)] \tau.\end{aligned}\tag{3}$$

The dynamics of the system are controlled by the equilibrium with all hosts and parasites present, which occurs at $h^* = s/[b(n - 1)]$ and $p^* = (1 - H^*)/(n - 1)$, where $H^* = nh^*$ and, by the symmetry of the system, $h_i^* = h^*$ and $p_j^* = p^*$ for all i and j . This equilibrium point is unstable when there are discrete time lags in the competitive effects among hosts and in the interactions between host and parasite. This equilibrium is neutrally stable when interactions occur in continuous time ($\tau \rightarrow 0$). A detailed analysis is given in the Appendix of Frank (1993a).

Figure 1 shows the dynamics of this system with two hosts and two parasites ($n = 2$). Each panel shows how one of the two host-parasite pairs changes from an initial condition. In each case the abundances follow a stable limit cycle that repeats at regular intervals. These cycles are stable because trajectories away from the cycle spiral toward and then remain on the cycle.

All three panels of figure 1 share the same parameters, equilibrium point and initial conditions except for the size of the time step, τ . Larger time steps destabilize the system. As τ increases from the left to the right panel, the oscillations increase in

magnitude. The very low parasite abundances that occur in the right panel suggest that the parasites in that system would be prone to extinction, which would change the subsequent course of the dynamics.

The difference between a repeating cycle and cyclic dynamics prone to extinctions can be seen in the next two figures. Figure 2 shows time-series plots for a model with two hosts and two parasites ($n = 2$). Extinction is simulated by setting to zero any abundance less than 0.01. In this figure abundances never drop that low and extinction never occurs. Colonization is simulated by adding 0.01 to the abundance of each host and parasite if a random number is less than the colonization rate (see figure legend). These colonizations have little effect on the dynamics because the system follows a stable limit cycle.

Figure 3 shows the same system with $n = 4$. An increase in the number of hosts and parasites has two effects on the dynamics. First, larger n lowers the equilibrium abundance of each host and parasite type. A lower equilibrium shifts the entire cycle down and to the left (see figure 1). Thus an increase in n shifts the cycle closer to the $p = 0$ and $h = 0$ boundaries.

The shift in the location of the cycle leads to the second effect, a tendency for genotypes to become locally extinct. When a host genotype is lost from the local population, the matching parasite genotype has a fitness advantage because it can attack all local host genotypes. Eventually the locally extinct host is reintroduced and spreads rapidly because it can resist attack by the locally dominant parasite. The spread of the resistant host causes a decline among the host's competitors and an increase among all nonmatching parasite genotypes. These extinctions followed by random immigration into the system cause unpredictable fluctuations in the composition of the four host and parasite genotypes (figure 3).

These theoretical examples show the qualitative shift in dynamics caused by colonization-extinction processes. Systems are more prone to extinctions of genotypes when local population sizes are small, the number of genotypes (dimensionality) is high, or nonlinear dynamics cause large, deterministic fluctuations. Colonization by locally novel alleles depends on the frequency of immigration and on the spatial variation in genotypes among populations.

Scale is clearly important. Frequent migration on a particular distance scale leads to high immigration but little differentiation among populations. Very rare migration enhances differentiation but increases the waiting time before locally extinct alleles are reintroduced by immigration. To complete the picture these spatial scalings must be tied to the temporal scales of local dynamics and extinctions (Frank 1991b).

Summary

It may seem rather disappointing to have only the simplest, single-patch Lotka-Volterra model for a metapopulation theory of host-parasite genetics. However, I believe this is the right way to seek theories that apply broadly. A brief justification may be useful before turning to the observations from natural systems.

What would it take to produce a full model of host-parasite genetics within the context of metapopulation dynamics? Since genetics is the question, we need several loci, and several alleles per locus. Natural systems often have this genetic complexity, which may play an important role in determining spatial and temporal dynamics. We must also consider sex and recombination, and the interaction between host and parasite. Mutation is important because rare events can have a large impact on diversity. We now have many parameters, but have not yet specified ecological processes. So we must add in birth and death rates, and explicit descriptions of spatial movement in the metapopulation.

We are ready to see that host-parasite genetics is like the weather. A epidemic arises seemingly without warning in the northwest, caused by a rare migrant parasite genotype that sweeps through the local host population. The patch is ravaged, perhaps extinct or left with only a depauperate set of genotypes and a few individuals. Colonizations occur over time. The new composition is very different from the original composition. And so on over space and time. Dial the migration parameter, and a different but equally beautiful map appears on the computer screen. We have many parameters, each with an effect over some range of the parameter space.

Of course, what we would really like to know about is invariance, regions where changes in a parameter do not matter, and “bifurcation” in the generic sense, parameter changes that cause a qualitative shift in the dynamics. We want to know about qualitative properties of invariance and change over this vast and immensely complex parameter space.

Here is my conjecture. Previous population genetic models missed the most interesting point because they always studied one or two loci with two alternative alleles per locus. At that dimensionality, one finds the usual nonlinear dynamics of cycles and chaos. Local dynamics dominate because, in each patch, all possible genotypes are usually present. However, if one increases the number of loci and alleles, the system “bifurcates,” changes generically. Colonization-extinction dynamics matter, times to extinction and recolonization dominate. Local dynamics are much less important.

Having discovered one major axis along which qualitative aspects are controlled, one can now pursue other interesting questions. Scale always comes up, but one has to put the problem in the context of the biology and the first major axis.

In summary:

1. The goal is to search for invariance over an interesting domain and “bifurcation” between domains because that is only way to learn something general about a complex problem.
2. Host-parasite systems “bifurcate” as they move from low to high dimension. At low dimension, local dynamics are probably more important for understanding genetic diversity. At high dimension, spatial processes dominate. This shift appears inevitable. The purpose of the simple one-patch model is to illustrate this point.
3. What about real systems? There is good evidence that many systems have surprisingly high dimension. The evidence is presented in the following sections. Data about spatial dynamics is sketchy, but where available, suggest the importance of colonization-extinction dynamics at the level of genotypes.
4. When analyzing these systems one is inevitably measuring diversity. One has to be aware of scale. Observed diversity can only be understood within the context of potential diversity and the spatial and temporal dynamics.

In the following sections I turn to data and theory for natural systems. As expected, dimension and scale are important. In addition, the details of extinctions, migration and the genetic system determine the particular attributes of each case. When one can measure these details, it may pay to consider a complex metapopulation model tuned to that system, although the size of the parameter space will make the analysis difficult. I summarize the general conclusions that can be drawn from current empirical and theoretical studies, which are still in an early stage of development.

Introduction to the Examples

Researchers working on two different host-parasite systems have recently turned their attention to spatial variation in allele frequencies. In plant-pathogen interactions the hosts often have numerous resistance genotypes and the pathogens have correspondingly diverse host-range genotypes. The limited data from natural populations suggest spatial variation in both the frequency of successful infections and in allele frequencies. Several authors propose metapopulation dynamics as the cause of spatial variation (e.g., Burdon et al., 1989; Thompson and Burdon, 1992; Frank, 1992, 1993b; Antonovics et al., 1994).

The second system is cytoplasmic male sterility in hermaphroditic plants. I will describe the details of this system later. The important feature is conflict between cytoplasmic genes and nuclear genes over the production of pollen. There are different

cytoplasmic genotypes, each of which is “resisted” by specific, matching nuclear genes. The interaction is similar to a system with several matching host (nuclear) and parasite (cytoplasmic) genotypes. Preliminary studies show spatial variation in the frequencies of nuclear and cytoplasmic genotypes. Several authors have analyzed this variation in terms of metapopulation dynamics (e.g., Gouyon and Couvet, 1985; Van Damme, 1986; Frank, 1989; Olivieri et al., 1990).

In the following sections I summarize the natural history and observations for plant-pathogen genetics and cytoplasmic male sterility. I then list other host-parasite interactions of high dimension that are candidates for metapopulation dynamics. These later examples include bacterial defense against viral pathogens and polymorphism of plant-herbivore systems. Finally, I consider how to test different explanations for the observed patterns of variation.

Plant-Pathogen Interactions

Genetic specificity is common in plant-pathogen systems. Each host genotype resists only specific pathogen genotypes; each pathogen genotype attacks only specific host genotypes. In this section I describe the details of genetic specificity, the dimensionality of the interaction, and spatial variation in natural populations.

Flor (1956, 1971) conducted the first detailed study of genetic polymorphisms for resistance in plants and the complementary polymorphisms for host-range in pathogens. The interaction between plant and pathogen genotypes turned out to have simple properties that Flor referred to as a ‘gene-for-gene’ system. In an idealized gene-for-gene system, each pair of resistance and susceptibility alleles in the host has a matching pair of host-range alleles in the pathogen.

Recent biochemical models suggest that resistance occurs only when a pathogen allele produces a particular gene product (elicitor) that can be recognized by a matching host receptor (Gabriel and Rolfe, 1990). If an elicitor-receptor match occurs, then the host induces a defensive response and resists attack. If the same pathogen elicitor is present, but the host produces a non-matching receptor, then disease develops. Infection also occurs when a pathogen lacks an elicitor that matches the specific host receptor.

In multilocus interactions each host polymorphism is matched to a unique, complementary locus in the pathogen. The host resists attack when at least one of the matching pairs of host-pathogen loci leads to recognition and resistance. The pathogen succeeds only when it escapes recognition at all the complementary loci.

The relation between plant and pathogen factors is simple in a gene-for-gene system, but the total interaction is complex because many loci are involved. Flor

and others have identified 29 separate host resistance factors in flax, each with a complementary host-range factor in flax rust (Flor, 1971; Lawrence et al., 1981). Similar gene-for-gene interactions are now known or suspected for over 25 different host-pathogen pairs (Burdon, 1987). These systems do not conform exactly to the idealized gene-for-gene assumptions (Christ et al., 1987), but these systems do have complementary major-gene interactions between hosts and pathogens.

These genetic analyses have been conducted in agricultural systems. They establish the possibility that plant-pathogen interactions in natural populations have genetic specificities of very high dimension. According to the theory described earlier, high dimensionality suggests that observed polymorphisms and the dynamics of disease are strongly influenced by colonization-extinction dynamics in a metapopulation.

That story of dimensionality and metapopulation dynamics is intriguing, but is it true? Data from natural populations are suggestive of metapopulation dynamics, but there is not enough information to draw firm conclusions. I briefly summarize the available data in the remainder of this section.

Dimensionality

The few studies on wild populations suggest widespread genetic polymorphisms for host resistance (Burdon, 1987; Alexander, 1992; Parker, 1992). For example, the matrix in Figure 4 shows the frequencies of different host phenotypes of wild flax when tested against seven races of flax rust. This matrix implies complementary major-gene effects at multiple loci with extensive polymorphism in the host. Similar studies of pathogen isolates in both natural and agricultural systems show that pathogen populations are often highly polymorphic (Wolfe and Caten, 1987; Burdon and Leather, 1990).

The most detailed study of a natural plant-pathogen system in natural populations has been on an annual weed, *Senecio vulgaris* (groundsel), and its fungal pathogen, *Erysiphe fischeri* (Clarke et al., 1990). In a recent study the authors obtained five pathogen isolates from each of two locations. These ten isolates were known to have different genotypes for the ability to attack specific host genotypes. The same two locations were used to obtain 360 host plants (Bevan et al., 1993a).

Progeny from 215 plants were tested against five of the pathogen isolates, and progeny from the other 145 plants were tested against all ten isolates. These two tests yielded large matrices of susceptible or resistant interactions. In both cases 70 percent of the hosts were susceptible to all pathogens tested. The case with five test races of pathogen yielded 12 different resistance phenotypes among the hosts. Each phenotype has a unique resistance/susceptibility classification against the pathogen test races. The case with ten test races yielded 14 different host phenotypes.

Variation in natural isolates of the pathogen was measured in a second study (Bevan et al., 1993b). Twelve isolates were obtained from each of the two locations used for the host study described above. These 24 pathogen isolates were tested against 50 inbred lines of host plants. Pathogen growth on each host was scored on a scale ranging from 0 (complete resistance) to 4 (vigorous fungal growth and sporulation). For the purposes of classifying genotype, each host-pathogen pair was labeled as either 'resistant' or 'susceptible', by splitting the continuous scale of fungal growth.

Table 1 shows that the majority of host and pathogen isolates have unique genotypes. The extensive variability in a limited sample suggests that natural populations are tremendously diverse for this particular plant-pathogen system. Put another way, the community matrix that describes the interactions between plant and pathogen genotypes has very high dimension.

Do other plant-pathogen systems have high dimensionality, or is the groundsel system unusual? The data are too limited to draw firm conclusions. There are several hints that diversity is high, but also some apparent exceptions.

Multilocus genetic diversity for resistance to fungal, viral and bacterial pathogens is typical in agricultural varieties and wild relatives of crops (Burdon, 1987). The pathogens of cultivated plants evolve quickly in response to changing host genotypes, suggesting complementary genetic complexity (Vanderplank, 1984).

Studies of natural plant-pathogen populations have often revealed high diversity. Examples include the groundsel study summarized here and Burdon and Jarosz's (1991) study of wild flax and flax rust (Figure 4). All analyses do not find variability of both host and pathogen in every sample. A study of a perennial herb, *Silene alba* and anther-smut fungus, *Ustilago violacea*, found genetic variability among hosts for resistance to the pathogen (Alexander, 1989). However, no variability of the pathogen was detected when six isolates from a single location were tested against 15 host lines (Alexander et al., 1993).

Colonization-Extinction Dynamics of Alleles

Given high dimensionality it seems inevitable that there will be occasional extinctions of alleles from a local population and subsequent recolonizations by immigration. The problems now concern pattern, process and inference. What are the temporal and spatial patterns of allele frequencies, disease intensity and population sizes? What is the relative influence (scaling) of colonization-extinction processes compared with other ecological and genetic processes? What measurable properties can be used to infer process?

Only a few studies of natural systems have measured spatial variation. I briefly summarize two projects that have focused on genetic variation.

Parker (1985) used field transplant experiments to study variability in the legume *Amphicarpaea bracteata* and its fungal pathogen *Synchytrium decipiens*. I describe the details of his work because transplant experiments are a relatively simple method to measure the scale of spatial variation in host-parasite interactions. The first experiment analyzed three sites: the focal population, 1 km away from the focal population, and 100 km away from the focal population. Seeds were collected from two self-fertilized plants in each of the three populations. For each of the six groups of selfed progeny, 15-20 seedlings were transplanted into the focal population.

All of the seedlings derived from the focal population developed severe infection when transplanted back into their natal location. Progeny from one of the plant lines derived from 1 km away was free of disease when transplanted and grown in the focal population. The other line from 1 km away had 88 percent of the progeny infected, but the average intensity of infection was about one-fifth that of the native plants. Infection intensity was measured as number of sori per plant (a sorus is the initial fungal lesion). All of the progeny derived from 100 km away were completely free of infection when transplanted into the focal population.

This transplant experiment suggests spatial variation in the genotypes of hosts and pathogens over distances of 1 km or greater. Fungal infection was heavy in each of the three locations. When a plant was moved to a new location, it developed little or no infection, suggesting that the pathogen populations differ between the focal site and the other two sites. The variation in infection among the host lines derived from different locations and transplanted into the focal site suggests spatial differentiation among the host populations.

In a second experiment Parker (1985) obtained stronger evidence for spatial variation over 1 km. He tested one pathogen isolate from the focal population against 13 plant families from the focal population and 11 families from 1 km away. All 13 local families developed infection, but 10 of the 11 families from 1 km away were completely resistant to this pathogen isolate.

The final experiment analyzed variation on a smaller spatial scale within the 100 km population. Plant lines were established by collecting along a linear transect from six sites separated by 30 m. The sites were labeled in order from one end of the transect to the other. A pathogen isolate from site 5 was tested against each plant line. I describe the details to show the difficulties that often arise when measuring variability in the interactions between host and parasite. Three different measures of resistance provide information about genetic variation.

First, when resistance or susceptibility was measured as the presence or absence of initial infection, there was no significant variation among sites, with a mean infection frequency of 74 percent. Second, if resistance was measured by percentage of sori that

abort before fungal reproduction, then all plants from site 6 were 100 percent resistant. The other five sites aborted 0–20 percent of sori. Third, the sites varied significantly when the number of sori per plant was used to measure response. For example, site 1 was the least resistant, with a mean \pm s.e. of 11.8 ± 3.2 . Site 6 was the most resistant, with 2.3 ± 0.4 , but neighboring site 5, where the pathogen was derived, was the second highest, with 8.0 ± 2.5 . These results suggest that quantitative components of resistance may be race specific, as in the groundsel study discussed above. In Parker's study, details about race-specific quantitative variation would require tests of the plant lines with different pathogen isolates.

Parker's work shows that genetic variation can occur over short distances. In this case, pathogens are highly successful on plants near the location at which they were found, but had poor success on plants from other locations. It appears that immigrant host genotypes, with resistance to local pathogens, could increase in frequency and change the spatial patterns of differentiation. Experimental movement of genotypes followed by time-series monitoring of consequences may provide a method for inferring the joint roles of selection and colonization-extinction dynamics.

The second major study of spatial variation in natural populations was conducted on flax (*Linum marginale*) and its pathogen, flax rust (*Melampsora lini*) (Jarosz and Burdon, 1991; Burdon and Jarosz, 1992). A summary of spatial variation in genotype is shown in Figure 5. To study the role of metapopulation dynamics, the authors measured the composition of nine pathogen populations over two to four consecutive years. This is the most extensive study of temporal and spatial variation in natural populations, but limitations of the data must be considered before drawing any conclusions. First, the host plant is perennial, so the time span of the study does not cover genetic changes in the host populations. Second, it is not clear how far the wind-borne spores can move each year, in other words, the scaling of spatial distance relative to migration distance is not known. In spite of these constraints, a few tentative conclusions are interesting.

(i) Four pathogen races dominated the metapopulation over all four years of the study. (ii) The majority of host populations contained little or no resistance to any of the four dominant pathogen races. Thus host resistance alone cannot explain temporal and spatial variation in the pathogen. (iii) Pathogen races occasionally became locally extinct in a particular population but were often reintroduced within a year or two. (iv) Fluctuations in the genetic composition of local pathogen populations may be strongly influenced by the dynamics of population size. Twenty-two host populations were sampled for the presence or absence of infection in two consecutive years. One population had no pathogen infections in the first year but was infected in the next

year. Another population had infections in the first year but was free of disease in the next year. Finally, two populations were free of infection in both years.

Burdon and Jarosz (1992) suggest that, over the temporal and spatial scale of their study, the observed fluctuations in the pathogen's genetic structure were driven by colonization-extinction events and drift. Thus the populations in that region may act as a cohesive unit linked by frequent migration, with selection playing a limited role in the dynamics of allele frequency. Put another way, the time scale of pathogen movement among these populations may be on the order of host generation time, and thus too short for colonization-extinction dynamics of alleles among these populations to exert strong coevolutionary pressures. Perhaps at a larger spatial scale the migration rate is small relative to the length of host generations—the time scale over which selection is effective. At that scaling between migration and selection, the colonization-extinction dynamics of alleles may cause occasional major shifts in genotypic composition.

To summarize these two studies on plant-pathogen systems, it is easy to imagine how metapopulation dynamics can influence genetics, but very difficult to measure space-time variation over the proper scales. How can convincing data be obtained? One way is to observe colonizations of locally absent alleles and the subsequent local dynamics. It may be difficult to observe such rare events, but there is one suggestive study of cytoplasmic male sterility that I describe in the next section.

Cytoplasmic Male Sterility

Most organisms inherit mitochondrial DNA from their mother, with no input from their father. By contrast, most other genetic material is obtained equally from the mother and father. Typically these different modes of transmission, matrilineal versus biparental, have no consequences for the direction of evolutionary change favored by selection. For example, efficient respiration increases both matrilineal and biparental transmission.

The allocation of resources to sons and daughters affects matrilineal and biparental transmission differently. Traits that enhance the production of daughters at the expense of sons always increase the transmission of matrilineally inherited genes. For example, in some hermaphroditic plants the mitochondrial genes may inhibit pollen development and simultaneously enhance the production of seeds (Edwardson, 1970; Hanson, 1991). Selection of genetic variants in the mitochondria would favor complete loss of pollen production in exchange for a small increase in seed production because the mitochondrial genes are transmitted only through seeds (Lewis, 1941).

Reallocation of resources from pollen to seeds can greatly reduce the transmission of nuclear genes because biparental transmission depends on the sum of the success

through seeds and pollen. Thus there is a conflict of interest between the mitochondrial (cytoplasmic) and nuclear genes over the allocation of resources to male (pollen) and female (ovule) reproduction (Gouyon and Couvet, 1985; Frank, 1989). Consistent with this idea of conflict, nuclear genes often restore male fertility by overcoming the male-sterility effects of the cytoplasm.

The nuclear-cytoplasmic conflict is very similar to a host-parasite system: there is antagonism over resources for reproduction, cytoplasmic (parasite) genes determine the host-range for exploitation, and cytoplasmic genes interact with nuclear (host) resistance genes to determine the specificity of the interaction. Cytoplasmic inheritance influences the patterns of “parasite” transmission but, on the whole, the genetics and population dynamics are typical of host-parasite interactions (Gouyon and Couvet, 1985; Frank, 1989; Gouyon et al., 1991).

The reduction of pollen caused by cytoplasmic genes is called Cytoplasmic Male Sterility (CMS). Laser and Lersten (1972) list reports of CMS in 140 species from 47 genera across 20 families. More than one-half of these cases occurred naturally, about 20 percent were uncovered by intraspecific crosses, and the rest were observed in interspecific crosses. Moreover, this listing is an underestimate of the true extent of CMS because detecting a cytoplasmic component to a male sterile phenotype requires genetic analysis of polymorphism (Frank, 1994).

Wild populations of CMS maintain several distinct cytoplasmic genotypes (cytotypes). Each cytotype is capable of causing male sterility by an apparently different mechanism because each is susceptible to a particular subset of nuclear restorer alleles. Nuclear restorer alleles are typically polymorphic at several loci, with each allele specialized for restoring pollen fertility when associated with particular cytotypes. The observations are summarized in Frank (1989), Couvet et al. (1990), and Koelewijn and Van Damme (1995a,b).

CMS has reciprocal genetic specificity of nucleus and cytoplasm and widespread polymorphism. The basic questions of dimensionality and colonization-extinction dynamics are similar to other host-parasite systems. What are the temporal and spatial patterns of female and hermaphrodite (phenotype) frequencies, allele frequencies, and population sizes? What is the relative influence of colonization-extinction processes compared with other ecological and genetic processes? What measurable properties can be used to infer process? As before, the data are not sufficient to answer all these questions, but the literature provides intriguing hints about dimensionality and colonization-extinction dynamics.

Dimensionality and Spatial Variation

Two or more different cytoplasmic genotypes may cause CMS within a particular species. The cytoplasmic types are recognized as distinct because they react differently to particular nuclear restorer genotypes. The dimensionality of the system increases with the number of different cytoplasmic types that cause male sterility, each with its own associated set of specific nuclear restorer loci.

Table 2 summarizes data on the dimensionality of agricultural and wild species. The 'cross type' describes whether variability was discovered with intraspecific crosses or with hybridizations between species. Molecular evidence matches different mitochondrial markers to genetic and phenotypic properties observed in crosses. The 'nuclear genes' column lists the total number of loci involved in male sterility. Although the existence of nuclear-cytoplasmic specificity is clear, the details are very difficult to work out. The numbers must be considered minimum estimates because a cytoplasmic polymorphism can only be detected when present in a study that also has matching nuclear polymorphism for restoration. Similarly, nuclear polymorphism requires matching cytoplasmic polymorphism. Each study requires tedious crosses and nurturing of many progeny to draw unambiguous conclusions. As mentioned above, CMS is widespread. The table shows only those studies in which attempts have been made to analyze the number of genotypes.

The data in Table 3 show that the frequency of females varies widely among populations of the same species. The column for 'genetics' describes how information was obtained on the spatial variation of cytoplasmic and nuclear genes. Evidence is 'direct' for *Plantago lanceolata* because the two cytoplasmic genotypes are associated with different morphological abnormalities of failed pollen production and anther development. In addition, crosses were performed to measure the frequency of the cytoplasmic types and associated restorer alleles. Spatial variation in *P. lanceolata* will be discussed below. For *Beta maritima*, crosses were performed to infer the frequency of cytoplasmic types and restorer alleles for each population. It appeared that cytoplasmic frequencies did not vary between the two populations. The large difference in female frequency was the result of variation in the frequency of restorers between the two locations.

Spatial variation was inferred from crosses between different populations in *Thymus vulgaris* and *P. coronopus*. These long-distance crosses yielded higher frequencies of females than were observed within each population. High frequencies of females in the crosses imply that, within each population, restorers are common for the locally common cytoplasm but relatively rare for other cytoplasmic types. If different populations are dominated by different cytoplasmic types, then the crosses will expose

cytoplasmic genotypes from the female parent to nuclear backgrounds of the male parent that have a low frequency of matching restorers.

For the *Plantago* species, the 'IN' rows show the frequency of partially male-sterile (IN) plants. Partial male sterility also depends on an interaction of cytoplasmic and nuclear genes. As noted by Koelewijn (1993), partial male sterility is a common phenomenon in CMS, but phenotypes are often reported with dichotomous classification. This is similar to the partial resistance that is common in plant-pathogen interactions, as noted in the previous section. In both CMS and plant-pathogen interactions, the intermediate phenotypes often depend on specific interactions between genetic polymorphisms of the host and parasite.

Colonization-Extinction Dynamics

The frequency of females in a population is the frequency of unrestored male-sterile cytoplasm. The data suggest that the frequency of females varies among populations. Phenotypic variation appears to be associated with widespread genotypic variation in cytoplasmic types and restorer frequencies.

Two related metapopulation scenarios have been proposed to explain phenotypic and genetic variation. The first theory concerns the colonization-extinction dynamics of alleles among existing populations (Gouyon and Couvet, 1985; Frank, 1989). The second theory focuses on the colonization-extinction dynamics of populations (Gouyon and Couvet, 1985). I will briefly outline the allelic theory, along with a field study that hints at how natural populations may be influenced by these processes. At the end of this section I mention the population colonization-extinction theory.

To understand the colonization-extinction dynamics of alleles one must imagine a sequence of events.

(i) Initially, one of the cytoplasmic type is lost from a local population. Loss may occur by drift or because the alternative types have higher fitness. Increasing dimensionality (more types) raises the probability that one or more cytoplasm will be absent locally.

(ii) When a cytoplasmic type is absent, the associated nuclear restorer alleles do not have any beneficial effects. These specific restorer alleles may be lost from the local population by a variety of processes. If there are no fitness differences between restorer and alternative non-restorer alleles, then the restorers may be lost by drift. If the restorers, which must in some way influence pollen development, reduce efficiency when their matching cytoplasm is absent, then the specific restorers will be lost by selection.

(iii) After steps (i) and (ii), a cytoplasmic genotype and its specific restorers are absent locally. If an unrestored cytoplasm arrives by immigration, it will have a fitness

advantage and spread quickly in the population. The fitness advantage occurs because an unrestored cytoplasm causes a male-sterile phenotype. Male-sterile plants typically produce more seeds than hermaphrodites (Lloyd, 1976; Van Damme, 1984; Van Damme and Van Delden, 1984). Because cytoplasmic fitness depends only on success through the maternal line (seeds) and not on pollen success, the male-sterile plants have greater cytoplasmic fitness than hermaphrodite plants. Thus the cytoplasmic genotypes that cause male sterility spread in the local population, causing an increase in the frequency of females.

(iv) Cytoplasmic genotypes are essentially alternative alleles at a haploid locus. When one genotype increases in frequency, then the other genotypes necessarily decline in frequency. In the case of mitochondria, an increase in the frequency of one mitochondrial type will cause a decline in other mitochondrial types. Thus the selective spread of an unrestored cytoplasm may cause the local extinction of alternative cytoplasmic genotypes. Loss of cytoplasmic genotypes may be associated with loss of matching restorers, as in step (ii).

(v) The population now has a high frequency of females and a dominant cytoplasmic genotype. The restorers matching the dominant cytoplasm are locally extinct. If a matching restorer arrives by immigration, it will combine with the dominant cytoplasmic type to produce hermaphrodites. The restorer allele spreads rapidly because pollen is rare locally, thus the few hermaphrodites are the source of paternal alleles for all members of the population. As the restorer spreads, the frequency of females declines. The frequency of cytoplasmic genotypes may be unaffected by the initial spread of restorers.

(vi) A locally absent cytoplasmic genotype can invade and spread if its specific restorers are absent. The cycle then repeats, with a genotypic turnover in the local population. The greater the dimensionality—the number of cytoplasmic genotypes and matching specific restorers—the more likely an immigrant cytoplasmic type will be locally absent and can start a new round of genotypic turnover.

Van Damme's study of *Plantago lanceolata* provides just enough detail to show how parts of the above scenario may work in a natural population. Van Damme and Van Delden (1982) distinguished two cytoplasmic genotypes in *P. lanceolata* each with its own set of nuclear restorers. Table 4 shows phenotypic frequencies in 12 populations in two habitat groups; the original paper lists data for 27 populations in five categories. The labels for each population are abbreviations for locations.

The cytoplasmic genotype *R* causes the male-sterile phenotype MS1 when unrestored and IN1 when partially restored. The cytoplasm *P* causes MS2 when unrestored and IN2 when partially restored. All four types are morphologically distinct and can be scored by direct examination. Restored cytoplasmic genotypes of either type are

hermaphroditic, *H*. The cytoplasmic type of a hermaphrodite can be determined only by crossing until the cytoplasm is exposed in an unrestored nuclear background.

The two population groups shown in Table 4 are the most differentiated of the five groups listed in the original paper. Five of the hayfield populations either lacked the *R* cytoplasm or were fixed for the *R* restorers. In the pasture populations, either the *P* cytoplasm was very rare or the *P*-specific restorers were common. The other three population groups were relatively more mixed for MS1 and MS2 phenotypes.

Van Damme (1986) made an intensive study of spatial variation within the Westduinen (*Wd*) population listed in Table 4. A picture of the field at Westduinen is shown in Figure 6, with some of the data listed in Table 5. Females were rare over the whole population, with MS1 more common than MS2. However, in a few locations the frequency of MS1 was high (Figure 6). Within the larger clusters of MS1, *p1-p4*, the frequency of MS1 phenotypes was close to zero at the borders and rose to 60 percent near the center.

The field as a whole was dominated by the *P* (MS2) cytoplasm, with an overall frequency of 0.94. The frequencies of the *P*-specific restorer alleles were also high. Thus most plants were hermaphrodites with a *P* cytoplasm and *P* restorers. The overall frequency of the *R* cytoplasm was 0.06, and the *R*-specific restorers at the two restorer loci had frequencies of 0.02 and 0.08.

Genotypic composition was very different in those few areas that had high frequencies of the MS1 phenotype (Figure 6 and Table 5). The *R* (MS1) cytoplasm, rare in the population as a whole, had frequencies ranging between 26 and 39 percent in populations *p1-p4*. The *R*-specific restorers, also rare in the whole field, were more frequent in the MS1 clusters, although the exact frequencies were difficult to estimate.

Van Damme's interpretation agrees with the scenario outlined above. Initially most of the field was dominated by *P* cytoplasm and *P*-specific restorers. *R*-bearing colonists founded the MS1 spots and, since the *R*-specific restorers were initially rare, the MS1 females spread from a central focus. MS1 plants produce more seeds that are larger and survive better than seeds from hermaphrodites (Van Damme and Van Delden, 1984), so the females have a competitive advantage locally. Seeds disperse at a slow rate (8cm/year; Bos et al., 1986), thus well-defined patches can form. As the frequency of unrestored *R* cytoplasm rises in an area, selection favors an increase in *R*-specific restorers. In an area with a high concentration of *R* cytoplasm, the main pollen donors will be *R*-restored hermaphrodites.

The low frequency of the *R*-specific restorers in the overall population suggests that these alleles are at a selective disadvantage when the *R* cytoplasm is absent. If so, then a population dominated by the *P* cytoplasm is likely to lack the *R* restorers, as at

Westduinen. That genotypic composition is susceptible to invasion by *R* cytoplasm, followed by a subsequent change in genotypic composition.

Many details about *P. lanceolata* require further study. But this first glimpse does suggest that colonization-extinction dynamics and the strong selective pressures on cytoplasm and nucleus may be responsible for the observed spatial variability.

The *P. lanceolata* example emphasizes the colonization and spread of a locally novel genotype into an existing population. Cytoplasm may also “escape” their restorers when a empty patch is founded by one or a few colonists (Gouyon and Couvet, 1985). Species that are subject to local population extinctions and colonizations of empty habitat patches may be particularly variable in the frequency of females and the spatial variation in genotypes. Studies of *Thymus vulgaris* in southern France suggest that disturbed populations and recently colonized patches are likely to have higher frequencies of females than undisturbed, older populations (Gouyon and Couvet, 1985; Belhassen et al., 1989; Olivieri and Gouyon, this volume). However, it is difficult to obtain convincing data on processes that cover large temporal and geographic scales.

All studies do not find evidence of a dynamic process. Koelewijn (1993) summarized his work on *Plantago coronopus* by noting that the frequency of phenotypes in each of four locations was “remarkably constant” over ten years. The evidence also suggested that both cytoplasmic male-sterile genotypes occurred at intermediate frequency in all four locations. Koelewijn’s (1993) comments serve as a reminder that we have only the haziest picture of a few cases, with no empirical guidelines about appropriate temporal and spatial scales at which nonequilibrium fluctuations may be important.

Other Systems of High Dimension

I have discussed dimensionality and spatial variation for plant diseases and cytoplasmic male sterility. Are these systems unusual, or are other host-parasite interactions similarly diverse?

There are very few systems with good data available on both the host and parasite. I briefly describe a few cases to illustrate the kind of information that has been collected. My interpretation is that high dimensionality occurs often, although there will certainly be many exceptions.

Bacteria have a simple recognition-based immunity system that protects them from invasion by foreign DNA (Wilson and Murray, 1991). There are two components to the system. Restriction enzymes cut DNA molecules that carry a particular sequence of nucleotides. Modification enzymes recognize the same nucleotide sequence but, instead of cutting the DNA, these enzymes modify the recognition site in a way

that protects that molecule from restriction. A bacterial cell's own DNA is modified, otherwise the restriction enzymes would cut the DNA and kill the cell.

Restriction-modification (RM) enzymes are known for over 200 different recognition sites (Kessler and Manta, 1990; Roberts, 1990). Circumstantial evidence suggests that defense against bacteriophage viruses has been a powerful force promoting diversity. (1) RM can protect host cells from invading phage (Luria and Human, 1952; Arber, 1965). (2) Phage that develop in bacteria with a particular RM type are modified for the associated recognition sequence. These modified phage can attack other bacteria of the same RM type, but are sensitive to restriction by different RM systems. Rare RM types are favored because few phage will be modified for their recognition sequence. This frequency dependent selection promotes diversity of RM as a defense against phage (Levin, 1986, 1988). (3) Phage carry a variety of antirestriction mechanisms (Kruger and Bickle, 1983; Sharp, 1986; Korona et al., 1993). For example, many phage lack particular RM recognition sequences. The probability of having these recognition sequences is very high if no selective pressure were acting on sequence composition.

These details suggest that the interaction between RM and phage is of high dimension. Not enough sampling has been done to draw any conclusions about spatial variation, but it seems likely that the genotypic composition of communities varies widely among different locations.

A second bacterial system acts in a very different way from RM but is also highly diverse. This allelopathic system affects competition between bacterial strains rather than what is usually thought of as a host-parasite interaction. However, the genetic specificity of attack and defense promotes widespread polymorphism in much the same way as in host-parasite dynamics.

In this system of bacterial allelopathy, cells often carry plasmids that encode a bacterial toxin (bacteriocin) and immunity to that toxin (Reeves, 1972; Lewin, 1977; Hardy, 1975). Immunity works by neutralizing the toxin after it has entered the cell. Bacteria may also be resistant to bacteriocins because they lack a compatible receptor through which the toxin can enter the cell.

Many distinct bacteriocin types are found within a population. A type is defined by its susceptibility to a set of toxin-producing test strains. With n test strains, there are 2^n possible types. Epidemiological studies frequently use bacteriocin typing to identify and follow pathogenic strains of bacteria. These studies provide information about the diversity of bacteriocin production and susceptibility in populations. For example, Chhibber et al. (1988) summarize data on the number of isolates, test strains, and bacteriocin susceptibilities for ten studies of *Klebsiella pneumoniae*. The fewest number of observed types occurred in a study with 200 isolates, four test strains, and

11 types of a possible $2^4 = 16$; the most occurred in a study with 553 isolates, seven test strains, and 64 types of a possible $2^7 = 128$. Similar levels of diversity have been reported for a variety of species (Gaston et al., 1989; Senior and Vörös, 1989; Rocha and Uzeda, 1990; Traub, 1991; Riley and Gordon, 1992).

The next example is disease resistance in vertebrates. There is great diversity at the loci that encode specific recognition of parasites, the Major Histocompatibility Complex (MHC) genes. However, this host diversity has rarely been matched to specific polymorphisms of parasites.

The molecules that bind intracellular protein fragments and bring them to the surface are coded by genes that reside within the MHC region. Each antigen-presenting molecule from the MHC has a groove that accommodates nine amino acids. Each particular MHC molecule can recognize and present on the cell surface only a subset of protein fragments. An individual has several different MHC types that, taken together, determine the set of protein fragments that can be recognized and carried to the cell surface for presentation.

The MHC loci are highly polymorphic, with between 10 and 80 different alleles known for each locus. Two lines of evidence suggest that resistance to particular diseases can strongly affect the frequency of MHC alleles. First, most of the variation among alleles occurs in the groove that binds protein fragments—the specific recognition area. Second, a few cases are known in which there is a strong spatial correlation between endemic diseases and MHC alleles that are associated with resistance to those diseases. For example, the allele HLA-B53 is associated with resistance to a severe strain of malaria that occurs in children in The Gambia. HLA-B53 occurs at a frequency of 25% in this west African nation; by contrast, the frequency of this allele in Europe is 1% (McMichael, 1993). Other MHC alleles are implicated in resistance to HIV, the cause of AIDS, and to Epstein-Barr virus, the cause of various cancers. Disease correlations with MHC alleles suggest that selective pressures influence the evolution of the immune system polymorphisms (Thomson, 1991; Mitchison, 1993).

The final example concerns genetic variation in plant resistance to herbivores. The resistance may be biochemical or structural. Karban (1992) lists 37 studies that show evidence of genetic variability in resistance to herbivore attack. These studies usually demonstrate genetic variability by growing different plant genotypes in a common environment and measuring variation in herbivore damage. The details of variable resistance and the number of independent traits involved (dimensionality) are typically unknown.

Insect herbivores are often genetically variable in their ability to attack different plant varieties (Gould, 1983). Edmunds and Alstad (1978) suggested that insect species

often differentiate into populations that are locally adapted for the host genotypes in their area. Karban (1992) summarizes studies that examine geographic specialization of insect herbivores. He concludes that the data are not convincing because of limited sampling, but the hypothesis that herbivores are geographically specialized remains an important idea that deserves further study.

Theories and Tests

The evidence summarized in the previous sections suggests that host-parasite interactions can be very diverse. The few careful studies of natural populations indicate a spatial component of diversity when the system is viewed on the appropriate spatial scale. In this final section I review the processes that can explain spatial variation in host-parasite allele frequencies. I then summarize the plant-pathogen and cytoplasmic male sterility studies in light of the alternative explanations for spatial variation.

Five factors may influence spatial variation in host-parasite genetics.

(i) Migration-drift dynamics occur when selection is a relatively weak force and allele frequencies fluctuate stochastically. Locally extinct alleles can return to a population by immigration if populations are connected in a metapopulation. Drift is relatively more important than selection in causing fluctuations when local populations are small or have frequent bottlenecks. Migration can overcome selection when the movement of alleles occurs more quickly than selection can change local allele frequencies.

(ii) Local, nonlinear dynamics cause spatial variation when populations fluctuate in an uncoupled manner. Selection causes changes in allele frequencies, and migration does not cause major perturbations of local dynamics. Migration must be sufficiently rare to prevent synchronization of population fluctuations.

(iii) Environmental heterogeneity can favor different allelic combinations in particular locations. This will be particularly important in inbreeding or asexual species, where chance linkage will occur between alleles involved in host-parasite interactions and alleles affecting success in different habitats.

(iv) The sexual system will, in general, determine the role of linkage in changing allele frequencies. With low recombination, selection at one host-parasite locus can change allele frequencies at many other loci.

(v) Local extinctions caused by selection coupled with global migration lead to colonization-selection-extinction dynamics. These are the processes that I emphasized in my descriptions of plant-pathogen and CMS systems. In this case immigration of locally extinct alleles will sometimes cause a major perturbation of local dynamics. Spatial variation may be dominated by the timing of local extinctions of alleles and

the waiting time until those alleles are reintroduced by immigration. The complicated details of nonlinear dynamics (limit cycles, chaos, etc.) may be relatively unimportant in systems of high dimension because the timing of extinctions and colonizations determines local and regional variation.

These five processes can all occur in a single system when measured over different spatial and temporal scales. For example, in Burdon and Jarosz's (1992) study of a plant-pathogen system, the evidence suggested that migration-drift dynamics dominated the spatial distribution of pathogen genotypes over approximately 75km. Local pathogen populations apparently experience frequent bottlenecks, with immigration or recolonization from neighboring populations. The movement of pathogen alleles occurs on a time scale that is shorter than host generation time, suggesting that migration is more powerful than coevolutionary selection pressures in determining the spatial dynamics of pathogen allele frequencies.

The rate of pathogen migration will be low at some sufficiently long spatial scale. The colonization of a region by a long-distance migrant allele could cause a major local perturbation. For example, once in a hundred years a locally novel resistance allele may land in a region, changing the selective pressures on the pathogens and favoring the immigration of new host-range alleles. These perturbations may be rare compared to the usual scale of study, but could be a major cause of regional variation. Other systems, such as CMS in *P. lanceolata*, may have relatively low rates of migration over short distances. Thus colonization-selection-extinction dynamics may occur over smaller scales that are easier to study (Van Damme, 1986).

Problems of inference can be severe. On the measurement side, polymorphism in coevolutionary systems can be difficult to detect (Frank, 1994). For example, two different male sterile cytoplasms both yield the same hermaphroditic phenotype when the study sample contains matching nuclear loci that are fixed for restorer alleles. Thus the potential diversity (dimensionality) of systems is difficult to measure. On the statistical side, very different processes may yield the same patterns of host-parasite polymorphism when the observer uses a particular sampling scheme. For example, drift models and strong selective, coevolutionary models often have similar patterns when sampled without long time-series data (Frank, 1995). The only remedy is thorough understanding of both the patterns expected under alternative processes *and* the consequences of different sampling schemes and methods of data analysis.

Two standards of empirical progress will help. First, manipulation experiments in the field are an easy way to discover spatial variation. Parker's (1985) study of a plant-pathogen system is an excellent example of how transplant experiments can be used to document the extent and scale of genetic variability. Van Damme (1986) did not manipulate his populations of cytoplasmically male sterile plants. But it is easy to

imagine an experiment in which locally absent cytoplasmic or restorer alleles are introduced into fields in which those alleles are extinct. Then, over several years, the natural spread of the alleles could be monitored.

The second avenue of progress will come from molecular methods of sampling. At present, host and parasite genotypes are identified by laborious methods of genetic crossing experiments and phenotypic testing. The time required severely restricts the scope of data collection. Molecular probes will eventually allow widespread sampling of host and parasite genotypes over different spatial and temporal scales. The preliminary work on plant diseases and male sterility suggests that host-parasite systems will be highly variable and strongly influenced by metapopulation dynamics.

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Table 1: Numbers of resistance and host-range phenotypes inferred from a test matrix of 25 pathogen isolates by 50 inbred host lines. Each row shows results when a particular infection intensity is used to define the binomial split between resistance and susceptibility. For example, if category 2 is used for the split, then categories 0-2 are defined as resistant, and categories 3-4 are defined as susceptible (from Bevan et al. 1993b).

Infection type category used to define resistance/host-range	Number of different groundsel resistance phenotypes discriminated	Number of different fungus host-range phenotypes discriminated	Minimum number of hypothetical resistance/host-range gene pairs required to explain the observed variation ^a
0	12	12	10
1	21	18	14
2	34	23	23
3	43	24	24

a. The calculation assumes that resistance occurs when the host has a resistance allele that matches a particular host-range allele at a complementary locus in the pathogen. One match at any of the complementary host-pathogen loci is sufficient to cause resistance. See Bevan et al. (1993b).

Table 2. Summary of available evidence on number of cytoplasmic genotypes and nuclear loci that have been detected in various agricultural and wild species. Copied from Koelewijn and van Damme (1995a).

Species	Cross Type	Molecular Evidence	Cytoplasmic Genotypes	Nuclear Genes
<i>Agricultural Species^a</i>				
<i>Beta vulgaris</i>	within	+	2	2–7
<i>Daucus carota</i>	within	+	2	3
<i>Helianthus spp.</i>	between	–	many	?
<i>Nicotiana spp.</i>	between	+	8	?
<i>Oryza spp.</i>	between	+	2	3
<i>Solanum spp.</i>	both	+	4	many
<i>Triticum spp.</i>	between	+	2	2
<i>Zea mays</i>	both	+	3–4	5
<i>Wild Species</i>				
<i>Beta maritima^b</i>	–	+	2	?
<i>Origanum vulgare^c</i>	within	–	2	2–7
<i>Nemophila menziesii^d</i>	within	–	2	2
<i>Thymus vulgaris^e</i>	within	+	2–many	?
<i>Plantago lanceolata^f</i>	within	+	2	3–5
<i>Plantago coronopus^g</i>	within	–	2	3–5

a. Compiled from Hanson and Conde (1985), Kaul (1988).

b. Boutin et al. (1987)

c. Kheyr-Pour (1980, 1981).

d. Ganders (1978).

e. Belhassen et al. (1991).

f. Van Damme and Van Delden (1982), Van Damme (1983).

g. Koelewijn and van Damme (1995a,b).

Table 3. Spatial variation in wild populations with cytoplasmic male sterility. The second and third columns show the range and median in percentage of females per population for samples from N populations.

Species	Range	Median	N	Study	Genetics
<i>Origanum vulgare</i>	1–62	?	100	Kheyr–Pour 1980	
<i>Thymus vulgaris</i>	5–95	>50	110	Gouyon & Couvet 1985	Inferred
<i>Plantago lanceolata</i>	1–23	8	27	van Damme & van Delden 1982	Direct
<i>with IN</i>	1–34	15	27		
<i>Plantago coronopus</i>	0–35	13	8	Koelewijn 1993	Inferred
<i>with IN</i>	13–61	31	8		
<i>Beta maritima</i>	19–62		2	Boutin–Stadler et al. 1989	Direct

Table 4. Phenotype percentages in natural populations of *Plantago lanceolata*. From Van Damme and Van Delden (1982).

Population	MS1	IN1	MS2	IN2	H	Sample size
<i>Hayfield</i>						
Dr	0	0	0.2	0.2	99.6	811
Ze	0	0	5.0	0.8	94.1	742
An	0	0	8.2	1.3	90.5	754
Re	0	0	5.0	3.6	91.4	695
Me1	0	0	3.9	5.5	90.6	688
Ve	12.2	2.2	0	0.6	85.0	623
Br	23.0	7.0	0.3	0.2	69.5	601
<i>Pasture</i>						
Wd	4.6	0.6	0.5	0.9	93.4	6902
Bm2	7.3	3.9	0	1.3	87.5	386
Pa	7.6	7.8	0.5	0.9	83.2	437
Ac2	11.8	10.8	0	1.0	76.4	305
Ju	21.5	7.0	0	0.5	71.0	414

Table 5. Percentage of phenotypes of *Plantago lanceolata* at a Westduinen field. MS3 is a rare phenotype controlled by variation at autosomal loci. The locations of populations p1-p4 are shown in Figure 6. Data from Van Damme (1986).

Description	MS1	IN1	MS2	IN2	MS3	H	Sample size
Total field	4.6	0.6	0.5	0.9	0.5	92.9	6902
p1	28.6	5.4	0	0	0	66.1	112
p2	25.6	1.6	0	0	0	72.8	188
p3	21.3	3.0	0.3	1.2	0	74.3	695
p4	22.7	1.6	0	4.7	0	71.1	688
remainder	1.9	0.4	0.6	0.9	0.5	95.7	6140

Figure Legends

Figure 1. Dynamics for the matching-allele model with two hosts and two parasites. (a, b) Limit cycles in which abundances fluctuate in a periodic and stable way. (c) Spiral from an initial condition out to a limit cycle, where parasite abundances repeatedly drop very close to zero. In this case the parasite is likely to become locally extinct, leading to colonization-extinction dynamics. The panels show the changes in abundance for one of the two host-parasite pairs in equation (3), with $b = 1.2$, $s = 0.4$, and $\tau = 0.125, 0.375, 0.625$ for the three panels, with increasing τ moving from left to right.

Figure 2. Time series for the matching-allele model with two hosts and two parasites, from equation (3) with $n = 2$, $b = 2.4$, $s = 0.4$, and $\tau = 0.25$. The dynamics are shown over a time period of 500 steps of length τ . Extinction is simulated by setting to zero any abundance less than 0.01. Colonization is simulated by adding 0.01 to the abundance of each host and parasite in each time step τ if a random number between zero and one is less than 0.01. Thus the average time between colonization events for each type is 100τ .

Figure 3. Time series for the matching-allele model with four hosts and four parasites. The parameters and methods are the same as in Figure 2 except that $n = 4$.

Figure 4. Qualitative resistance in a wild population of flax. The matrix shows the frequency distribution of resistant patterns from 67 different host plants collected from a single population when tested against seven pathogen races of flax rust (races A and H are grouped together). Redrawn from Burdon and Jarosz (1991).

Figure 5. Spatial variation in pathogen genotypes and host resistance among wild populations of flax (*Linum marginale*) and flax rust (*Melampsora lini*). Both host and pathogen isolates were obtained from several different sites. Each panel shows the racial composition of the pathogen population and the frequency of host resistance to each pathogen race when summarized over a different geographic scale. (a) Data from a one-hectare plot for 67 host lines and 94 pathogen isolates. (b) Combined data for 40 host lines and 37 pathogen isolates from two populations 300m and 2.7km away from the plot summarized in the first panel. (c) Combined data for 108 host lines and 80 pathogen isolates from six populations 13.8–75km away from the plot summarized in the first panel. Redrawn from Jarosz and Burdon (1991).

Figure 6. Distribution in a pasture of areas with MS1 and IN1 plants of *P. lanceolata*. Single plants are represented by dots and groups of plants by circles. The number within each circle is the area in square meters covered by the local group of plants.

The four largest groups are labeled $p1-p4$. The shaded areas are pools that cattle use for water. Redrawn from Van Damme (1986).

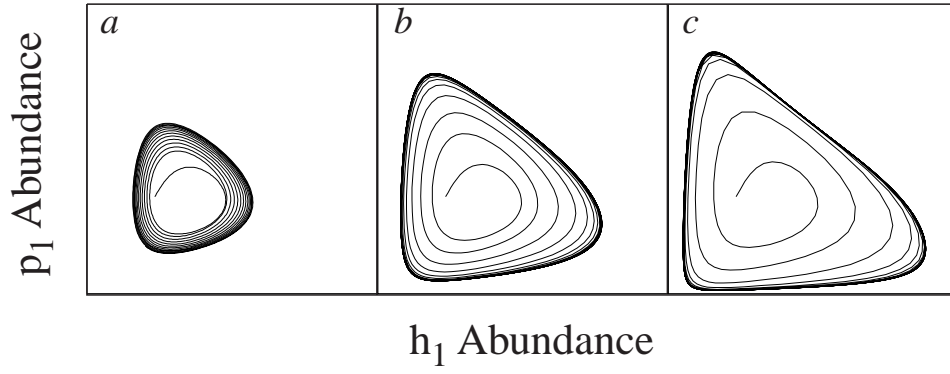


Figure 1

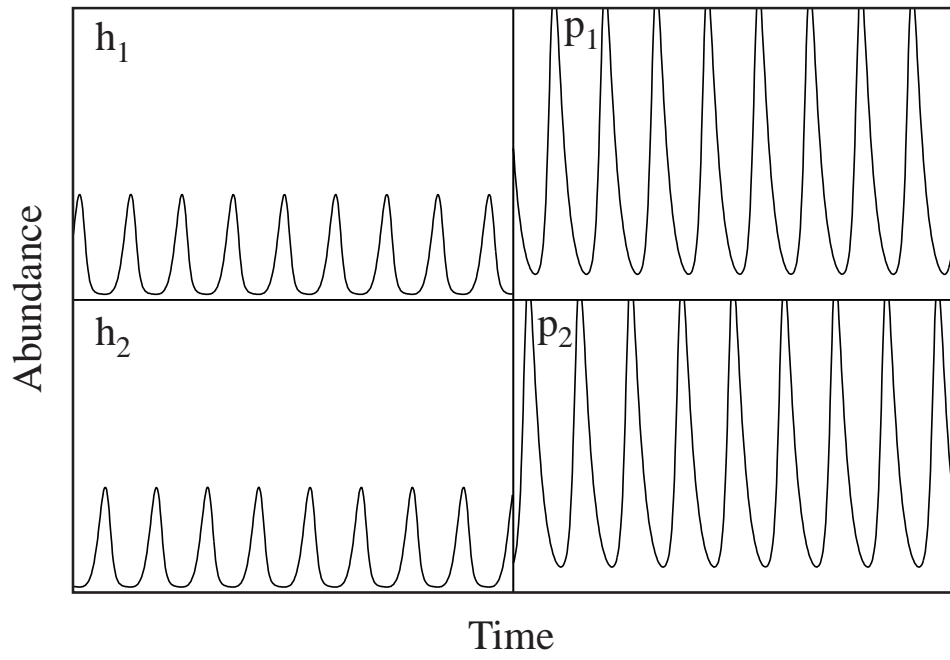


Figure 2

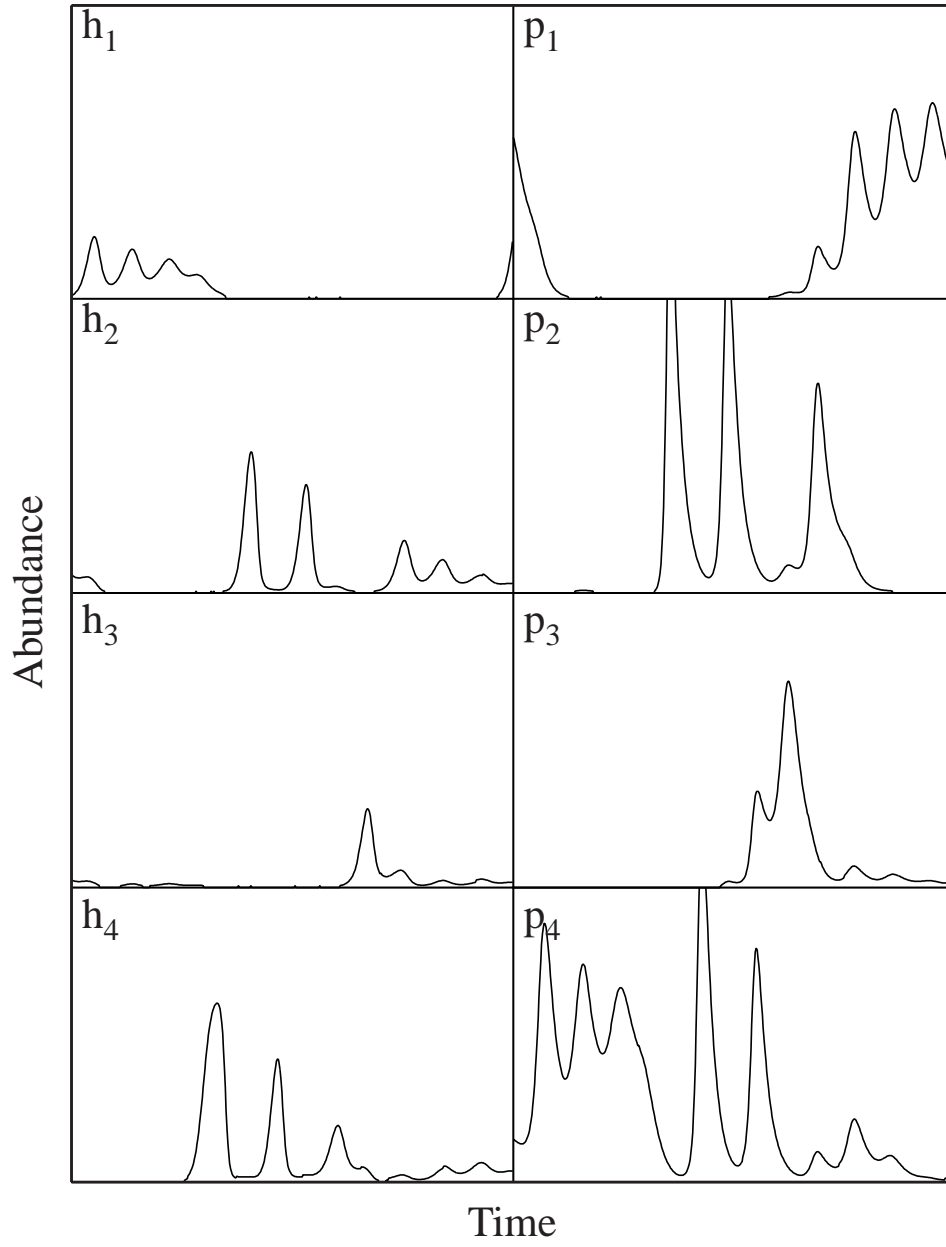


Figure 3

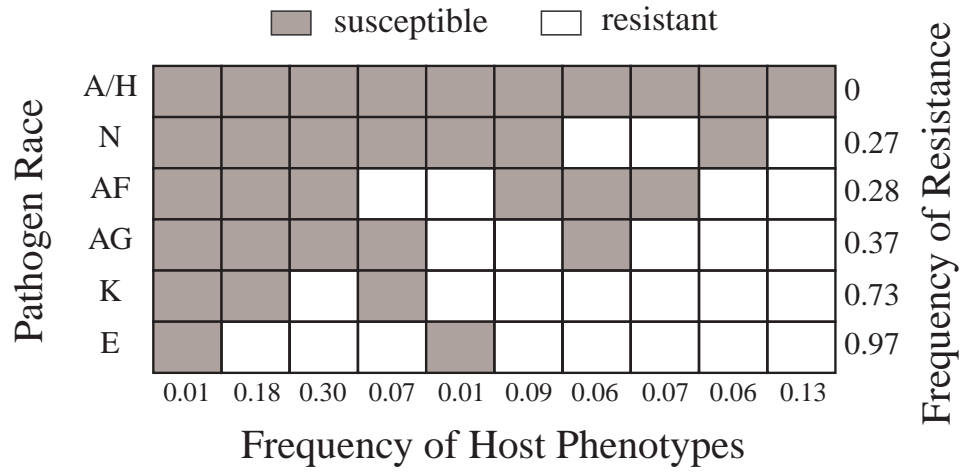


Figure 4

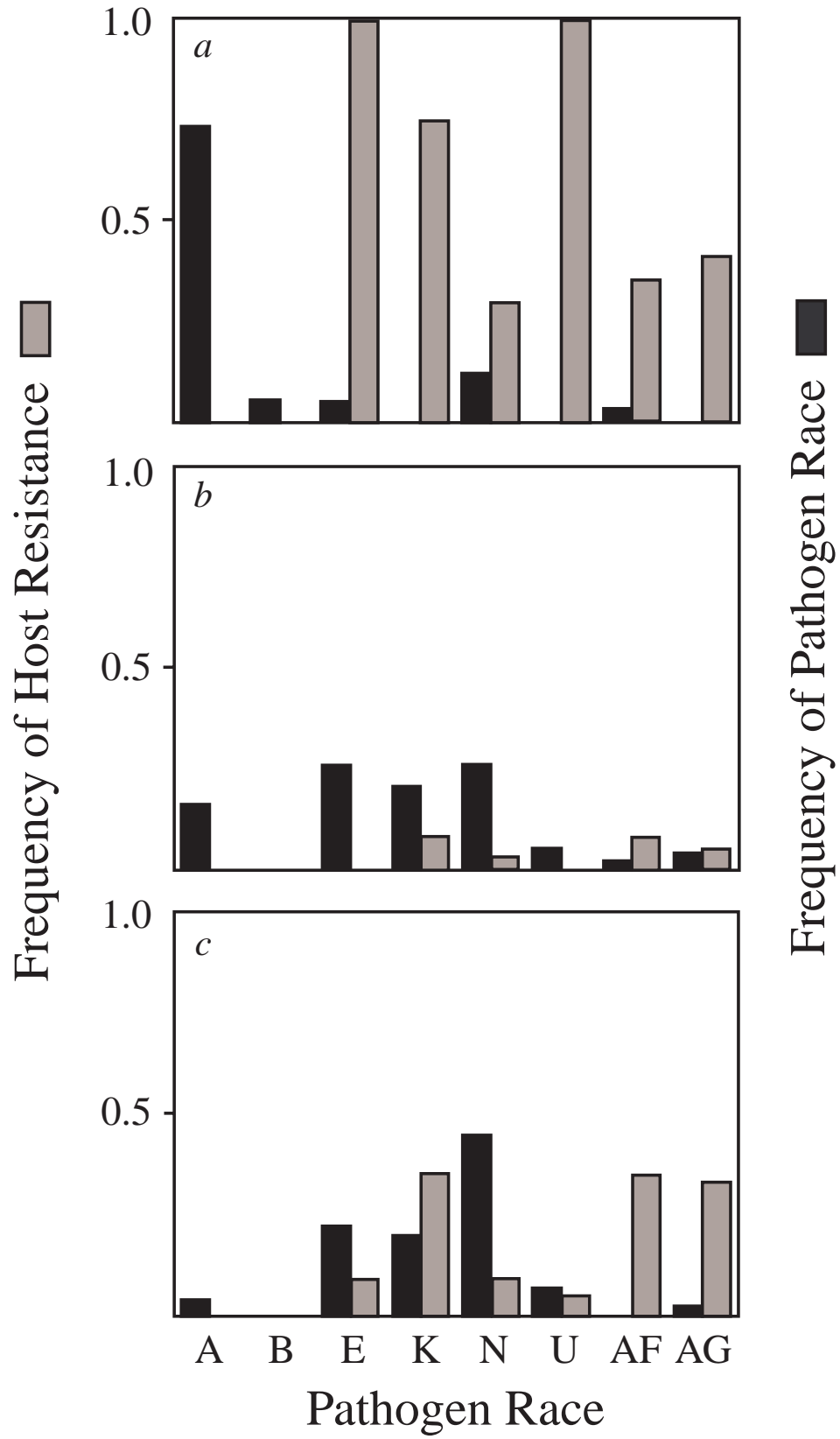


Figure 5

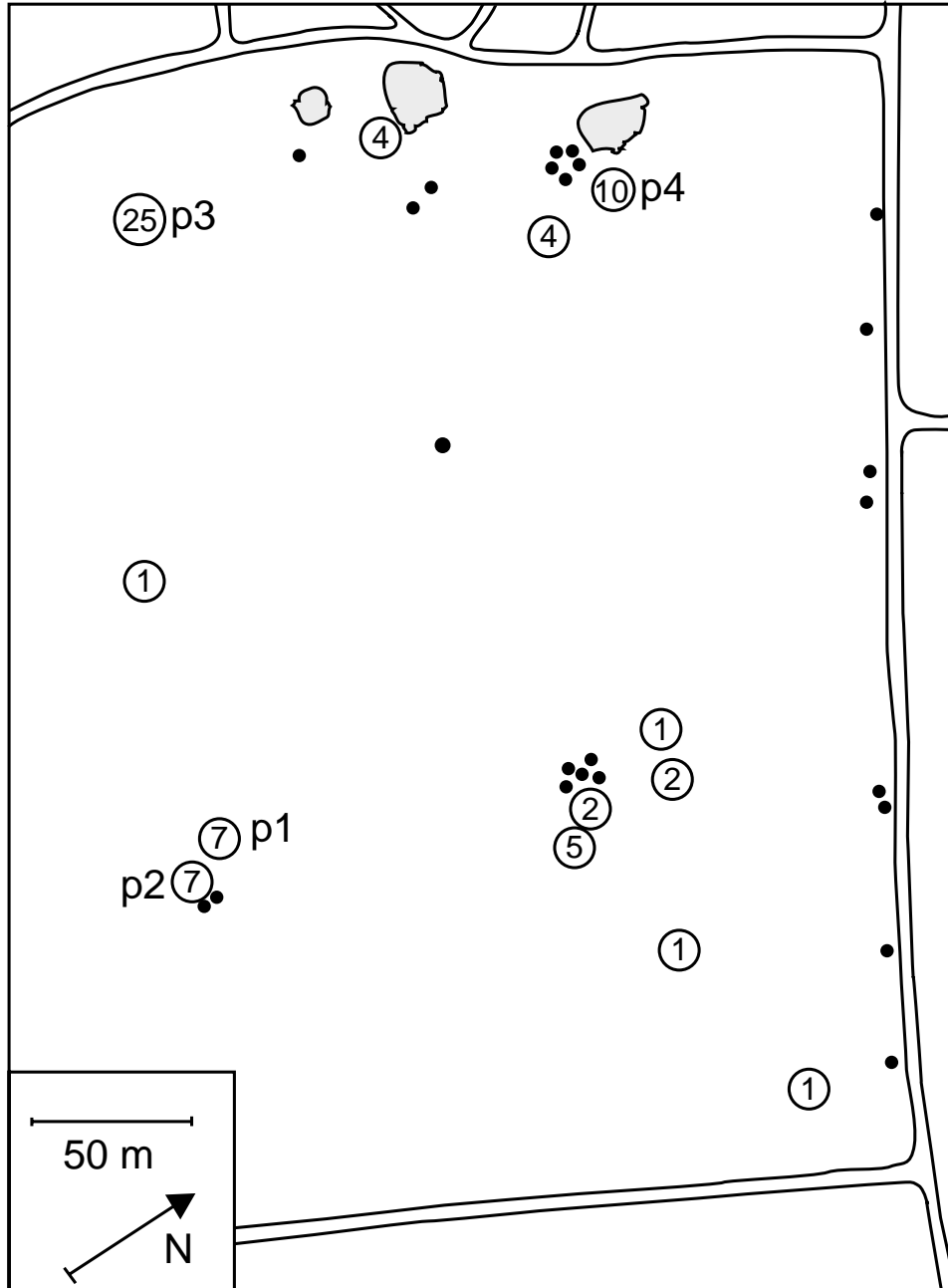


Figure 6