Title: How clonal are bacteria over time?

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Abstract

Bacteria and archaea reproduce clonally (vertically), but exchange genes by recombination (horizontal transfer). Recombination allows adaptive mutations or genes to spread within (or between) species. Clonality – the balance between vertical and horizontal inheritance – is therefore a key microbial trait, determining how quickly a population can adapt. Here, I consider whether clonality can be considered a stable trait of a given population. In some cases, clonality changes over time: non-clonal (recombining) populations can give rise to clonal expansions. However, an analysis of time-course metagenomic data suggests that a bacterial population's past clonality is indicative of its future clonality. Thus, a population's evolutionary potential – whether it is likely to retain genetic diversity or not – can in principle be predicted from its past.

Introduction

Here, I revisit the question posed in the title of a classic paper by John Maynard Smith and colleagues [1]: How clonal are bacteria? More specifically how does clonality vary among different microbial populations and over time? First, what do we mean by clonality? Perfectly clonal bacteria replicate by cell division (vertical descent) and evolve by random mutations that occur during DNA replication. There is negligible horizontal transfer of DNA by recombination across the resulting tree of vertical descent. Very few (if any) natural bacterial populations fit this theoretical definition of clonality. Or, as discussed below, they might only fit it for a short amount of time. However, knowing where a bacterial population happens to fall along a spectrum of clonality can help us understand its biology, and even make predictions about its evolution.

The opposite of clonality is panmixis – a situation in which the rate of horizontal transfer is higher than the rate of vertical cell division [1,2]. However, rates of horizontal transfer (recombination) vary widely across the genome, such that a population can be mostly clonal, except for a few loci in the genome. These loci came to be termed genomic islands – a metaphor I will build upon below. Some of the first islands identified were called pathogenicity islands because they contained virulence factors [3]. However, non-pathogenic environmental bacteria also contain islands, conferring adaptation to different ecological niches. For example, genes in *Prochlorococcus* genomic islands confer adaptation to light and nutrient conditions [4,5]. But islands need not confer niche adaptation to their host genome; they can be neutral to host fitness or even detrimental, selfish parasites. Here, I define genomic islands broadly as any piece of DNA that is transferred horizontally (by either homologous or nonhomologous recombination) from cell to cell and therefore evolves independently (*i.e.* is unlinked) from the rest of the genome.

Are some islands really peninsulas?

In the classic analogy, an island is totally disconnected from the mainland, meaning that genes in the island evolve independently of the genome (**Table 1**). Examples of islands that fit this strict independence might include integrated phages and other “selfish” elements, or genes that reside in a particular niche but not in a particular genome (*e.g.* a gene ecology model [6]). Peninsulas provide an analogy that might better describe how islands are related to microbial genomes. A peninsula (or "presque-ile," from the French for "almost island") is a geographic term for a very narrow strip of land connected to (but distinct from) the mainland. An island is evolutionarily independent of the mainland genome, but their fates may become linked, forming a peninsula. For example, a bacterium may acquire a gene from a vast microbial gene pool. This gene allows the bacterium to invade a new ecological niche, triggering a clonal expansion in which the fate of the gene and its new host genome are linked, at least for the duration of the clonal expansion. One such example could be *Yersinia pestis,* which acquired a single gene allowing flea-borne transmission and triggering a clonal expansion in the form of Plague pandemics [7]. Another peninsula, the prophage-encoded cholera toxin, and its links to the mainland *Vibrio cholerae* genome [8,9], is discussed below.

Are some genomes archipelagos?

The very concept of one or a few islands implies a contrast with the large, clonal genomic mainland or continent. But some microbial genomes may contain so many islands that there is no mainland, only a vast archipelago (**Table 1**). A striking recent example is a population of hotspring cyanobacteria in which virtually every gene in the genome evolved independently due to frequent recombination [10], leading the authors to call the population “quasi-sexual” (panmictic). The Asian ocean population of *Vibrio parahaemolyticus* also form a panmictic gene pool, with each recombination block of ~1.8 kbp evolving independently [11]. Similarly, almost every gene in a population of *Vibrio cyclitrophicus* genomes showed signals of recombination over relatively recent time scales [12]. Such apparently high rates of recombination in natural

populations were mysterious at first, contradicting recombination rates measured in the lab [13,14] and predicted by theory [15,16]. However, new models (discussed below) suggest mechanisms capable of explaining such surprisingly panmictic populations [17,18].

Clonal expansions from panmictic pools

Archipelagos are not necessarily static over time; they can sometimes coalesce into continents. Given the right ecological opportunity, a genome from a panmictic gene pool can escape the "gravitational pull" of recombination and take off into a clonal expansion (resulting in “epidemic” population structure [1]). An example mentioned earlier is *V. cholerae*, a genetically diverse group of coastal marine bacteria, some of which cause cholera. Virulence is mainly determined by two loci in the genome: the cholera toxin and the toxin-coregulated pilus. Both genes are frequently gained and lost by recombination [19,20], but are always found in one lineage of *V. cholerae* – the lineage causing severe disease with pandemic potential, known as the phylocore genome (PG) group [9]. It remains a mystery why the PG lineage evolved once, and only once. If PG *V. cholerae* really did evolve just once, this would be surprising because *V. cholerae* draws on a diverse, global gene pool and can be considered panmictic [21]. Therefore multiple different lineages would be expected to acquire the two (or perhaps a handful of) genetic elements required for pandemic disease. This leads to the hypothesis that pandemic cholera emergence is *selection limited* rather than *diversity limited*. In other words, benign *V. cholerae* strains constantly acquire virulence genes. However, these strains rarely encounter the right ecological niche to flourish, *e.g.* a human population consuming brackish water. "The right niche" has appeared a few times in human history: for example in India in the 1800s, when the Classical lineage evolved, and again in Indonesia in the 1950s, when the El Tor lineage evolved [22]. El Tor and Classical lineages have different cholera toxin alleles, but both evolved from within the PG group, suggesting that the PG genomic background is adapted to acquire and exploit virulence genes. When the “right” conditions appear, the PG lineage, along with its virulence factors, takes off in a clonal

expansions which continue to wreak havoc today (*e.g.* cholera pandemics from the 1800s to today, all caused by the PG clonal group). The virulence factors, previously islands in an archipelago, became a peninsula connected to the PG mainland. The linkage between virulence factors and PG remains imperfect because different variants of the cholera toxin continue to flow in and out of the PG continent [9,19]; hence the toxin remains a peninsula, not firmly part of the mainland.

V. cholerae is a particularly well-characterized example of a panmictic gene pool giving rise to a clonal expansion, but similar evolutionary dynamics are seen in other pathogens as well. For example, enterotoxigenic *Escherichia coli* (ETEC) seems to behave similarly, with deep branches of the phylogeny obscured by frequent recombination and plasmid exchange, but more recent branches experiencing mostly clonal descent, with tight linkage between virulence factors and the genomic mainland [23]. These observations are consistent with an ancient, diverse panmictic gene pool giving rise to clonal expansions, which can last for decades or centuries.

The balance between recombination and selection

Let us consider the evolutionary forces that determine clonality: natural selection and recombination. The effect of recombination on clonality is straightforward: more recombination means less clonality. The effect of natural selection is more complex, but is defined here simply as a force which favors clonal expansions of adaptive mutants within an ecological niche. When driven by ecological selection, clonal expansions are called selective sweeps, in which one clone outcompetes all others, purging genetic diversity in the population [15,16].

Recombination and selection interact to determine the clonality of a population. Recombination rates depend both on the ability of DNA to enter a cell and be incorporated into the genome (the baseline rate) and the ability of that DNA to be retained by a balance of genetic drift and natural selection (the realized rate). Some bacteria, such as *Helicobacter pylori,* have realized recombination rates that are much higher than point mutation rates, exchanging at least

10% of their genome within a single four-year human infection [24]. Others, such as *Staphylococcus aureus* [25,26] and *Mycobacterium tuberculosis* [27-29] are decidedly more clonal. Recombination rates (both realized and baseline) vary widely across the genome. Of 10 pathogenic bacterial species studied, all had identifiable recombination 'hot' regions, although their length, genomic location and gene content varied [30]. Genes of different functions had different realized recombination rates, implying a role for natural selection on gene function in determining whether newly acquired genes are retained.

Modeling the recombination-selection balance

When rates of recombination are relatively low compared to rates of natural selection (s) on adaptive genes within niches, entire genomes will sweep to fixation before they can be shuffled by recombination. The $s >> r$ regime is well described in the Stable Ecotype Model [15], which predicts that most of the genome will follow a single, clonal phylogeny. Genome-wide sweeps thus increase clonality and can be considered a hallmark of clonal populations (**Table 1, Figure 1a**). In the $r >> s$ regime, individual genes (rather than entire genomes) will sweep to fixation (*i.e.* reach 100% frequency) in ecological niches to which they are adapted, without affecting genetic diversity elsewhere in the genome (**Figure 1b**). A recent model showed how these gene sweeps can occur at moderate (not unrealistically high) rates of recombination [18]. In this model, a microbial habitat is bombarded with genetically maladapted migrants, allowing gene sweeps to occur, although the adaptive allele never reaches 100% frequency due to the constant input of migrants. In another model, Takeuchi et al. [17] show that gene sweeps can occur when r is either very high or – counter-intuitively – when r is very low, but only when negative frequency-dependent selection (NFDS) reduces the rate of genome-wide selective sweeps. NFDS might be commonly imposed on bacteria and archaea by viral (phage) predation, providing a selective advantage to rare alleles of phage receptor genes [31].

151 **Genome-wide and gene-specific sweeps in nature**

152 To date, empirical evidence for gene-specific and genome-wide sweeps has come mostly from
153 cross-sectional studies of a single population of genomes at a single point in time, with
154 recombination and selection inferred backward in time [10-12,32]. Sequencing microbial
155 genomes or metagenomes sampled over time – already a typical practice in genomic
156 epidemiology (e.g. [26,33]) – promises to elucidate the rates of gene-specific and genome-wide
157 sweeps in nature (**Figure 1**).

158 In a pioneering study, Bendall et al. [34] sampled a lake over 9 years and followed single-
159 nucleotide polymorphism (SNP) and gene frequencies in 30 bacterial populations by
160 metagenomic sequencing. They inferred that one of the populations (*Chlorobium*-111) had
161 undergone a near-complete genome-wide sweep over the 9-year study, with most SNP diversity
162 purged genome-wide (**Figure 1a**). In 6 other populations, they identified regions of the genome
163 with unexpectedly low diversity compared to the genome-wide average, throughout the time-
164 course. Either strong purifying selection on these regions or gene-specific selective sweeps
165 (completed before the start of the time-course) could explain the low diversity. During the 9-year
166 study, they also observed examples "where a few adjacent SNPs trended toward fixation while
167 genome-wide diversity was maintained" (**Figure 1b**). They took this observation as consistent
168 with gene-specific selective sweeps, but did not attempt to determine whether the sweeps were
169 due to selection or drift. As a whole, the study showed that both genome-wide and gene-specific
170 sweeps can occur in different microbial populations from the same environment. Whether
171 microbial populations behaved differently due to differences in their ecology (*i.e.* regime of
172 natural selection) or in their baseline recombination rates remains a question for future study. The
173 fact that a genome-wide sweep was observed over a 9 year period suggests that such events might
174 be relatively rapid but rare (only observed in 1 of 30 populations). Meanwhile, gene-sweeps
175 might be more common historically (affecting 6 of 30 populations), but could take longer to
176 proceed to completion.

Is clonality a stable trait?

As described in the *V. cholerae* example, some pathogenic bacterial populations can switch between panmictic and clonal lifestyles. Therefore clonality can vary over time, but how much and how often? To quantify the stability of clonality over time, I re-analyzed the lake time-course of Bendall et al. [34]. Because estimates of selection and recombination rates were not readily available for this dataset, I defined clonality based on the frequency of genome-wide selective sweeps. Frequent genome-wide selective sweeps suggest $s >> r$, suggesting clonality. I identified 20 "old, diverse" populations as those with a high density of SNPs (>1500 SNPs/Mbp) at the beginning of the time-course. These populations are likely "old" because they have gone a relatively long time since the last genome-wide purge of genetic diversity and are relatively non-clonal. They include the 6 populations inferred to have undergone gene-specific sweeps [34]. The remaining 10 populations were defined as "young, low-diversity," having more recently experienced a genome-wide purge of diversity. The "old, diverse" populations have a relatively low ratio of nonsynonymous (N) to synonymous (S) SNPs, suggesting large effective population sizes and ample time for purifying selection to remove (mostly deleterious) nonsynonymous mutations (**Figure 2**). In contrast, the "young, low-diversity" populations are more likely to have high N:S ratios, suggesting smaller effective population sizes and less time for purifying selection to have acted.

With young (clonal) and old (less clonal) populations thus defined, I asked whether "old, diverse" populations tended to maintain their diversity through the 9-year period of the study. Bendall et al. defined two alternative population types: 1) those that maintained stable SNP diversity over 9 years, and 2) those that experienced significant fluctuations in diversity due to clonal expansions – defined when one, but not all timepoints are dominated by a single allele (≥95% frequency) at >40% of SNP sites in the genome [34]. By definition, the 19 populations of the first type did not experience genome-wide sweeps during the study, while the 11 populations

203 of the second type did experience genome-wide purges of diversity, which were transient in 10
204 cases and apparently permanent in 1 case (*Chlorobium*-111). Strikingly, 17 out of 20 "old,
205 diverse" populations maintained their diversity over the 9-year study, compared to only 2 out of
206 10 "young, low-diversity" populations (Fisher test, Odds Ratio = 19.4, $P < 0.001$). This result
207 suggests that populations with a history of genome-wide sweeps (and/or population bottlenecks)
208 tend to experience subsequent genome-wide sweeps, and those that have maintained genetic
209 diversity in the past tend to maintain their diversity into the future. In other words, clonality can
210 be considered a relatively stable microbial trait.
211
212 **History repeats itself**
213 It appears that pathogens are more likely than free-living bacteria to undergo clonal expansions,
214 due in part to their ecology and transmission dynamics [1,35]. Free-living aquatic bacteria, on the
215 other hand, seem to be more likely to live in large, panmictic populations and behave like
216 archipelagos [10-12,34]. If clonality is indeed a stable trait, this implies that history will repeat
217 itself, and that the future behavior of microbial populations can be predicted with some
218 confidence from their past behavior. Diverse populations tend to stay diverse. Clonal populations
219 (that experience frequent genome-wide sweeps) tend to stay clonal. But history is not doomed to
220 repeat itself forever. As we have seen, clonal expansions, such as pandemic *V. cholerae,* may
221 originate when a panmictic gene pool (an archipelago) coalesces into a clonal continent, with
222 virulence factors linked as peninsulas. Many such pathogenic clones have been documented, with
223 life spans of decades to thousands of years [23,26,36,37]. Other pathogens, such as *Streptococcus*
224 *pneumoniae*, may retain their panmictic population structure throughout an outbreak [38-40].
225 Why some pathogens are clonal and others are panmictic is an open question, but surely depends
226 on the balance between recombination and selection, and on the time scales considered.
227

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231 **Table 1. Extended island metaphors of microbial genome evolution.**
232

Geographic metaphor	Genetic unit to which the metaphor applies	Type of selective sweep experience by the unit	Dominant mode of genetic transmission	Example
Island	Gene	Gene-specific	horizontal	genes in the *V. cholerae* integron [20,21]
Peninsula	Gene	Genome-wide	vertical (clonal)	the cholera toxin gene, acquired horizontally, then linked to a clonal *V. cholerae* genome [8,19]
Continent	Genome	Genome-wide	vertical (clonal)	clonal expansions of *S. aureus* [26] and *M. tuberculosis* [29,37]
Archipelago	Genome	Gene-specific	horizontal	hotspring cyanobacteria [10], ocean vibrios [11,12], pneumococcus [38,40]

233
234
235 **Figures**
236
237 **Figure 1. Temporal dynamics of genome-wide and gene-specific selective sweeps**
238 **inferred from metagenomic data.** Genetic diversity can be measured by mapping
239 metagenomic sequence reads to a reference genome, identifying SNPs, and calculating
240 the allele frequencies at each SNP position in the genome over time. The lowest possible
241 genetic diversity occurs when a single allele is present in 100% of metagenomic reads.
242 Alternatively, diversity could be defined in terms of gene presence/absence, based on
243 relative coverage of a gene in the reference genome by metagenomic reads. **(a)** In a
244 hypothetical genome-wide selective sweep, all positions in the genome tend toward low
245 diversity over time. **(b)** In a hypothetical gene-specific selective sweep, only one or a few
246 positions in the genome tend toward low diversity, while the rest of the genome maintains
247 high or intermediate diversity.
248
249 **Figure 2. Past diversity predicts future diversity.** Based on data from Table 2 of
250 Bendall et al. [34], the genome-wide average nonsynonymous to synonymous (N:S) SNP
251 ratio was plotted against the total SNP density (SNPs per megabasepair) for each of 30
252 bacterial populations. A pseudocount of 1 was added to both N and S counts. These 30
253 populations were divided into 20 "old, diverse" populations (>1500 SNPs/Mbp) and 10
254 "young, low-diversity" populations (<1500 SNPs/Mbp), highlighted in blue and yellow,
255 respectively. Each point represents one of the 30 populations, colored in black if diversity
256 was maintained over a 9-year metagenomic time-course, or in red if it was not. Seventeen
257 out of 20 "old, diverse" populations maintained their diversity over the 9-year study,
258 compared to only 2 out of 10 "young, low-diversity" populations (Fisher test, Odds Ratio
259 = 19.4, $P < 0.001$). Consistent with previous observations that N:S depends on the
260 evolutionary time available for purifying selection to act [41,42], N:S is negatively
261 correlated with SNPs/Mbp, a proxy for evolutionary time or the time since the last
262 genome-wide purge of genetic diversity in this dataset (Pearson's correlation of $\log_{10}$
263 transformed data, $r = -0.81$, $P = 5.6e-8$).

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Figure 1

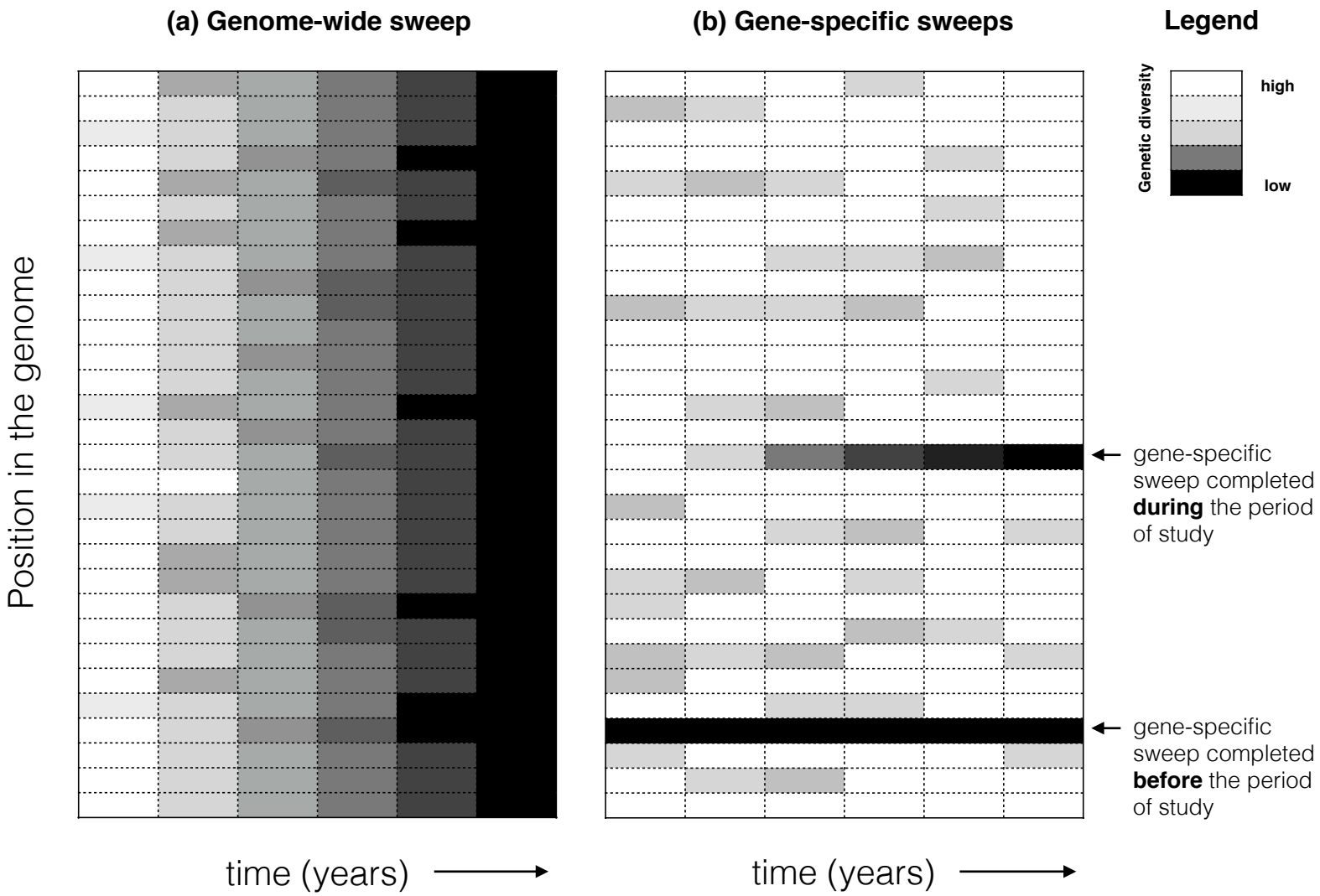
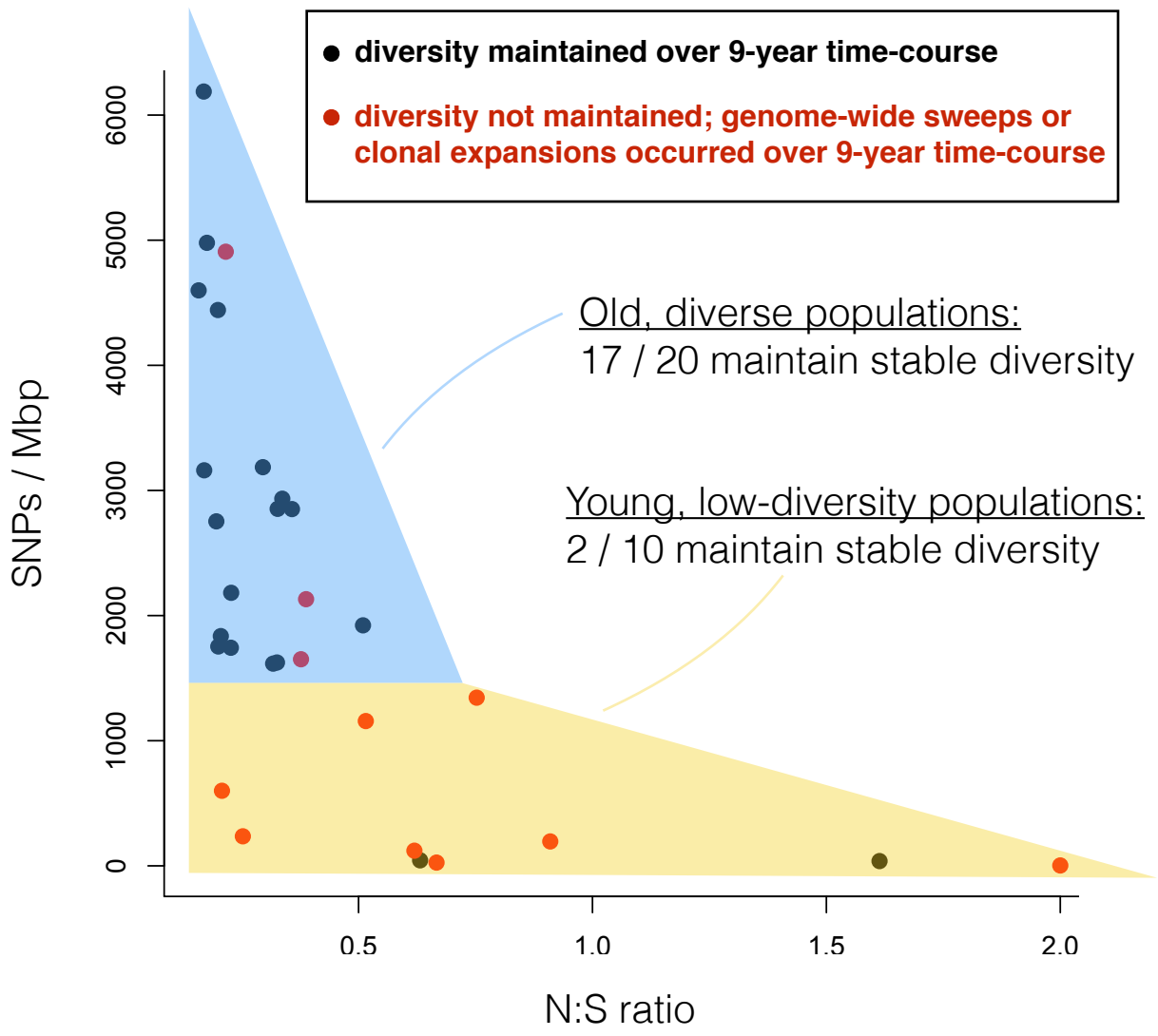

(a) Genome-wide sweep
(b) Gene-specific sweeps
Legend
Genetic diversity
high
low
Position in the genome
gene-specific sweep completed **during** the period of study
gene-specific sweep completed **before** the period of study
time (years)
time (years)

Figure 2


diversity maintained over 9-year time-course
diversity not maintained; genome-wide sweeps or clonal expansions occurred over 9-year time-course
Old, diverse populations:
17 / 20 maintain stable diversity
Young, low-diversity populations:
2 / 10 maintain stable diversity
SNPs / Mbp
0
1000
2000
3000
4000
5000
6000
0.5
1.0
1.5
2.0
N:S ratio