Modelling bacterial speciation

William P. Hanage, Brian G. Spratt, Katherine M. E. Turner and Christophe Fraser*

Department of Infectious Disease Epidemiology, Imperial College London, St Mary’s Hospital Campus, Norfolk Place, London W2 1PG, UK

A central problem in understanding bacterial speciation is how clusters of closely related strains emerge and persist in the face of recombination. We use a neutral Fisher–Wright model in which genotypes, defined by the alleles at 140 house-keeping loci, change in each generation by mutation or recombination, and examine conditions in which an initially uniform population gives rise to resolved clusters. Where recombination occurs at equal frequency between all members of the population, we observe a transition between clonal structure and sexual structure as the rate of recombination increases. In the clonal situation, clearly resolved clusters are regularly formed, break up or go extinct. In the sexual situation, the formation of distinct clusters is prevented by the cohesive force of recombination. Where the rate of recombination is a declining log-linear function of the genetic distance between the donor and recipient strain, distinct clusters emerge even with high rates of recombination. These clusters arise in the absence of selection, and have many of the properties of species, with high recombination rates and thus sexual cohesion within clusters and low rates between clusters. Distance-scaled recombination can thus lead to a population splitting into distinct genotypic clusters, a process that mimics sympatric speciation. However, empirical estimates of the relationship between sequence divergence and recombination rate indicate that the decline in recombination is an insufficiently steep function of genetic distance to generate species in nature under neutral drift, and thus that other mechanisms should be invoked to explain speciation in the presence of recombination.

Keywords: Fisher–Wright model; simulation; species; recombination; multilocus genotypes; genetic cartography

1. INTRODUCTION

Despite the well-documented extent of lateral gene transfer among the prokaryotes (Gogarten et al. 2002), which has led some researchers to doubt whether the term ‘species’ has any meaning for these organisms (Lawrence 2002; Gevers et al. 2005), we can define clusters of similar phenotype or genotype which often correspond to named species. However, these clusters show a variety of forms, levels of within-cluster diversity and degree of resolution from neighbouring clusters. This should not be surprising, because bacteria may have very different lifestyles and rates of recombination (Hanage et al. 2006a). Surprisingly few studies have addressed the necessary conditions for the formation of genotypic clusters, their dynamics or properties, which could shed light on the reasons why, even in the face of promiscuous recombination, we can define entities among the bacteria which we recognize as species (Hanage et al. 2005a,b).

In recent years, the ability of the sequences of multiple house-keeping genes to identify distinct genotypic clusters among populations of closely related species has been explored. This approach (reviewed elsewhere in this volume; Hanage et al. 2006b) is predicated upon the success of multilocus sequence typing (MLST) for both precise strain characterization in the context of epidemiology (Hanage et al. 2004) and application to species definition termed ‘multilocus sequence analysis’ (MLSA; Gevers et al. 2005). In MLSA, the sequences of several (usually about seven) house-keeping genes are determined, and the concatenates of these are used to determine the presence (or otherwise) of clusters of related genotypes in sequence space, which may be related to existing species or used to inform the process of species assignment. This approach has demonstrated that at least some of the species presently recognized by microbiologists are concordant with genotypic clusters, even when a large number of strains of frequently recombining species are considered (Hanage et al. 2005a,b).

A complementary approach is to identify by simulation the conditions under which an initially uniform bacterial population diverges and resolves into distinct genotypic clusters. While much of the previous work in this field has concentrated on the role of periodic sweeps in ecologically structured populations in the formation of distinct genotypic clusters (ecotypes; Majewski & Cohan 1999a; Cohan 2002), we deliberately explore the behaviour of systems under neutral drift. Neutrality provides a useful null model and identifies conditions under which genotypes do, or
do not, form resolved clusters in the absence of selection or population subdivision (Fraser et al. 2005). In addition, neutrality is not necessarily a statement of lack of selection or structure, but rather an effective description of situations where the evolutionary landscape is highly complex, and thus specific genotypes are rarely advantageous over extended periods of time or space. The effect of more persistent selection or population substructure in affecting basic neutral speciation models can subsequently be explored.

2. SIMULATING POPULATIONS USING HIGH-RESOLUTION MULTILOCUS SEQUENCE TYPING

In MLST, internal fragments (approx. 500 bp) of seven house-keeping genes are sequenced from each strain (Maiden et al. 1998). The different sequences at each locus are assigned different allele numbers and each strain is defined by a string of seven integers (the allelic profile), corresponding to the alleles at seven loci. Large MLST datasets are available for several bacterial species, and we have described a population genetic model that can be applied to this rich source of data (Fraser et al. 2005; Hanage et al. 2006a).

This Fisher–Wright neutral model of bacterial evolution defines the genotypes of strains in the same way as MLST, by the alleles present at seven house-keeping loci. Multilocus genotypes in generation \( n + 1 \) of the neutral model are randomly sampled from generation \( n \), with individual loci changing at specified rates by point mutation or recombination. The analytical solution for the expected distribution of allelic mismatches of multilocus genotypes at equilibrium for any mutation and recombination rate allows these model parameters to be estimated from samples of real bacterial populations characterized by MLST (Fraser et al. 2005). We may also simulate bacterial populations for any values of the mutation and recombination rates. To explore speciation, we have increased the number of loci that define each strain from 7 to 140, as this provides a greatly enhanced ability to discriminate between strains. Our choice for the number of loci as well as an allelic structure rather than full genotype simulations were motivated by the goal of substantially extending models in terms of population size and discrimination between genotypes, and were bounded by computational limitations.

Simulating the evolution of populations with strains defined by large allelic profiles rather than full sequences for a limited numbers of alleles was hypothesized to limit the distorting effects of recombination in assessing genetic distance between different strains.

We simulate populations of constant size \( 10^6 \), with each strain defined as a string of integers corresponding to the alleles at 140 loci (each of 500 bp) distributed around the chromosome. In each generation of the model, loci mutate with probability \( m \) and recombine with probability \( r \), as previously described (Fraser et al. 2005). We assume an infinite alleles model in which each mutation generates an allele not previously recorded in the population. In the limiting case of full panmixis, we model recombination as replacing the allele at a single locus with another drawn at random from the population. We consider recombination to be equally probable at any of the 140 loci. By analogy with \( \theta \) (the population mutation rate), we define the population recombination rate \( \rho = 2rN \).

In order to simulate the effect of sequence divergence on the probability of successful recombination (distance-scaled recombination), we use the allelic distance between the strain that donates the allele and the recipient strain (the proportion of allelic differences at the 140 loci) as a proxy for the sequence divergence between the strains. The probability of successful recombination in the distance-scaled recombination model declines in a log-linear fashion with increasing divergence between donor and recipient strains, as found to be the case in Bacillus subtilis (Majewska & Cohan 1999b), Escherichia coli (Vulic et al. 1997) and Streptococcus pneumoniae (Majewska et al. 2000). While in these cases the degree of local divergence between donor and recipient sequences determines the probability of successful recombination, owing to the high level of discrimination offered by the large number of loci studied we argue that our model based on mismatches in allelic profiles captures this relationship in a probabilistic sense.

Starting with an initially uniform population of \( 10^6 \), we allow the simulation to run. At intervals, samples of 1000 strains are drawn at random and are used to examine the pattern of genotypic clustering. To display the clustering of genotypes in the samples of the simulated populations (the genetic cartography), we use a multidimensional scaling (MDS) algorithm implemented in R (Venables & Ripley 2002; Team 2005), which represents in two dimensions the overall genetic distance between each strain and all others in the population.

3. CLONAL POPULATIONS AND THE INFLUENCE OF INCREASING RECOMBINATION

The relative contributions of point mutation and recombination to the divergence of multilocus genotypes differ greatly among bacterial populations (Feil & Spratt 2001). In some species, such as Mycobacterium tuberculosis, convincing evidence for recombination is lacking and genotypes diverge exclusively (or nearly so) by mutation (Smith et al. 2003). At the other extreme, in some populations, alleles at house-keeping loci change much more frequently by recombination than point mutation (Spratt et al. 2001; Hanage et al. 2006a). Therefore, we explore the patterns of clustering observed within simulated populations evolving with a fixed population mutation rate \( (\theta = 2) \) and a range of population recombination rates, from \( \rho = 0 \) (clonal) to 20. In the initial simulations, recombination occurs at the same defined rate between any pair of strains. We then introduce the more plausible scenario of distance-scaled recombination, incorporating the log-linear reduction in recombination rate with increasing divergence between strains.

Figure 1 shows the clusters obtained using MDS for population samples drawn every \( 2.5 \times 10^7 \) generations for a clonal population with \( \theta = 2 \). The diversification of the initially uniform population in
the absence of recombination leads within about 250 000 generations to distinct clusters of closely related strains. The initial cluster persists, but through stochastic drift it has become extinct by the 800 000th generation. If we introduce recombination at the same rate as mutation (θ = 2, ρ = 2), then diversification proceeds as under the totally clonal simulation, with multiple distinct clusters emerging

(figure 2). Under conditions of much higher recombination rates (θ = 2, ρ = 20; figure 3), transient diffuse clusters of strains still emerge, but fail to become established as distinct resolved clusters, being drawn back into the main cluster by recombination with the other strains in the population. The dynamics of clonal clustering and the cohesive effects of recombination can be observed more clearly in the movies in the electronic supplementary material.

4. THE EFFECT OF DISTANCE-SCALED RECOMBINATION

Figure 4 shows the effect of introducing a log-linear decline in the probability of recombination with increasing overall allelic distance. For all strains θ = 2, and the probability of recombination occurring between identical strains is very high (ρ₀ = 50). The probability of recombination occurring between strains with allelic distance D is given by ρ = ρ₀ exp[-αD] and the resulting relationship between ρ and allelic distance is shown in figure 4a, corresponding to α = 0.1. As shown in figure 4b (and a movie in the electronic supplementary material), the initially uniform cluster rapidly forms distinct clusters, which then continue to diversify and form new clusters by the same process. Between the similar strains within these distinct clusters, the rate of recombination is high (figure 4a). Between strains in different clusters it is low, owing to the log-linear drop-off of recombination with genetic distance. The integrity of clusters is therefore maintained by frequent recombination. Major new clusters are formed rarely, as stochastic drift infrequently leads to the establishment of new strains that are sufficiently distant from the progenitor cluster that they can no longer be reabsorbed by recombination. The number of such clusters presumably increases monotonically as a function of θ.
5. DYNAMICS OF MAJOR CLUSTER FORMATION

Figure 5 shows an alternative way of displaying the formation and dynamics of the emergence and persistence over time of genotypic clusters under the scenarios described previously. In this representation, the change over time in the proportion of pairs of strains differing at \( n \) of 140 loci is shown for the entire population of \( 10^6 \) (as opposed to samples of 1000). This analysis is unable to detect the minor transient clusters visible in the MDS diagrams, but instead focuses on the major lineages of similar strains. Genetic cartography of samples taken during the evolution of a population with distance-scaled recombination. \( \theta = 2 \) and \( \rho = 50 \) for recombination between identical strains and \( \rho \) declines as a log-linear function of the genetic distance between strains, as described in the text.

6. DISCUSSION

While any satisfying definition of bacterial species remains elusive, the present work demonstrates that distinct clusters of similar genotypes can emerge under
many parameter values for both mutation and recombination rates. Distinct clusters fail to arise where there are high levels of recombination between strains, with no decline, or a slow decline, in the probability of recombination with increasing genetic distance. In this situation, subclusters appear to arise but become drawn back into the main population, presumably owing to the cohesive effect of recombination. In contrast, where recombination declines sharply with increasing genetic distance, separate clusters arise and then are maintained by distance-scaled recombination—high rates of recombination within each cluster and low rates between different clusters. In this scenario, clusters arise even though rates of recombination between similar isolates are substantially higher than those that prevent clusters from emerging in simulations where recombination rate is not scaled to genetic distance. These distinct clusters are effectively ‘species’, and the cohesive role of recombination between similar strains, with no decline, or a slow decline, in the probability of recombination with increasing genetic distance should be very low, except when very few alleles match at all, and the degree of sequence divergence should be nearly equal to that between identical sequences.

Under neutral drift, we therefore do not predict speciation in sympatric populations with high rates of recombination, unless the empirically determined reduction in recombination rate with genetic distance (divergence) we have used to generate clusters is much sharper than this empirically determined one. By linearizing the binomial probability for sequence identity based on randomly scattered polymorphisms, we infer that \( D \approx Lx \), where \( L \) is the total length of sequence compared. Thus, the degree of sequence divergence should be very low, except when very few alleles match at all, and the degree of recombination should be nearly equal to that between identical sequences.

Recombination is believed to often involve the replacement of small regions (a few kilobases) of a recipient chromosome with the corresponding region from a donor strain. An important caveat of our simulations is that studies of natural populations, and the general features of RecA-mediated recombination, suggest that the rate of recombination will depend on the local sequence similarities between the donor and recipient strains in the regions involved in the localized genetic exchange. In this work, we assume that recombination is a function of overall genetic distance, measured as the proportion of the 140 alleles that differ between strains. We chose this as our initial approach, as computationally it allows an examination of large populations defined at large numbers of alleles. Further developments of our simulations incorporating local measures of genetic distance will be described elsewhere. Our observation of a recombination threshold, lying between \( \rho/\theta=1 \) and \( \rho/\theta=10 \) for situations where recombination is not distance-scaled, above which population cohesiveness is maintained and below which clonal clusters emerge, is not dependent on this assumption. Interestingly, Falush et al. (2006) present a simulation using local measures of genetic distance, which shows similar patterns of clustering and ‘speciation’, although we would argue that (as in our simulations) speciation at high recombination rates is only observed in their simulations under conditions where the recombination rate reduces with sequence divergence very much more steeply than found in empirical studies.

Bacteria exist as diverse populations that can be resolved into clusters which can be assigned to various taxonomic divisions (lineages, species, genera, etc.). The study of these populations and their taxonomy can be enhanced by the widespread application of...
multilocus sequencing approaches, with the prospect of future sequencing technologies making it ever more feasible to sequence hundreds of genes from thousands of strains. Within this context, it is important that we have some theoretical means of describing what we expect to observe in nature, of interpreting what we observe, and of integrating these findings with the biology and ecology of the organisms under study. Future work should address the impact of selection and population subdivision (or allopatry) on the nature and dynamics of genotypic clustering, as well as better models of genetic distance, and it should explicitly attempt to compare the clusters derived from simulation with those observed among natural populations.

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REFERENCES

Cohan, F. M. 2002 What are bacterial species? Annu. Rev. Microbiol. 56, 457–487. (doi:10.1146/annurev.micro.56.012302.160634)

Falush, D., Torpøldal, M., Didelot, X., Conrad, D. F., Wilson, D. J. & Achiman, M. 2006 Mismatch induced speciation in Salmonella: model and data. Phil. Trans. R. Soc. B 361, 2045–2053. (doi:10.1098/rstb.2006.1925)

Feil, E. J. & Spratt, B. G. 2001 Recombination and the population structures of bacterial pathogens. Annu. Rev. Microbiol. 55, 561–590. (doi:10.1146/annurev.micro.55.1.561)

Fraser, C., Hanage, W. P. & Spratt, B. G. 2005 Neutral microepidemic evolution of bacterial pathogens. Proc. Natl Acad. Sci. USA 102, 1968–1973. (doi:10.1073/pnas.0406993102)

Gevers, D. et al. 2005 Opinion: re-evaluating prokaryotic species. Nat. Rev. Microbiol. 3, 733–739. (doi:10.1038/nrmicro1236)

Gogarten, J. P., Doolittle, W. F. & Lawrence, J. G. 2002 Prokaryotic evolution in light of gene transfer. Mol. Biol. Evol. 19, 2226–2238.

Hanage, W. P., Feil, E. J., Brueggemann, A. B. & Spratt, B. G. 2004 Multilocus sequence typing: strain characterization, population biology and patterns of evolutionary descent. In Molecular microbiology: diagnostic principles and practice (ed. D. H. Persing, F. C. Tenover, J. Versalovic, Y.-W. Tang, E. R. Unger, D.A Relman & T. J. White), pp. 235–243. Washington, DC: American Society for Microbiology.

Hanage, W. P., Fraser, C. & Spratt, B. G. 2005a Fuzzy species among recombinogenic bacteria. BMC Biol. 3, 6. (doi:10.1186/1741-7007-3-6)

Hanage, W. P., Kajilalainen, T., Herva, E., Saukkoripii, A., Syrjanen, R. & Spratt, B. G. 2005b Using multilocus sequence data to define the pneumococcus. J. Bacteriol. 187, 6223–6230. (doi:10.1128/JB.187.17.6223-6230.2005)

Hanage, W. P., Fraser, C. & Spratt, B. G. 2006a The impact of homologous recombination on the generation of diversity in bacteria. J. Theor. Biol. 239, 210–219. (doi:10.1016/j.jtbi.2005.08.035)

Hanage, W. P., Fraser, C. & Spratt, B. G. 2006b Sequences, sequence clusters and bacterial species. Phil. Trans. R. Soc. B 361, 1917–1927. (doi:10.1098/rstb.2006.1917)

Koufopanou, V., Hughes, J., Bell, G. & Burt, A. 2006 The spatial scale of genetic differentiation in a model organism: the wild yeast Saccharomyces paradoxus. Phil. Trans. R. Soc. B 361, 1941–1946. (doi:10.1098/rstb.2006.1922)

Lawrence, J. G. 2002 Gene transfer in bacteria: speciation without species? Theor. Popul. Biol. 61, 449–460. (doi:10.1006/tpbi.2002.1587)

Maiden, M. C. et al. 1998 Multilocus sequence typing: a portable approach to the identification of clones within populations of pathogenic microorganisms. Proc. Natl Acad. Sci. USA 95, 3140–3145. (doi:10.1073/pnas.95.6.3140)

Majewski, J. & Cohan, F. M. 1999a Adapt globally, act locally: the effect of selective sweeps on bacterial sequence diversity. Genetics 152, 1459–1474.

Majewski, J. & Cohan, F. M. 1999b DNA sequence similarity requirements for interspecific recombination in Bacillus. Genetics 153, 1525–1533.

Majewski, J., Zawadzki, P., Pickrell, P., Cohan, F. M. & Dowson, C. G. 2000 Barriers to genetic exchange between bacterial species: Streptococcus pneumoniae transformation. J. Bacteriol. 182, 1016–1023. (doi:10.1128/JB.182.4.1016-1023.2000)

Mayr, E. 1942 Systematics and the origin of species. New York, NY: Columbia University Press.

Smith, N. H., Dale, J., Inwald, J., Palmer, S., Gordon, S. V., Hewinson, R. G. & Smith, J. M. 2003 The population structure of Mycobacterium bovis in Great Britain: clonal expansion. Proc. Natl Acad. Sci. USA 100, 15 271–15 275. (doi:10.1073/pnas.2036554100)

Spratt, B. G., Hanage, W. P. & Feil, E. J. 2001 The relative contributions of recombination and point mutation to the diversification of bacterial clones. Curr. Opin. Microbiol. 4, 602–606. (doi:10.1016/S1369-5274(00)00257-5)

Team, R. D. C. 2005 R: a language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing.

Venables, W. & Ripley, B. 2002 Modern applied statistics with S. New York, NY: Springer.

Vulic, M., Dionisio, F., Taddei, F. & Radman, M. 1997 Molecular keys to speciation: DNA polymorphism and the control of genetic exchange in enterobacteria. Proc. Natl Acad. Sci. USA 94, 9763–9767. (doi:10.1073/pnas.94.18.9763)