‘Drifting’ *Buchnera* genomes track the microevolutionary trajectories of their aphid hosts

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ABSTRACT

Coevolution of *Buchnera*–aphid host symbioses is often studied among species at the macroevolutionary scale. Investigations within species offer a different perspective about how ecoevolutionary processes shape patterns of genetic variation at the microevolutionary scale. Our study leverages new and publicly available whole-genome sequencing data to study *Buchnera*–aphid host coevolution in *Myzus persicae*, the peach potato aphid, a globally invasive and polyphagous pest. Across 43 different aphid clonal lineages, we examined patterns of genomic covariation between *Buchnera* and their aphid host, and considered the distribution of mutations in protein-coding regions of the *Buchnera* genome. We found *Buchnera* polymorphism within aphid clones, suggesting that aphids harbour populations of different *Buchnera* strains. Genetic distance between pairs of *Buchnera* samples was positively correlated to genetic distance between their hosts, indicating shared

evolutionary histories. However, there was no segregation in the genetic variation of both *M. persicae* and *Buchnera* with plant host (Brassicaceae and non-tobacco Solanaceae) and there was also no isolation-by-distance within both organisms at global or regional spatial scales. Abundance patterns of non-synonymous mutations were similar to synonymous mutations, and both mutation classes had similar site frequency spectra. We hypothesize that a predominance of neutral processes results in the *Buchnera* of *M. persicae* to simply 'drift' with the evolutionary trajectory of their aphid hosts. Our study presents a unique microevolutionary characterisation of *Buchnera*–aphid host genomic covariation across multiple aphid clones. This provides a new perspective on the eco-evolutionary processes generating and maintaining polymorphisms in a major pest aphid species and its obligate primary endosymbiont.

INTRODUCTION

Endosymbiotic bacteria can play significant roles in the physiology of their host organisms. Among the most well studied endosymbionts is *Buchnera aphidicola* (herein, '*Buchnera*'), a maternally inherited proteobacteria found in aphids. *Buchnera* has a long coevolutionary history with aphids, which has led to the two organisms being entwined in an obligate symbiosis. *Buchnera* have lost many core genes for their own regulation, but maintain genes involved in the biosynthesis of essential amino acid missing from the diet of their sap-sucking aphid hosts (Moran & Mira, 2001; Shigenobu, Watanabe, Hattori, Sakaki, & Ishikawa, 2000). Because of the importance of *Buchnera* to the fitness of its aphid host, it is often described as a primary endosymbiont. This contrasts with secondary endosymbionts, which are other non-obligate endosymbiotic bacteria that can have important, but variable, phenotypic effects on their aphid host (Guo et al., 2017). At broad macroevolutionary scales (among species), there is strong congruence between the phylogenies of aphid species and their *Buchnera*, reflecting unique coevolutionary histories of adaptation and (or) drift in the genomes of these organisms over evolutionary time (Chen, Wang, Chen, Jiang, & Qiao, 2017; Chong, Park, & Moran, 2019; Jousselin, Desdevises, & Coeur D'Acier, 2009; Nováková et al., 2013).

Coevolution between *Buchnera* and their aphid hosts can also be studied at the microevolutionary scale (within species), providing a population genetic perspective and an appreciation for processes that generate and maintain genetic polymorphisms in these symbioses over ecological time (Bennett & Moran, 2015; Wernegreen, 2015, 2017). To date, microevolutionary studies on the *Buchnera*–aphid host symbiosis have primarily focused on the model species, the pea aphid, *Acyrthosiphon pisum* (as reviewed in: Bennett and Moran 2015, Smith and Moran 2020). In *A. pisum*, specific genetic variants in the *Buchnera* genome have been linked to thermal tolerance of their aphid host (Dunbar, Wilson, Ferguson, & Moran, 2007; Perreau, Zhang, Maeda, Kirkpatrick, & Moran, 2021) and performance under histidine depleted diets (Chung, Parker, Blow, Brisson, & Douglas, 2020). The rapid evolution of the *Buchnera* genome and maternal inheritance of this endosymbiont has

been a useful molecular tool in tracking plant host specialization of *A. pisum* across different species of Fabaceae (Peccoud, Simon, McLaughlin, & Moran, 2009). Other laboratory studies on *A. pisum* have helped develop insight into the (lack of) plasticity of *Buchnera* gene expression in response to nutrient variability (Moran, Plague, Sandström, & Wilcox, 2003) and possible interactions with gene expression patterns in their aphid host (Smith & Moran, 2020). Whilst *A. pisum* has provided a valuable system for understanding microevolutionary dynamics in the *Buchnera*–aphid host symbioses, we lack a broader perspective of how variation in *Buchnera* might affect the evolutionary ecology in other aphid species (including major pest species).

Myzus persicae, the peach potato aphid, is in many ways a prime species for studying coevolution between *Buchnera* and its aphid host on microevolutionary scales. *Myzus persicae* originated in Asia, but is now a major globally invasive agricultural pest (Li et al., 2015). This global distribution of *M. persicae* is interesting with respect to considering possible genomic changes that might be associated with post-invasion adaptation or drift. Clonal diversity in invasive ranges can be low, presumably through the joint action of post-invasion bottlenecks and strong selective sweeps from agricultural insecticides (de Little, Edwards, van Rooyen, Weeks, & Umina, 2017; Umina, Edwards, Carson, Van Rooyen, & Anderson, 2014). However, the extent to which related, but geographically separated, clones diverge from each other post-invasion has been poorly characterized, with previous work largely interested in quantifying beta diversity in clonal composition (e.g., Margaritopoulos, Kasprowicz, Malloch, & Fenton, 2009; Singh et al., 2021). *Myzus persicae* is also an incredibly polyphagous pest that is able to infest more than 40 different plant families (CABI Compendium, 2024); this strongly contrasts the model *A. pisum*, which is restricted to plants in the family Fabaceae (Peccoud et al., 2009). Unlike many other aphids species, *M. persicae* tends to lack polymorphism in secondary endosymbionts, especially in its invasive range (Yang et al., 2023). The rarity of these secondary endosymbionts in *M. persicae* would simplify the possible microevolutionary dynamics between the aphid host and *Buchnera*, as well as attempts to link genomic variation in their genomes to environmental variables.

We know very little about segregating patterns of *Buchnera* variation within and among different clonal lineages of *M. persicae*. Some prior work has suggested that *M. persicae* and its associated *Buchnera* have retained an unusually high functional capacity relative to other aphid species, which may be linked to the polyphagous nature of this aphid species (Douglas, 1988; Smith, Li, Perreau, & Moran, 2022; J. Wang et al., 2013). Prior global analysis of *M. persicae* clones revealed an association between the aphid host genome and different plant host families (Singh et al., 2021). In that study, the major axis of aphid host genetic structuring was related to the primary peach host and recent tobacco specialization, but genetic structuring with respect to other plant hosts was less clear, and structuring of genetic variation in *Buchnera* was not considered. Some additional work in tobacco specialized *M. persicae* clones suggests that adaptive genetic changes underlying this plant host shift have occurred in the aphid host rather than in the *Buchnera* genome (Jiang et al., 2013; Singh et al., 2020). A greater understanding of how *Buchnera* may (or may not) contribute to host plant specialization in *M. persicae*

could be gained from examining a broader diversity of clones from other plant hosts.

Here, we investigate coevolution of *Buchnera*-aphid symbiosis in *M. persicae* on a macroevolutionary scale. Our analyses focus on patterns of genomic covariation between the *Buchnera* and aphid host genome *within* aphid clones and the structuring of this genomic covariation *among* aphid clones across space and on different host plants. *Buchnera*–aphid host genomic covariation could arise from the near-neutral processes of mutation accumulation and genomic decay, so that lineage specific genomic changes in *Buchnera* simply track the lineage of their aphid host via drift (McCutcheon & Moran, 2012). Adaptive processes could also contribute to patterns of covariation, such as selection favoring coadaptations between the aphid host and endosymbiont that increase overall fitness (Gilbert et al., 2010), or antagonistic selection for adaptations and counter-adaptations in a 'tug-of-war' between these organisms (Bennett & Moran, 2015; Smith & Moran, 2020). Under coadaptation, genetic variants in both the endosymbiont and aphid host could rapidly spread through a population and predominate descendent lineages, or else drive codivergence among lineages under diversifying selection, such as in response to different host plants and climates.

Our study had two primary aims. Our first aim was to quantify genomic variation within, and covariation between, *Buchnera* and its aphid host with respect to geography and plant host. This allowed us to investigate how genomic (co)variation is segregating among different clones, providing insight into post-invasion genomic changes and plant host specialization, respectively. Our second aim was to characterize the distribution of mutations in protein-coding regions across *Buchnera* from different aphid clones. This allowed us to specifically test for the relative contributions of adaptive versus neutral processes in shaping the distribution of variation within the *Buchnera* genome. We compiled a globally distributed dataset of clonal *M. persicae* strains using publicly available sequencing data and new sequence data from Australia. We focused on clones associated with two less well studies plant families in *M. persicae* host specialization: Brassicaceae (cruciferous vegetables) and Solanaceae (peppers). We excluded clones from tobacco (also a member of Solanaceae) in light of evidence suggesting that specialization on this plant host is due to genomic changes in the aphid host (Jiang et al., 2013; Singh et al., 2020) and support for tobacco specialized clones representing a distinct subspecies (*M. p. nicotianae*) (Singh et al., 2021). Our study provides among the first major characterizations of coevolutionary patterns between aphid clones and their primary endosymbiont at the microevolutionary scale.

METHODOLOGY

Sample collection and metadata curation

Our study used a global sample of *M. persicae* (n = 43), leveraging previously sequenced *M. persicae* clones from Singh et al. (2021) (n = 24) and newly sequenced clones collected in this study from Australia (n = 19). All

clonal strains were found on plant hosts belonging to the families Brassicaceae or Solanaceae. For the 19 Australian *M. persicae samples*, we extracted genomic DNA from pools of 5 individuals using Qiagen's DNeasy® Blood and Tissue kit. Whole-genome library construction was performed by Novogene (Novogene, Hong Kong, China) with sequencing performed on an Illumina HiSeq paired end 150 bp. We treat each clonal sample as a pooled sample of individuals (pool-seq). Herein, clonal samples follow the naming convention 'Country_Study_ID', where 'Country' is a country-of-origin code, 'Study' is one of 'Z' for this present study or 'S' for Singh et al. (2021), and 'ID' is a unique identifier number. Sample information is recorded in supplementary Table S1, and the global distribution of samples is illustrated in Figure 1. We retrospectively obtained microsatellite genotypes for the majority of Australian clones sequenced in this study (n = 14) to align our genomic information against historical measures of clonal variation in Australia (de Little et al., 2017; Umina et al., 2014),

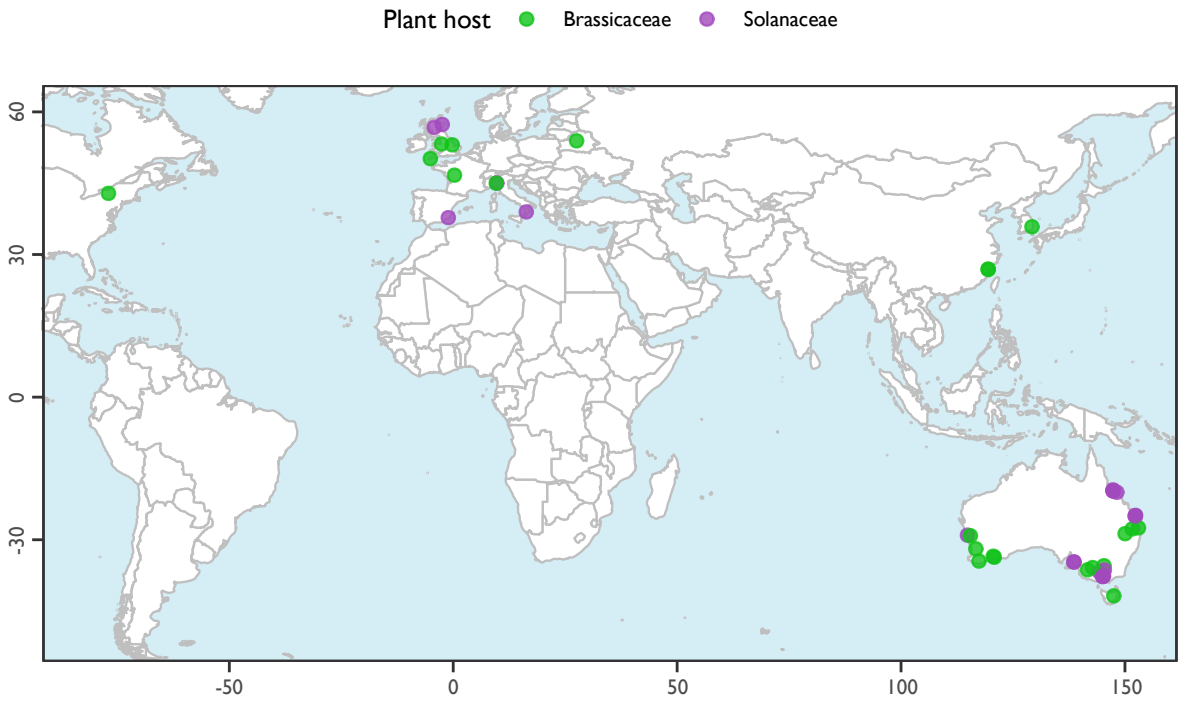

Figure 1. Global distribution of clonal *Myzus persicae* samples used in this study. Points are coloured by plant host family (see legend). See supplementary Table S1 for associated metadata.

Read trimming, read mapping, and variant calling

Raw reads for our newly sequenced *M. persicae* and those from Singh et al. (2021) were trimmed and quality-filtered using *fastp* v0.12.4 (Chen et al., 2018). We then mapped trimmed reads against the G006 v3 nuclear reference genome for the aphid host (Aphid Base) and against the USDA strain *Buchnera* genome (GenBank

Accession: CP002697), using *bowtie2* with the 'very-sensitive' end-to-end mode (Langmead et al., 2012). Alignments were sorted, filtered for a map quality >30, and deduplicated using *samtools* v1.16.1 (Danecek et al., 2021). The samples from Singh et al. (2021) had much greater sequencing depth than our low-coverage samples. We therefore down-sampled all Singh et al. (2021) reads to the maximum number of mapped reads observed for our samples to make the two datasets comparable: 15.6 million reads for *M. persicae* and 1.6 million reads for *Buchnera*. Down-sampling was performed with *samtools*. After down-sampling, we called variants in both the *M. persicae* host and *Buchnera* genomes using *freebayes* v1.3.2 (Garrison and Marth 2012) with the '--pooled-continuous' (treating each sample as a pool of individuals) and '--min-alternate-count 3' arguments. This dataset was then separately filtered for analyses of (1) genetic diversity in the *M. persicae* host and *Buchnera* genomes, (2) genetic differentiation among *M. persicae* hosts and *Buchnera* genomes, and (3) mutational effects in the *Buchnera* genomes. We describe filtering for these analyses in the following subsections.

Genetic diversity within clones

We quantified the genetic diversity in the genomes of *Buchnera* and *M. persicae* host as the genomic heterozygosity, the relative proportion of the total genome that is polymorphic. We filtered each *Buchnera* and *M. persicae* host sample separate (n = 43 clones): (1) *Vcftools* v0.1.16 was used to subset variants to a minimum depth threshold (20 reads for *Buchnera* and 10 reads for *M. persicae* host genomes) and no missing data for each sample; (2) the number of SNP loci was extracted using custom code; (3) the total number of covered genomic sites meeting the minimum depth threshold was determined using the *samtools depth* function; (4) the genomic heterozygosity was calculated by dividing the number of observed SNPs in a sample over the total covered genomic sites.

We tested the hypothesis that genetic diversity differs between plant hosts. We fitted the model:

$$\text{Heterozygosity} = \text{Plant family}$$

Here, genomic heterozygosity in either *Buchnera* or *M. persicae* was modeled as a function of plant family (Brassicaceae or Solanaceae) as categorical variable. We also tested the hypothesis that genetic diversity in *Buchnera* is a function of the genetic diversity in its *M. persicae* host. We fitted the model:

$$\textit{Buchnera}\ \text{heterozygosity} = \textit{M. persicae}\ \text{heterozygosity}$$

We used the *lm* function to fit models and the *anova* function to determine significance. Genomic heterozygosity was transformed using a log10 transformation and addition of a small constant (1e−6) to reduce skew and non-normality, and to allow transformation of 0 values. Some samples were outliers with respect to genomic heterozygosity; some clonal samples had notably higher heterozygosity in their *Buchnera* genome, and some clonal samples had no heterozygosity in their *Buchnera* genome. We therefore modeled the *Buchnera–M.*

persicae correlations twice, once with all samples, and again with outlier samples removed.

Genetic differentiation between clones

We tested several hypotheses on the structuring of clonal genetic variation with respect to genetic differences across space and plant hosts. We filtered *Buchnera* and *M. persicae* host SNPs, derived following a series of filtering steps for all n = 43 clones: (1) *Vcftools* was used to reduce the variants to biallelic loci with a minimum quality of 20; (2) we manually reduced the data to SNPs using string searching on the VCF file; and (3) we used *vcftools* to filter out SNPs with minimum depth <20 reads across samples and any SNPs with missing data. SNPs were imported into R using the *genomalicious* R package (Thia and Riginos 2019) with the *vcf2DT* function. We performed a series of iterative filtering steps to more carefully curate genetic variants for downstream analysis, which involved: (1) setting a minimum read depth threshold, (2) filtering by a mean minor allele frequency of 0.05 across all samples, and (3) filtering to retain SNPs at a minimal distance threshold to reduce non-independence of sites. For *M. persicae* hosts, we set a minimum depth of 5 reads and a minimum SNP distance of 10,000 bp. For *Buchnera*, we set a minimum depth of 20 reads and a minimum SNP distance of 500 bp. This left 541 SNPs for the *M. persicae* host and 285 SNPs for *Buchnera*.

For both the *M. persicae* host and *Buchnera*, we calculated frequencies of the alternate allele as a continuous measure of genetic variation within each clonal sample. For *Buchnera*, we divided the number of alternate reads by the total read count to get the alternate frequency. However, SNPs with singleton reads for either the alternate or reference allele were set to 0 or1, respectively, because singleton reads could be sequencing errors. Characterisation of allele frequencies treats the *Buchnera* within an aphid as a population of bacteria with coexisting strains. Such a method has been used elsewhere to study genetic variation of coral endosymbionts (Matias et al., 2022), and other studies have used deep amplicon sequencing to study different strains of *Buchnera* in *A. pisum* (Perreau et al., 2021).

For *M. persicae*, use of individual allele frequencies helped to account for uncertainty in genotypes attributed to low-sequencing coverage (Clark et al. 2019). We performed a Bayesian estimation of individual allele frequency for each sample using the R package *polyRAD* (Clark et al. 2019). *PolyRAD* was designed to provide inferences of allelic dosage in the context of polyploids but flexibly extends to diploids. Over-dispersion was examined using the*TestOverdispersion* function, with the optimal value for the over-dispersion parameter estimated as 26. The *IteratePopStructLD* function incorporated this over-dispersion into estimates of the allelic dosage with information on linkage, inferences of population structure, and expectations under Hardy-Weinberg equilibrium. Although the assumption of Hardy-Weinberg does not hold true for clonal aphids, this approach allowed us to objectively infer individual allele frequencies from low-coverage data as a proxy for genotypes in aphid host samples (Figure S1).

Next, we estimated pairwise differentiation across all clonal sample pairs. We used the Δ_D statistic as our

measure of genetic differentiation, which measures beta diversity from relative abundance data based on Shannon's entropy (Hill number of order q = 1), weighting alleles by their relative frequency. This deviates from genetic differentiation measured as F_{ST} (Hill number of order q = 2) which is influenced by heterozygosity rate (Gaggiotti et al., 2018). Additionally, Δ_D does not have the same underlying population genetic assumptions as F_{ST}, which is arguably more appropriate for clonally reproducing species and for measuring 'pools' of alleles in *Buchnera* samples. Δ_D was calculated using R's IDIP function from the *HierDpart* package, available through GitHub (Gaggiotti et al., 2018). We produced a set of pairwise Δ_D values for *Buchnera* and another set for their *M. persicae* hosts.

Our first hypothesis tested for isolation-by-distance between pairs of clones. This hypothesis specifically tested whether sampled clones are increasingly genetically differentiated with increasing geographic distance. Geographically distant clones might be expected to diverge due to drift and (or) different local environments. Geographic distances between clonal samples were obtained using the *geosphere* package (Hijmans, 2022). We then correlated pairwise geographic distance against pairwise genetic differentiation, measured as Δ_D, in the *Buchnera* and *M. persicae* host genomes.

Second, we tested whether there was a pattern between aphid and *Buchnera* differentiation consistent with 'coevolution', with this term interpreted in the most general sense to encompass both neutral and adaptive processes producing joint differentiation among *M. persicae* clones and their *Buchnera*. We correlated pairwise Δ_D values between *Buchnera* and *M. persicae* genomes, whereby a signal of coevolution would be a positive correlation between genetic differentiation in both genomes. To visualize coevolutionary patterns, we constructed neighbor joining trees for *Buchnera* and *M. persicae* from Δ_D distance matrices using the *nj* function from R's *ape* package (Paradis, Claude, & Strimmer, 2004). Bootstrapping of node support was performed using *ape*'s *boot.phylo* function in conjunction with custom code to regenerate bootstrapped Δ_D distance matrices. Bootstrapping the Δ_D distance matrices required randomly redrawing SNP loci with replacement and then recalculating pairwise Δ_D values. Trees were constructed using R's *ggtree* (Yu, Smith, Zhu, Guan, & Lam, 2017) and *treeio* (Wang et al., 2020) packages.

Third, we tested for signals of plant host specialization. If *Buchnera* or *M. persicae* on the same plant host are genetically similar, pairwise genetic differentiation should be lower when comparing clones within a plant host relative to between plant hosts. To test this, we first reduced our dataset to only contain unique clonal lineages. Our neighbour joining tree (see below) showed that some samples formed clades that likely reflect groups of very closely related clones connected by short branch lengths. This included clonal samples from Australia, China, and the UK with pairwise Δ_D values ≤ 0.037. For those groups of closely related clones, we took the most derived sample within each clade to represent each plant host. We then tested our plant host specialization hypothesis using an analysis of residuals. We first fitted the models:

$$\Delta_D \textit{ Buchnera} = \Delta_D \textit{ M. persicae} + \text{Geographic distance} + \Delta_D \textit{ M. persicae}\text{:Geographic distance}$$

$$\Delta_D \textit{ M. persicae} = \Delta_D \textit{ Buchnera} + \text{Geographic distance} + \Delta_D \textit{ Buchnera}\text{:Geographic distance}$$

These models fitted the pairwise genetic differentiation in the focal species genome as a function of pairwise genetic differentiation in their partner (*M. persicae* host or *Buchnera* endosymbiont) genome, geographic distance, and their interaction. We then took the residuals and fitted two more models:

Buchnera residuals = Host plant

M. persicae residuals = Host plant

Here, the residual variation in pairwise genetic differentiation (unaccounted for by the partner's genetic differentiation or geographic distance) is fitted as a function of the host plant; that is, within Brassicaceae or Solanaceae, or between 'different' plant families. If there was a genome-wide signal of plant host specialization, we would expect residuals within Brassicaceae and Solanaceae samples to be smaller than those from different host plant samples. Models were fitted with R's *lm* function with significance tested using the *anova* function.

We tested each of our three hypotheses of genetic differentiation (isolation-by-distance, covariance between *Buchnera* and *M. periscae* hosts, and plant host specialization) using three different partitions of our dataset: global, Europe, and Australia. The global dataset provided a broad perspective but is complicated by potentially varying ecological factors among geographic regions and different evolutionary histories of clonal aphid lineages. We also had greater replication of samples from Europe and Australia, so conducted analyses on these separately to see if regional patterns differed from those observed at the global scale.

Mutations in *Buchnera* protein-coding regions within and among clones

We examined protein-coding mutations and their distributions among *Buchnera* from different clonal samples to assess the possible relative contributions of adaptive versus neutral processes shaping genetic variation. We filtered the raw variants with *vcftools* to retain only SNPs (excluding indels) with a minimum quality of 20, a minimum depth of 20, and no missing data. We did not filter for biallelic SNPs because we wanted to retain all possible segregating mutations in *Buchnera* that may have protein coding effects. This *Buchnera* SNP set was annotated with the program *snpEff* (Cingolani et al., 2012) and imported back into R. SNPs that were annotated as 'Missense' (amino acid changes) or 'Stop' (premature stop codon) mutations were designated as 'Non-synonymous' mutations and compared with those identified as 'Synonymous' mutations. It is important to note that the number and class of mutations depends on the reference genome. We did not use an ancestral reference sequence, so mutations cannot be considered as being derived *per se.* Instead, we consider counts of alternate alleles.

We created site-frequency spectra (SFS) for non-synonymous and synonymous SNPs to test for similar frequency distributions between these two mutation classes. Downward projection was used to place counts of alternate alleles into bins from '1' to '20' by rounding the product of $q \times 20$, where q is the alternate allele frequency. Prior to downward projection, any allele with a count of 1 read was set to a frequency of 0 to reduce the effect of singleton reads. Pearson's correlation between allele count bins for non-synonymous versus synonymous mutations was calculated using the *ppcor* package (Kim, 2015).

We tested for enrichment (proportional over-representation) and diminishment (proportional under-representation) of non-synonymous SNPs in genes contributing to different functional pathways. We had four hypotheses. First, our 'core cellular' pathway hypothesis posited that genes involved in core cellular pathways should have fewer non-synonymous mutations that might reduce functionality. Decay of core cellular pathway genes would be detrimental to *Buchnera*. Second, our 'core mutualism' pathway hypothesis posited that genes involved in vital pathways to the *Buchnera*–aphid host symbiosis (e.g., amino acid biosynthesis) should have fewer non-synonymous mutations that might reduce functionality. Decay of core mutualism genes would be detrimental to the *M. persica* host. Third, our 'ecologically relevant' pathway hypothesis posited that genes involved in environmental adaptation should be enriched for non-synonymous mutations. Polymorphisms at ecologically relevant genes would benefit *Buchnera* by enhancing *M. persicae* host fitness under different ecological conditions. Fourth, our 'drift' hypothesis posted that neutral evolution predominates, such that non-synonymous and synonymous mutations occur at similar abundance across the *Buchnera* genome. In that case, no functional pathways would be expected to exhibit enrichment or diminishment of non-synonymous mutations.

SNPs were assigned to KEGG functional pathways using the R packages *KEGGREST* (Tenenbaum, 2023) and *pathfindr* (Ulgen, Ozisik, & Sezerman, 2019). Contingency tables (2×2) were constructed for each focal *Buchnera* KEGG pathway: focal and non-focal genes (those genes in vs. not in the focal KEGG pathway, respectively) in rows, and non-synonymous and synonymous mutations in columns. Fisher's exact test was used to test whether non-synonymous mutations were enriched or diminished in the focal functional pathway, using R's *fisher.test* function with a two-sided test. Note, this analysis was performed using SNPs across all samples, and was not performed separately for each sample, to ensure a sufficient sample size and to obtain average effects across clones.

RESULTS

Bioinformatic summary

The mean depth of mapped reads to the *Buchnera* genome was 616,927 with a range of 314,589 to 1,614,489

for our sequenced samples, and 3,089,599 with a range of 1,681,159 to 11,992,629 for the Singh et al. (2021) samples. The mean depth of mapped reads to the aphid host genome was 12.8 million with a range of 8.9 million to 15.6 million for our new sequenced samples, and 79.1 million with a range of 38.1 million to 219.4 million for the Singh et al. (2021) samples.

Genetic diversity within clones

Genomic diversity, the proportion of polymorphic to monomorphic sites in the genome, was considerably lower in *Buchnera* relative to *M. persicae*. *Buchnera* had a mean genomic heterozygosity of 4.6e–5 with a range of 0 to 4.4e–4, whereas *M. persicae* had a mean genomic heterozygosity of 0.001 with a range of 0.0008 to 0.002 (Figure 2a). There were no significant differences in genomic heterozygosity between plant hosts in either *Buchnera or M. persicae* (Figure 2a). *Buchnera* clearly exhibited a much greater variance in genomic heterozygosity, which spanned several orders of magnitude, whereas *M. persicae* had a much smaller variance. When considering all samples, there was a significant positive association between *Buchnera* and *M. persicae* genomic heterozygosity ($F_{1,41} = 26.7$, $p < 0.001$), but this was non-significant when removing outliers ($F_{1,32} = 0.27$, $p = 0.6$) (Figure 2b). Evidence for aphid host diversity driving diversity in *Buchnera* is therefore mixed in this dataset. Importantly, however, *Buchnera* polymorphism (non-zero heterozygosity) within different clones of *M. persicae* suggest *Buchnera* may exist as populations of genetically different strains within their aphid hosts (Figure 2b).

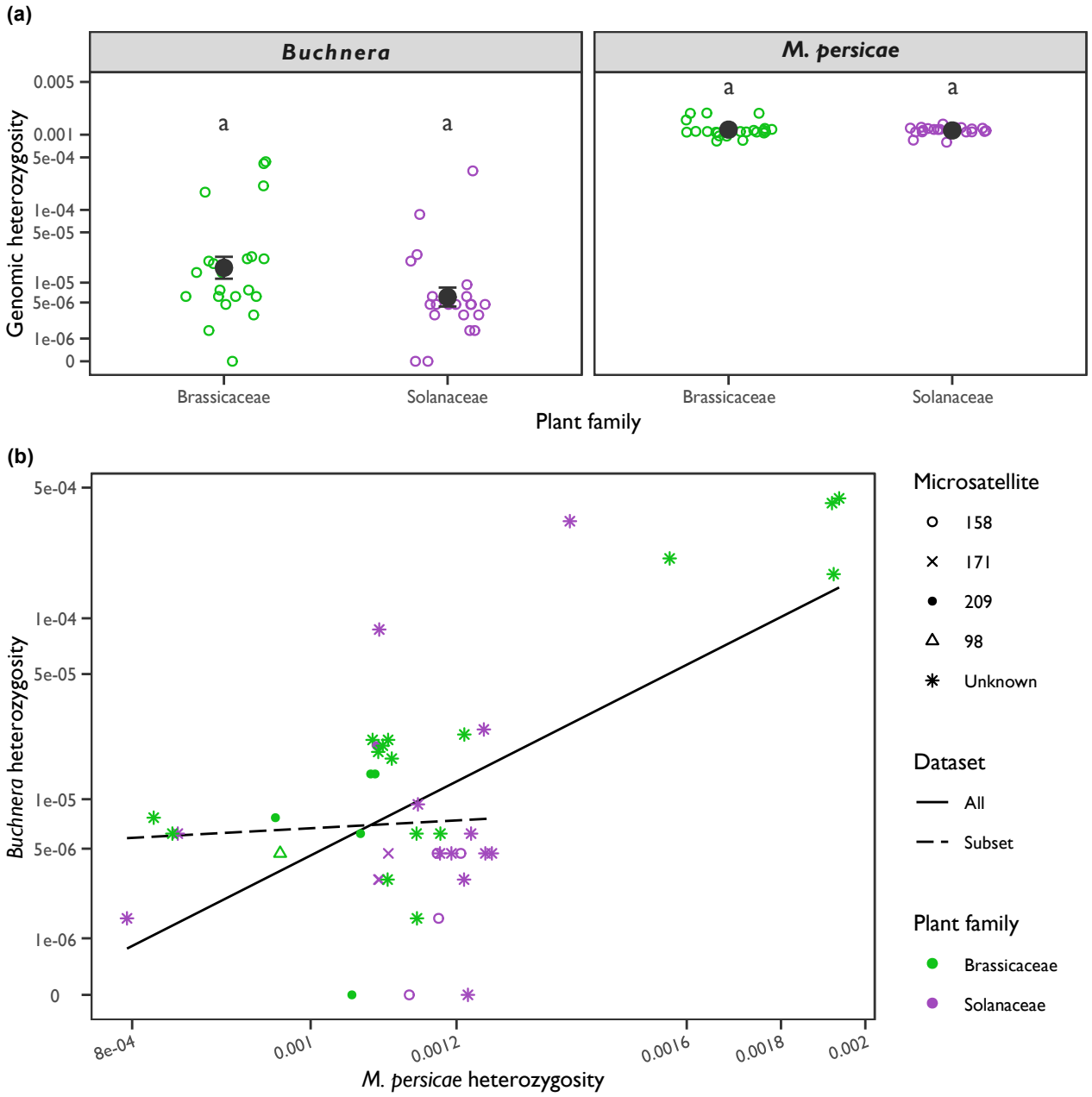

Figure 2. Patterns of genetic diversity in *Buchnera* and their *Myzus persicae* hosts. Genetic diversity was measured as the genomic heterozygosity, the proportion of the genome that is polymorphic. (a) Genomic heterozygosity (*y*-axis) as a function of host plant (*x*-axis). Open points represent individual samples, large closed circles represent the mean with standard error bars. Panels separate estimates for *Buchnera* (left) and *M. persicae* (right). (b) Genomic heterozygosity in *Buchnera* (*y*-axis) as a function of genomic heterozygosity in its aphid host (*x*-axis). Points are coloured by plant host, and where known, previous microsatellite clonal classification is depicted by point shapes (see legend). Linear regression lines for all samples, or subset samples (removing samples with *Buchnera* heterozygosity of 0 and >5e–5), are depicted by different line types (see legend).

Genetic differentiation between clones

Our global SNP set comprised 285 loci for *Buchnera* and 534 loci for *M. persicae*. Pairwise Δ_D values among *Buchnera* samples had a mean of 0.50, with a range of 0.0003 to 0.95. Pairwise Δ_D values among *M. persicae* samples had a mean of 0.27, with a range of 0.02 to 0.46. We found no evidence in support of isolation-by-distance in either *Buchnera* or *M. persicae* at the global scale, within Europe, or within Australia (Figures 2a, b, d, e, g, and h). Indeed, these patterns showed no obvious relationship; clonal samples separated by shorter geographic distances could be highly differentiated, and conversely, clonal samples separated by larger geographic distances could be genetically similar.

We did find strong support for coevolution between *Buchnera* and *M. persicae* (Figures 2c, f, and i). Pearson's correlations were r = 0.71, 0.37, and 0.91 in the global, European, and Australian datasets, respectively. This indicates that as aphid hosts diverge, their *Buchnera* track them with the same trajectory of divergence, although we found pairwise differentiation tended to be greater among *Buchnera* pairs relative to *M. persicae* pairs. This pattern is also evidenced in the co-phylogenetic tree, where there is a general congruence of topology between *Buchnera* and their aphid host trees but the topologies are not perfectly aligned (Figure 4).

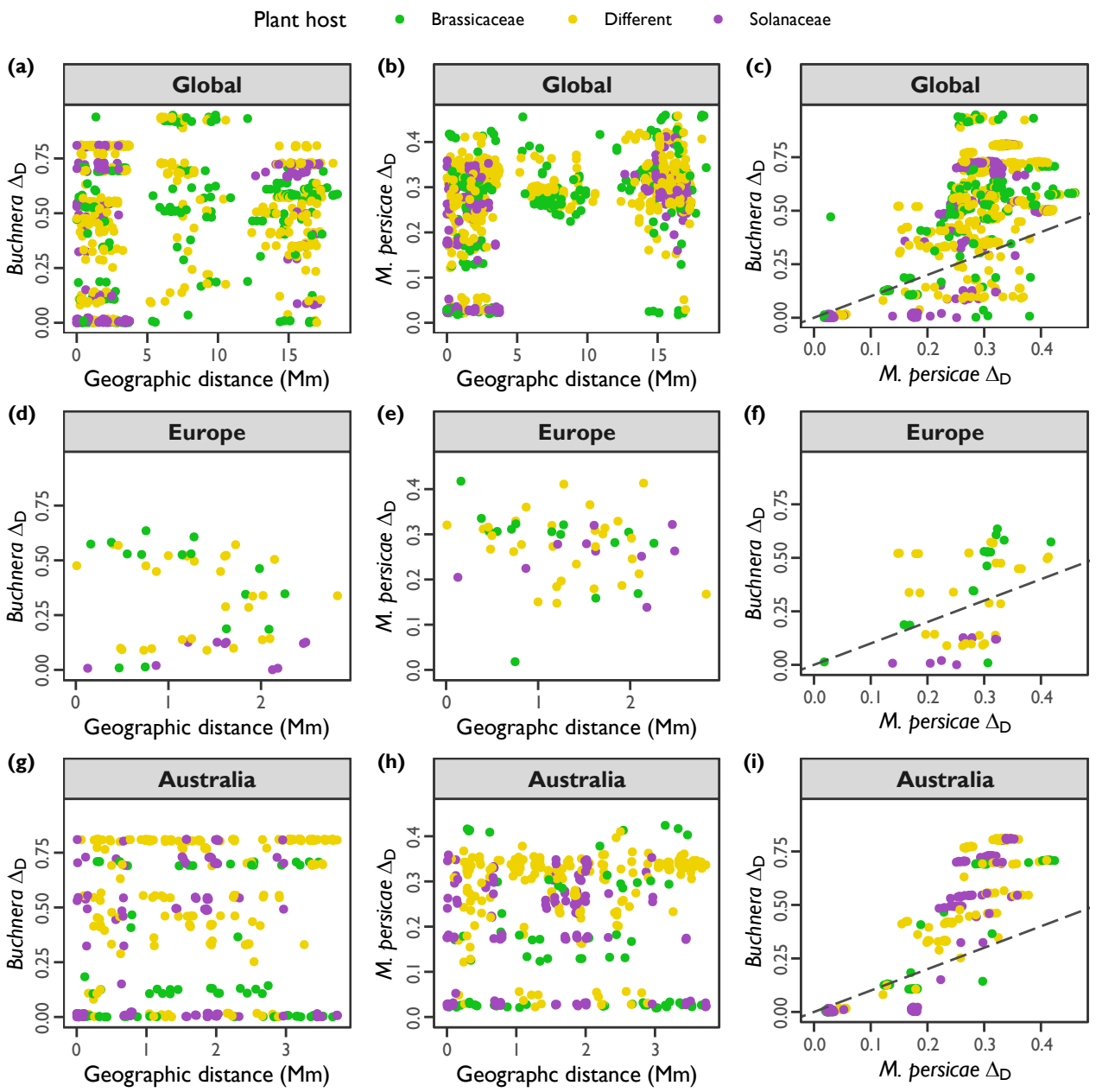

Figure 3. Patterns of pairwise genetic differentiation among samples. In all plots, points represent pairs of samples, colored by host plant (see legend: within Brassicaceae, within Solanaceae, or between 'different' plant families). Rows represent different partitions of our dataset: (a–c) global; (d–f) Europe; (g–i) Australia. Columns represent different comparisons of genetic differentiation: (a, d, g) between *Buchnera* samples (*y*-axis) as a function of geographic distance in megameters (*x*-axis); (c, e, h) between *M. persicae* samples (*y*-axis) as a function of geographic distance in megameters (*x*-axis); (c, f, i) between *Buchnera* samples (*y*-axis) as a function of genetic differentiation between *M. persicae* samples (*x*-axis), and hypothetical 1:1 relationship with dashed lines.

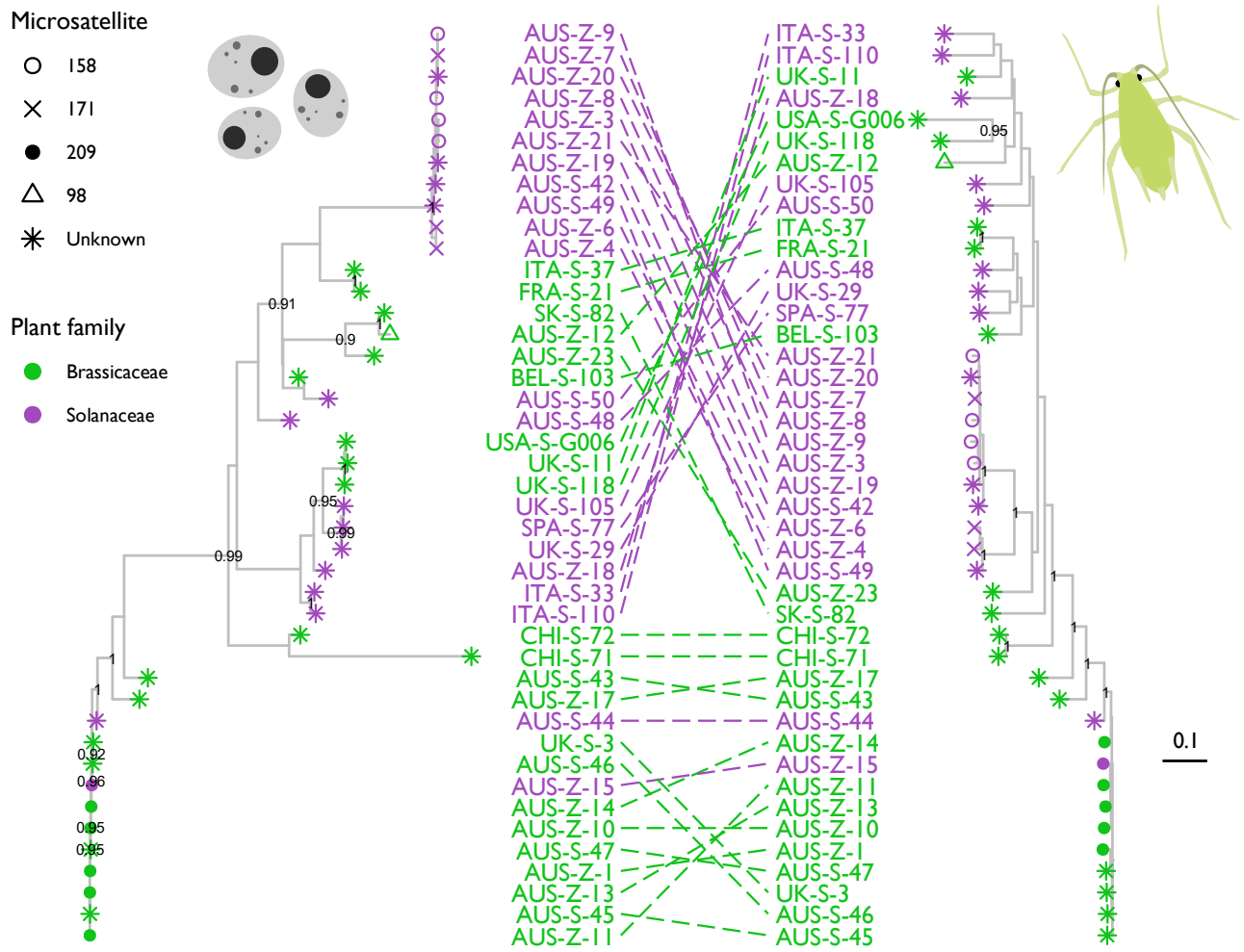

Figure 4. Aligned phylogenetic trees for *Buchnera* and aphid host genomes in *Myzus persicae*. The *Buchnera* tree is on the left, and the aphid host tree is on the right. Points on tree tips and sample labels are coloured by host plant; where known, post-hoc microsatellite clonal classification is depicted by point shapes (see legend). Node support is indicated as the proportion of 100 bootstrap replicates, with values >0.9 presented. The scale bar indicates the relative distance.

We did not find support for plant host specialization. Residual variation in pairwise Δ_D was not significantly different among plant hosts at the global scale, within Europe, or within Australia (Figure 5). The exception was in the European dataset, where *Buchnera* from Solanaceae exhibited lower residual Δ_D relative to within Brassicaecae or different plant family comparisons, but this is likely driven by spurious effects due to small sample size (n = 10 pairs). Notably, the residual variation in Δ_D values was consistently distributed around 0 for all host plants, suggesting that there was no additional information in pairwise Δ_D values in a focal organism that could be explained after controlling for pairwise Δ_D values in its partner organism and geographic distance.

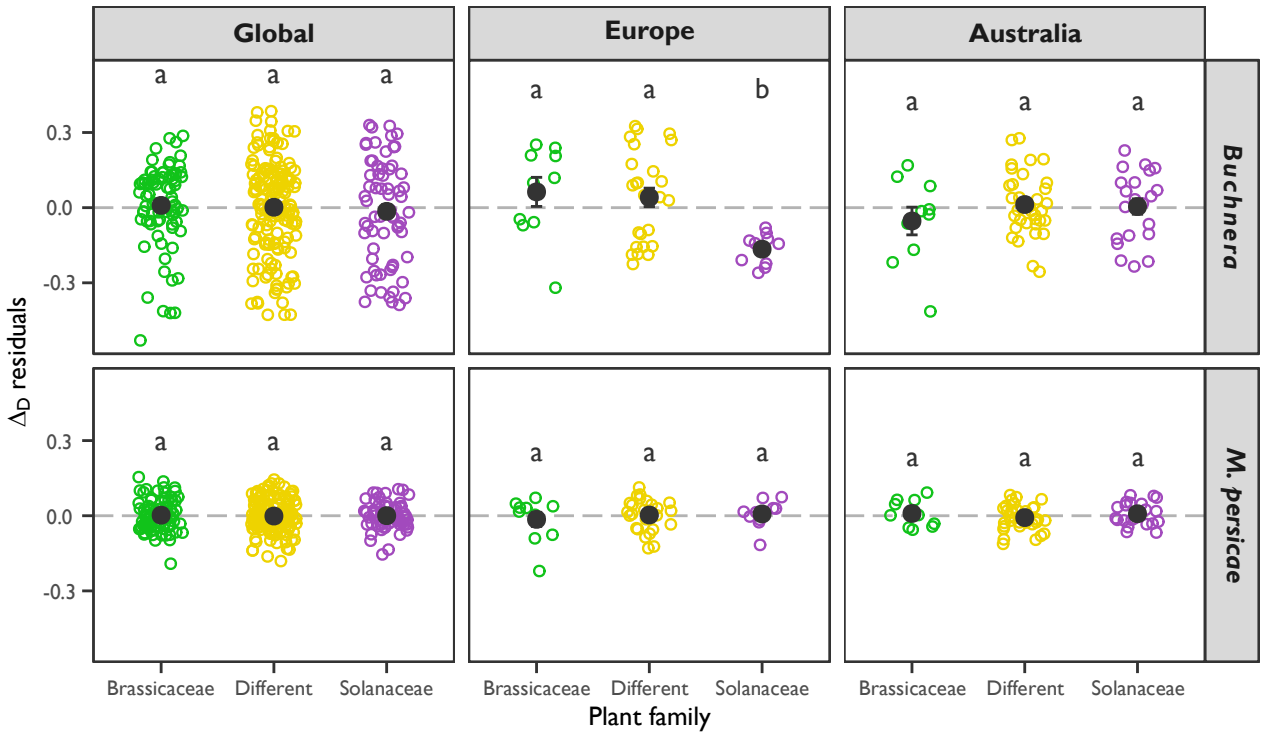

Figure 5. Genetic differentiation between samples of *Buchnera* or *M. persicae* from the same host plant family (within Brassicaceae or Solanaceae) or 'different' host plant (Brassicaceae vs. Solanaceae). Plots depict residual variation in pairwise genetic differentiation (*y*-axis) as a function of host plant (*x*-axis). Open points represent pairs of samples, and large filled points represent the mean with standard error bars. Lowercase letters denote a significant difference within each group. The dashed grey line delimits a mean of zero. Each panel represents a different combination of organism (*Buchnera* or *M. persicae*, in rows) and dataset partition (global, European, or Australian, in columns).

Mutations in *Buchnera* protein-coding regions

We recovered 958 SNPs found in protein-coding regions in the *Buchnera* genome: 448 non-synonymous (446 missense and 2 stop) mutations and 510 synonymous mutations. Within aphid clones, we observed very strong positive correlations between the SFS of non-synonymous and synonymous *Buchnera* mutations (Supplementary Figure S2). Pearson's correlation, *r*, had a mean of 0.98 and a range of 0.87 to 0.99 across all samples, indicating the relative allele frequency distributions of both mutation classes are very similar. However, there was a tendency for a slightly higher number of synonymous mutations relative to non-synonymous mutations (Supplementary Figure S3). Across all samples, the mean number of non-synonymous to synonymous mutations was 0.91:1, with a range of 0.62:1 and 1.24:1. There was a clear structuring of the number of mutations, and the non-synonymous and synonymous SFS, across the *Buchnera* genetic distance tree (Figure 6).

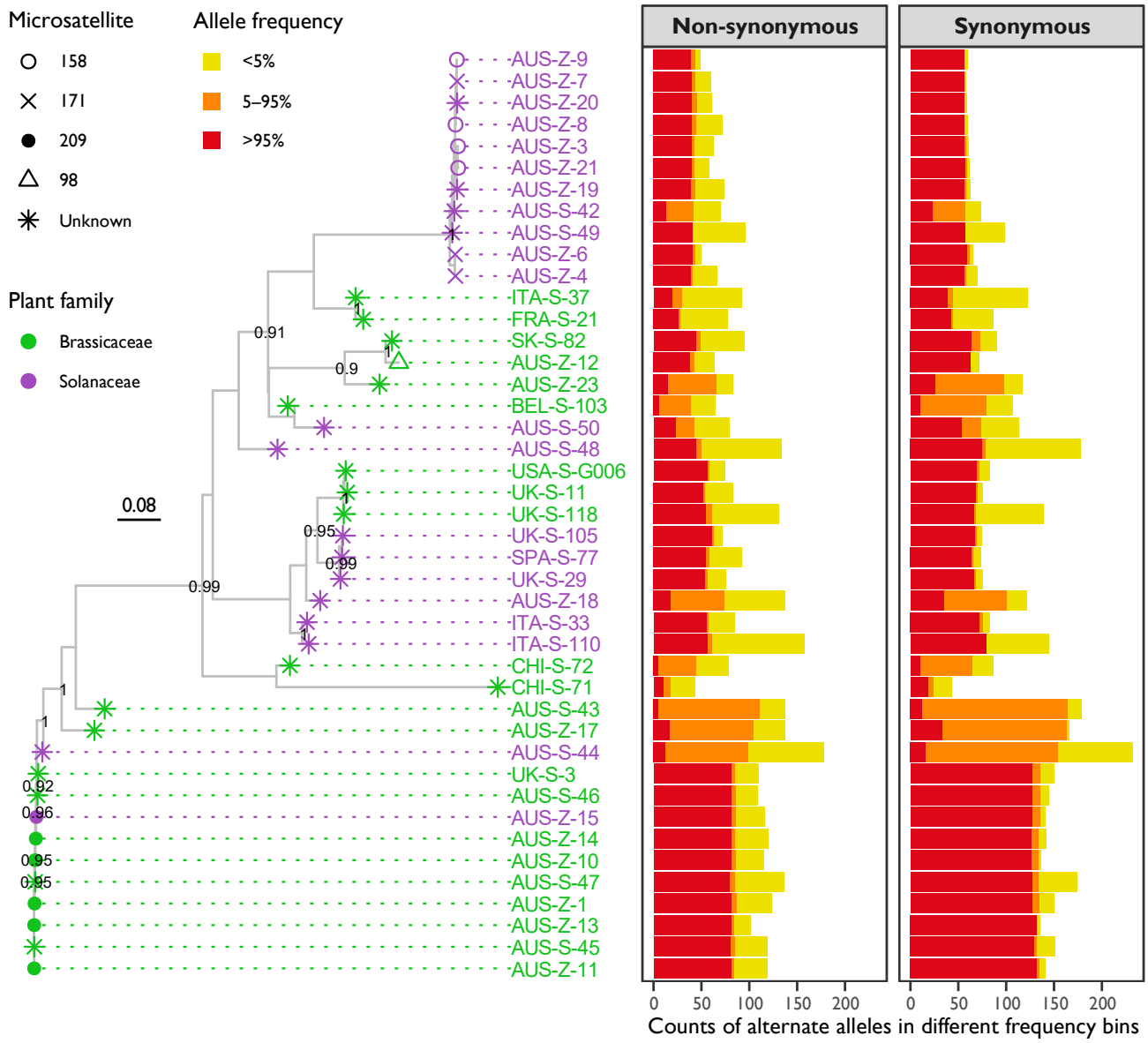

Figure 6. Distribution of non-synonymous and synonymous mutations along the *Buchnera* phylogenetic tree. Points on the trees tips and sample labels are colored by host plant; where known, a post-hoc microsatellite clonal classification is depicted by point shapes (see legend). Node support is indicated as the proportion of 100 bootstrap replicates, with values >0.9 presented. The scale bar indicates the relative distance. Panels depict the number of mutations (*x*-axis) per sample (*y*-axis) for non-synonymous (left) and synonymous (right) sites. Bars are portioned and colored by relative counts of different alternate allele frequency bins (<5%, 5–95%, and >95%, see legend). Classification of non-synonymous versus synonymous mutations is relative to the reference genome, GenBank Accession CP002697.1.

We tested for enrichment or diminishment of non-synonymous mutations in 68 different functional pathways across *Buchnera* samples. Following a Bonferroni correction, and significance at a threshold of α = 0.05/68 =

0.0007, only one pathway was significant: 'homologous recombination', with an odds ratio of 3.5 (p = 0.0004), indicating an enrichment of non-synonymous mutations. If we considered significance at an uncorrected threshold of α = 0.05, two more pathways were significant: 'D-amino acid metabolism', odds ratio of 0.14 (p =0.04), a diminishment of non-synonymous mutations; and 'Glutathione metabolism', odds ratio of 8.1 (p = 0.03), an enrichment of non-synonymous mutations.

DISCUSSION

Macroevolutionary studies have clearly shown that *Buchnera* and their aphid hosts exhibit significant covariance in their evolutionary histories (Chen et al., 2017; Chong et al., 2019; Jousselin et al., 2009; Nováková et al., 2013). But these studies among species shed little light on the ecoevolutionary processes within species, which require a focus on microevolutionary scales. This present study bridges an important knowledge gap by examining the genomic variation and covariation in 43 clonal lineages of *M. persicae*. Our findings indicate that multiple genetically different strains of *Buchnera* may coexist as a 'population' within their clonal *M. persicae* host. This parallels very recent work that has also identified coexisting *Buchnera* strains in four different clonal lineages of Russian wheat aphid, *Diuraphis noxia* (Burger, Nicolis, & Botha, 2023). Limited plasticity of *Buchnera*'s genetic regulatory capacity (Moran et al., 2003; Neiers, Saliou, Briand, & Robichon, 2021; Wilcox, Dunbar, Wolfinger, & Moran, 2003) suggests that physiological effects of *Buchnera* on their aphid host is likely via genetically encoded variants. In the model pea aphid, *Acyrthosiphum pisum*, different alleles at the *ibpA* (heat shock protein) genes among different *Buchnera* strains affect the performance of their host (within-host selection) and clonal lineage (among-host selection) under different thermal conditions (Dunbar et al., 2007; Perreau et al., 2021). Specific genetic variants have also been linked to performance of clonal lineages under histidine depletion in *A. pisum* (Chung et al., 2020). The density of *Buchnera* has largely been the focus of within-species investigations due to the importance of these endosymbionts in nutrient provisioning (Whittle, Barreaux, Bonsall, Ponton, & English, 2021), but the ecoevolutionary consequences of genetic polymorphisms within aphid hosts is virtually unknown outside the model *A. pisum*. Our results from *M. persicae* suggest that most *Buchnera* polymorphisms are not adaptive and that microevolutionary trajectories of *Buchnera* may simply 'drift' with that of their aphid hosts.

We found no evidence that genetic variation in *Buchnera*, or their *M. persicae* host, was structured relative to the host plant families Brassicaceae and Solanaceae (excluding tobacco which was not considered here). The *Buchnera* genome from *M. persicae* has retained genes that may be important in the polyphagous ecology of this species (Jiang et al., 2013), yet few studies have directly examined the role of *Buchnera* in plant host adaptation in this aphid species. In the tobacco specialized subspecies, *M. p. nicotianae*, plant host adaptation appears to be completely under control of the aphid host (Jiang et al., 2013; Singh et al., 2020). Genetic variation in *Buchnera*

might have little impact on the utilisation of Brassicaceae and (non-tobacco) Solanaceae, at least as measured in this study. Our more intensive sampling of invasive Australian clones did recover two genetic groups of closely related aphid clones associated with either Solanaceae or Brassicacea, a pattern that may reflect bottlenecks in *M. persicae* following invasion into Australia (Yang et al., 2023) or perhaps selective sweeps of clones carrying local insecticide resistance mechanisms (de Little et al., 2017; Umina et al., 2014).

Our analysis of mutations in protein-coding regions of the *Buchnera* genome are generally consistent with genomic decay (Silva, Latorre, & Moya, 2001; Wernegreen & Moran, 1999). We suspect that neutral processes predominate the microevolutionary changes in *Buchnera* from *M. persicae*, based on our results indicating an approximate 1:1 ratio of non-synonymous to synonymous mutations (mean of 0.91:1) and similar SFS between these mutation classes. Although the exact number of mutations identified depends on the sequence divergence of a focal *Buchnera* genome from the reference genome sequence, relative patterns of mutation classes tended to be consistent across *M. persicae* clones. Most non-synonymous mutations are expected to be deleterious and can be eliminated by efficient selection within and among clones (Rispe & Moran, 2000; Wernegreen & Moran, 1999). This should bring down the ratio of non-synonymous to synonymous mutations and keep deleterious mutations at low frequencies. However, most (non-synonymous or synonymous) mutations in protein-coding regions in our *Buchnera* analysis were near or at fixation within clonal populations. These results are more consistent with a high drift scenario that drives mutations (irrespective of functional effect) to high frequency, which might be expected if the effective population size of *Buchnera* is small, selection is weak, and mutation rates are high (Bourguignon et al., 2020; Wernegreen, 2015, 2017).

Non-synonymous mutations were generally found at equivalent abundances across different functional pathways. After false positive correction, only the homologous recombination pathway was significant, and enriched for non-synonymous mutations. Homologous recombination is part of the DNA repair process, which has undergone considerable degradation in the *Buchnera* genome as it transitioned to an obligate endosymbiont (Shigenobu et al., 2000). This observation does not align with our expectations about enrichment in core cellular, core mutualism or ecological relevant pathways, nor with the expectation of neutral evolution. Without false positive correction, we also found that non-synonymous mutations were detected as being (a) diminished in D-amino acid metabolism genes, and (b) enriched in glutathione metabolism genes. Diminished non-synonymous mutations in D-amino acid metabolism may align with our core cellular pathway hypothesis. D-amino acids are used to synthesize peptidoglycan and build the cell wall. *Buchnera* from the aphid tribe Macrosiphini (which includes *M. persicae*) contribute to building their own cell wall (Smith et al., 2022). Enriched non-synonymous mutations in glutathione metabolism might align with our hypothesis of ecologically relevant pathways. Prior work has suggested that glutathione metabolism in *Buchnera* may play a role in acquiring inorganic sulfur from plant phloem (Douglas, 1988; Jiang et al., 2013). Glutathione as a substrate for glutathione-S-transferases has also been reported as important for plant xenobiotic metabolism in *M. persicae*

(Francis, Vanhaelen, & Haubruge, 2005), and perhaps for resistance to synthetic insecticides (Bass & Field, 2011). This suggests a possible adaptive role of glutathione metabolism in *Buchnera* supporting polyphagy and (or) insecticide detoxification in its *M. persicae* host. However, such conjectures remain speculative and neutral processes seem to predominate the genome dynamics of *Buchnera* sampled in this study from *M. persicae*.

Lack of isolation-by-distance between pairs of clonal samples highlights the dispersive and invasive nature of *M. persicae* that has spread clones across the globe. In this study, we were specifically interested in whether pairs of clones from disparate locations tend to be more genetically dissimilar than clonal samples at more proximate locations. This contrasted the goals of other genetic studies using microsatellites (Margaritopoulos et al., 2009) or genomic data (Singh et al., 2021) focusing on the beta diversity of clonal lineages among different geographic locations. We show that genetic differences between pairs of clonal *M. persicae* hosts or their *Buchnera* does not scale with geographic distance, irrespective of whether we considered the global dataset or partitions of the European or Australian clones. Indeed, we found samples in Australia that were genetically very similar to those found in Europe. This indicates that few post-invasion genetic changes have occurred in *M. persicae* hosts or their *Buchnera*.

In conclusion, our study provides a novel perspective on *Buchnera*–aphid host coevolution in *M. persicae* by focusing at the microevolutionary scale, both within and among different clones of *M. persicae*. Although our study suggests that *Buchnera* may simply 'drift' with their aphid host, we cannot rule out weak selection on some protein-coding changes. Whilst we largely focused on variation across aphid clones, it is still possible that there are lineage-specific variants in the *Buchnera* genome involved in coadaptation (as mutualists, antagonists, or both) (Bennett & Moran, 2015). Future experimental manipulations of *Buchnera* in different aphid host genetic backgrounds (Perreau et al., 2021) provides interesting prospects to test the ecoevolutionary consequences of genetic interactions in the *Buchnera*–aphid host symbiosis.

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DATA AVAILABILITY

All sequencing data generated in this study has been deposited into GenBank, BioProject PRJNA987046, Sequencing Read Archive (SRA) SRR25064204 to SRR25064225. SRA Accessions for all samples used in this study are presented in Table 1, including those sourced from Singh et al. (2021). All scripts and data required to recreate these analyses are stored in a Dryad repository, doi.org/10.5061/dryad.gf1vhhmvz (Thia, 2023).

AUTHOR CONTRIBUTIONS

JAT, KR, AAH and QY designed the research. PAU organized the sourcing of aphid material. QY organized the molecular work and sequencing. JAT led the analyses, with support from AAH, DWZ and KR. JAT wrote the original manuscript. All authors contributed to revisions of the final manuscript.

CONFLICT OF INTERESTS STATEMENT

The authors declare no conflict of interests associated with this work.

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Supplementary Information

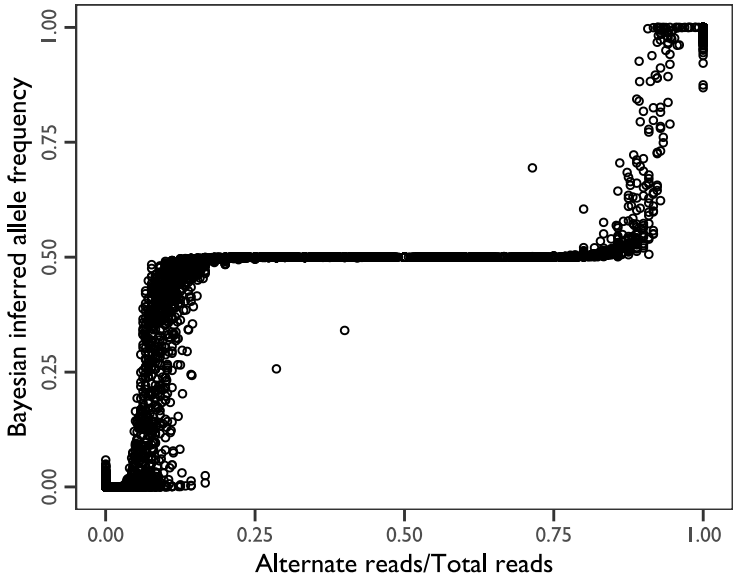

Figure S1. Bayesian inferred individual allele frequencies (*y*-axis) in aphid host samples as a function of alternate read proportions (*x*-axis) as the number of alternate reads over total read depth.

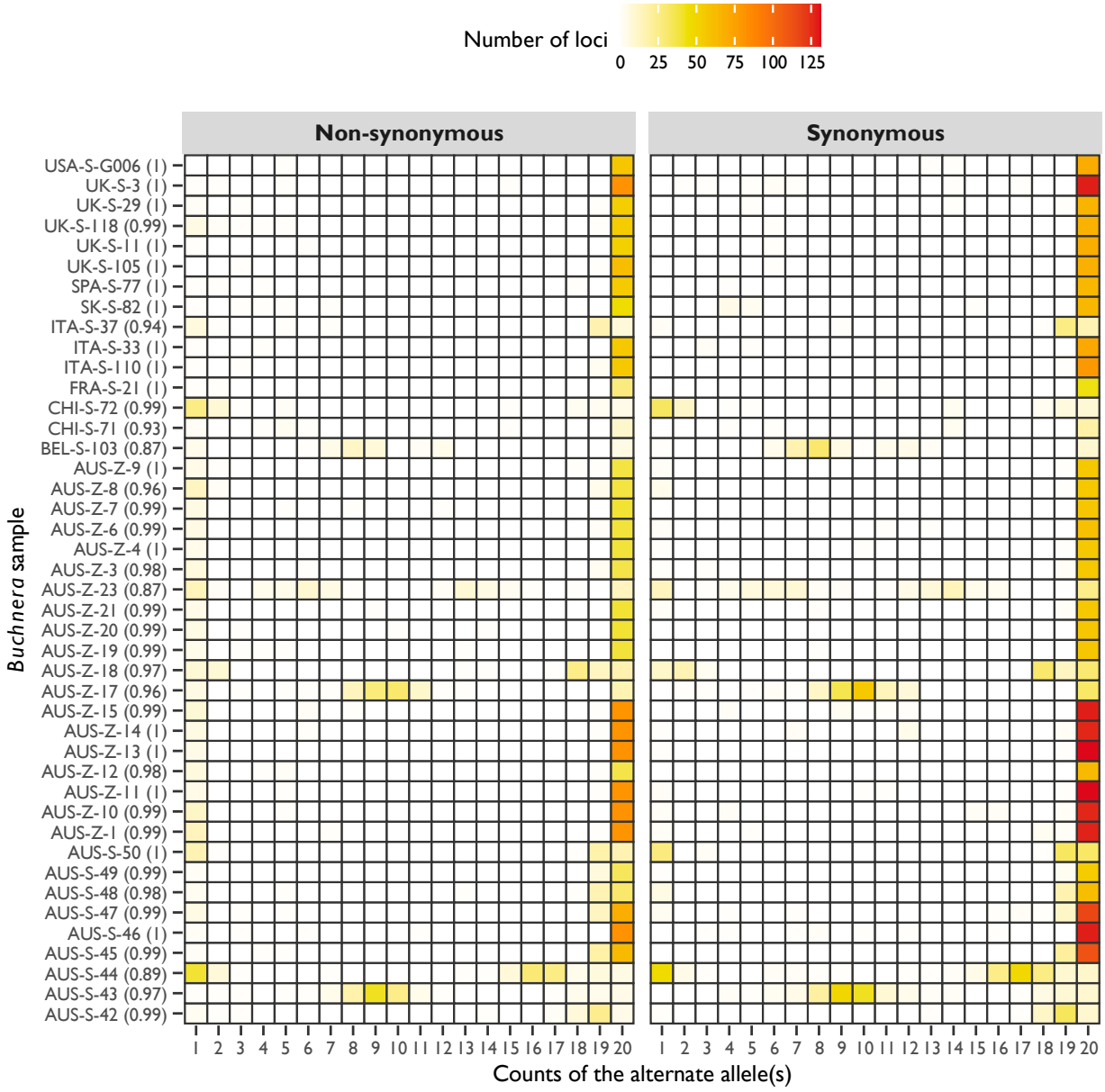

Figure S2. Site frequency spectra (SFS) for non-synonymous and synonymous mutations in the *Buchnera* genome. Counts of the alternate allele (*x*-axis) have been downward projected to bins of 1 to 20 for each *Buchnera* sample (*y*-axis). Values in parentheses next to each sample name indicates the Pearson correlation coefficient between non-synonymous and synonymous mutations. Cells are coloured based on the number of loci for each sample and allele count bin (see legend).

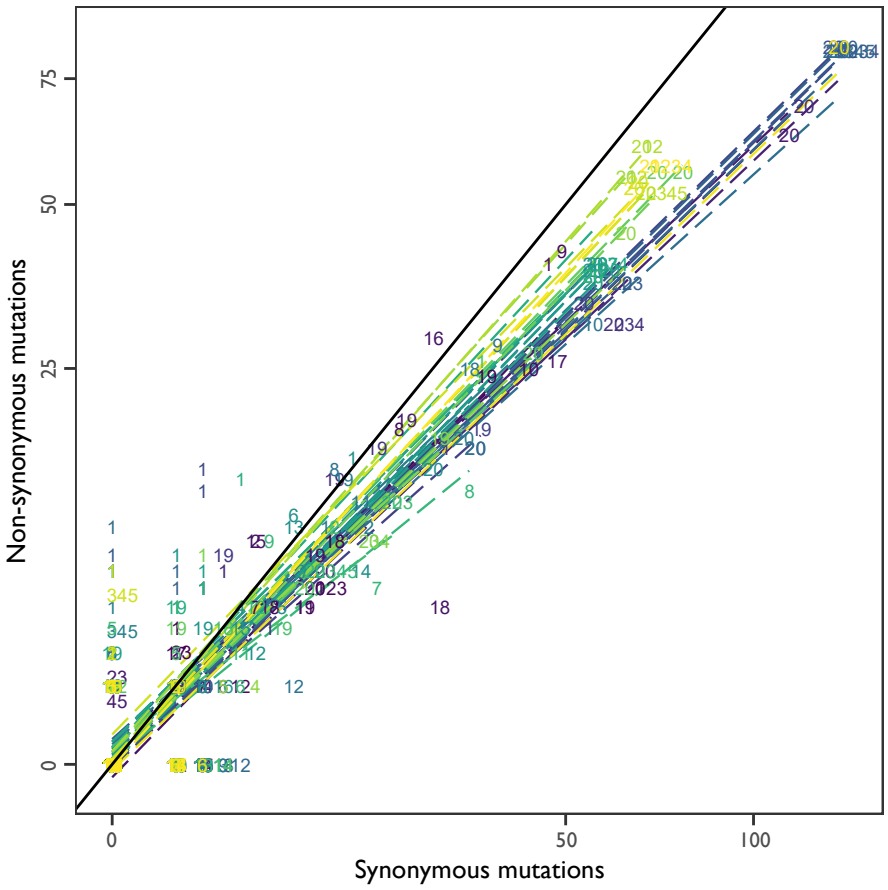

Figure S3. Correlations between the site frequency spectra (SFS) of non-synonymous and synonymous mutations in the *Buchnera* genome. The number of non-synonymous mutations (*y*-axis) is presented as a function of the number of synonymous mutations (*x*-axis). Numbers represent different bins of alternate allele counts (downward projected to fit in the range of 1 to 20), with dashed lines delimiting the linear relationship between mutation classes (non-synonymous vs synonymous). Numbers and dashed lines are coloured by different *Buchnera* samples. The solid black indicates a 1:1 relationship, that is, the number of non-synonymous and non-synonymous mutations for a given allele count bin are equal.

Table S1. Sample information for *Myzus persicae* clones. Microsatellite assignments (Msat) are based on nomenclature from previous studies conducted on Australian *M. persicae*. Locations for some samples are approximate and based on local townships near where they were collected; these are marked with an asterisk (*).

Source	Plant family	Continent	Country	Sample	Year collected	Plant host	Msat	Latitude	Longitude	SRA Accession
Singh et al. 2021	Brassicaceae	Asia	China	CHI-S-71	2005	Oilseed rape		26.9	119.5	SRR13326401
		Asia	China	CHI-S-72	2017	Oilseed rape		26.9	119.5	SRR13326400
		Asia	South Korea	SK-S-82*	Unknown	Cabbage		35.8	129.2	SRR13326389
		Australia	Australia	AUS-S-43*	2017	Oilseed rape		−36.3	141.6	SRR13326432
		Australia	Australia	AUS-S-45*	2018	Oilseed rape		−33.5	120.6	SRR13326430
		Australia	Australia	AUS-S-46*	2017	Broccoli		−27.7	151.6	SRR13326429
		Australia	Australia	AUS-S-47*	2017	Oilseed rape		−35.5	145.3	SRR13326428
		Europe	Belarus	BEL-S-103*	2018	Cabbage		53.9	27.5	SRR13326480
		Europe	France	FRA-S-21*	2015	Oilseed rape		46.7	0.3	SRR13326456
		Europe	Italy	ITA-S-37*	2015	Oilseed rape		45	9.6	SRR13326439
		Europe	UK	UK-S-11*	2018	Cabbage		50.2	−5.1	SRR13326483
		Europe	UK	UK-S-118*	1997	Brussel sprout		53.1	−0.2	SRR13326475
		Europe	UK	UK-S-3*	2004	Oilseed rape		53.2	−2.6	SRR13326457
		North America	USA	USA-S-G006*	2003	Pepper		42.9	−77	SRR3466613

	Solanaceae	Australia	Australia	AUS-S-42*	2017	Pepper		−24.9	152.3	SRR13326433
		Australia	Australia	AUS-S-44*	2017	Tomato		−36.8	144.3	SRR13326431
		Australia	Australia	AUS-S-48*	2014	Eggplant		−34.7	138.6	SRR13326427
		Australia	Australia	AUS-S-49*	2014	Pepper		−34.7	138.6	SRR13326426
		Australia	Australia	AUS-S-50*	2002	Pepper		−36.4	145.4	SRR13326425
		Europe	Italy	ITA-S-110*	unknown	Potato		39	16.3	SRR10199541
		Europe	Italy	ITA-S-33*	1996	Tomato		45	9.7	SRR13326443
		Europe	Spain	SPA-S-77*	unknown	Pepper		37.8	−1.1	SRR13326395
		Europe	UK	UK-S-105*	2000	Potato		56.7	−4.2	SRR10199546
		Europe	UK	UK-S-29*	2015	Potato		57.4	−2.4	SRR13326448
This study	Brassicaceae	Australia	Australia	AUS-Z-1	2020	Oilseed rape	209	−28.7	150	SRR25064225
		Australia	Australia	AUS-Z-10	2020	Oilseed rape	209	−29.2	115.5	SRR25064204
		Australia	Australia	AUS-Z-11	2021	Oilseed rape	209	−31.9	116.7	SRR25064223
		Australia	Australia	AUS-Z-12	2019	Oilseed rape	98	−34.5	117.4	SRR25064222
		Australia	Australia	AUS-Z-13	2018	Oilseed rape	209	−33.7	120.8	SRR25064221
		Australia	Australia	AUS-Z-14	2021	Cabbage	209	−27.5	153	SRR25064220
		Australia	Australia	AUS-Z-17	2019	Oilseed rape		−35.9	142.8	SRR25064218
		Australia	Australia	AUS-Z-23	2019	Oilseed rape		−41.8	147.5	SRR25064211

	Solanaceae	Australia	Australia	AUS-Z-15	2021	Tamarillo	209	−37.7	145	SRR25064219
		Australia	Australia	AUS-Z-18	2021	Tamarillo		−37.6	145.2	SRR25064217
		Australia	Australia	AUS-Z-19	2021	Tomato		−37.7	145.1	SRR25064216
		Australia	Australia	AUS-Z-20	2020	Chili		−19.7	147.4	SRR25064215
		Australia	Australia	AUS-Z-21	2017	Capsicum	158	−25	152.3	SRR25064214
		Australia	Australia	AUS-Z-3	2017	Capsicum	158	−25	152.3	SRR25064213
		Australia	Australia	AUS-Z-4	2021	Habanero	171	−19.5	147.3	SRR25064210
		Australia	Australia	AUS-Z-6	2020	Chilli	171	−19.7	147.4	SRR25064208
		Australia	Australia	AUS-Z-7	2020	Chilli	171	−19.7	147.4	SRR25064207
		Australia	Australia	AUS-Z-8	2021	Eggplant	158	−20	148.2	SRR25064206
		Australia	Australia	AUS-Z-9	2019	Capsicum	158	−29	114.8	SRR25064205