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Evolution of genomic variation in the burrowing owl in response to recent colonization of urban areas

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When a species successfully colonizes an urban habitat it can be expected that its population rapidly adapts to the new environment but also experiences demographic perturbations. It is, therefore, essential to gain an understanding of the population structure and the demographic history of the urban and neighbouring rural populations before studying adaptation at the genome level. Here, we investigate populations of the burrowing owl (*Athene cunicularia*), a species that colonized South American cities just a few decades ago. We assembled a high-quality genome of the burrowing owl and re-sequenced 137 owls from three urban–rural population pairs at 17-fold median sequencing coverage per individual. Our data indicate that each city was independently colonized by a limited number of founders and that restricted gene flow occurred between neighbouring urban and rural populations, but not between urban populations of different cities. Using long-range linkage disequilibrium statistics in an approximate Bayesian computation approach, we estimated consistently lower population sizes in the recent past for the urban populations in comparison to the rural ones. The current urban populations all show reduced standing variation in rare single nucleotide polymorphisms (SNPs), but with different subsets of rare SNPs in different cities. This lowers the potential for local adaptation based on rare variants and makes it harder to detect consistent signals of selection in the genome.

1. Introduction

Urbanization is one of the most prevailing causes of habitat transformation and biodiversity loss worldwide [1]. Urbanization typically involves a set of environmental changes including habitat fragmentation, increased temperature, air, noise and light pollution, altered resource availability and reduced predation or parasite pressure [2]. Not all species respond negatively to these transformations, and there are many examples of successful urban colonization. Among birds, urban colonization has been related to intraspecific variation in fear of humans: it has been proposed that urban life selects for individuals with a smaller flight initiation distance upon approach [3,4]. This and other phenotypic changes associated with urbanization [5], combined with the lower predation pressure in urban areas [6], can affect not only the demography but also the dispersal propensity of individuals, with consequences for the dynamics and spatial structure of rural and urban populations.

Colonization of urban habitats by animals and plants is ideal to study recent adaptive and non-adaptive processes at the genome level. The habitat of city centres and suburban areas and their historical development appear to be

similar across a wide geographical range and thus represent repeated natural experiments to study evolution in action [2,7]. Being exposed to a set of environmental changes during urbanization should lead to strong selection in the colonizer, whose signatures should be identifiable locally in the genome [5]. However, urban colonization typically goes hand-in-hand with demographic perturbations such as population bottlenecks or fragmentation, which can lead to similar genome signatures as adaptive processes, although across all loci [2,8]. Studying repeated urban settlements by the same species might help to disentangle random genome-wide demographic effects from local deterministic effects based on selection. While similar selective pressures among different cities could lead to the same selected regions or regulatory pathways in the genome, standing genomic variation (in particular the presence or absence of rare variants) on which selection can act may vary randomly among those cities if they were colonized independently. It is thus important to describe the genomic population structure and to understand the demographic effects on the genome and its consequences on potential adaptive processes. Models of the demographic history of the populations can then be used as null models when scanning for genomic targets of selection.

Urban colonization by birds has occurred on an ecological time scale, dating back more than 150 years (in case of the European blackbird *Turdus merula*; [9]) to only a few decades (e.g. in the dark-eyed junco *Junco hyemalis*; [10] or the monk parakeet *Myiopsitta monachus*; [11]). Because of the short time scale and the short geographical distance between neighbouring urban and rural populations, population structure is expected to be weak. Furthermore, only those genomic characteristics that change sufficiently strongly during such short time scales are potentially informative for elucidating the recent demographic history. Founder effects during the colonization and subsequent inbreeding typically lead to (i) reduced genetic diversity, but also to (ii) increased linkage disequilibrium (LD) between genetic markers, whereby such LD should decay with distance between markers over multiple generations. Recent studies show that population-level genomic sequence data can reveal weak population structures [12] and can be used to extract LD values for any distance class [13].

Here, we analyse the population structure and demographic history of burrowing owls (*Athene cunicularia*) in recently colonized Argentinian cities in comparison to neighbouring rural populations. Burrowing owls, a species typically associated with open grasslands in North and South America, have been reported as breeding birds in South American suburban areas for a few decades [3]. Burrowing owls have been historically associated with fossorial mammals such as prairie dogs (*Cynomys* sp.) in North America or the plains viscachas (*Lagostomus maximus*) in South America, whose burrows are used for nesting [14]. However, the owls of the Southern range evolved the ability to excavate their own burrows for nesting [14], which may have facilitated moving into the urban environment [6]. We do not know when this behaviour first emerged, but today all urban burrowing owls and most rural individuals in our study area excavate their own nests (less than 25% of the rural pairs use burrows of plains viscacha for nesting; M. Carrete 2018, unpublished data). The colonization of urban areas by these owls appears to be quite successful given their relatively high population densities in comparison to rural populations [15]. Reduced

predation pressure has been described as one of the driving forces of this success [6]. Moreover, changes in behavioural traits due to selection or selective immigration have been documented in urban populations. Risk perception—measured as flight initiation distance—is an individually consistent and heritable trait and differs consistently between urban and rural individuals [16,17]. Information from previous studies of urban and rural burrowing owls thus suggests that the species represents a suitable study system for rapid and successful adaptation to the new urban environment.

In this paper, we present a high-quality genome assembly of the burrowing owl and we re-sequenced 137 individuals from three urban–rural population pairs to address the following questions: (i) what is the population structure of urban and rural populations of burrowing owls? We expected a weak structure given the supposedly recent urban colonization and the high dispersal ability of birds; (ii) were the different cities independently colonized, or were they colonized from a single source population that spread across all cities? (iii) what are the contemporary gene flow patterns among neighbouring populations? (iv) does the demographic history differ between the young urban populations and the rural populations? We discuss the implications of our results in terms of our ability to detect local adaptation and signatures of selection in the burrowing owl genome.

2. Materials and methods

(a) Sampling

As part of a long-term study, a population of burrowing owls has been individually marked, monitored and blood-sampled since 2006 in and around Bahia Blanca, Argentina [3,15]. Between 2012 and 2016, breeding burrowing owls have also been sampled in and near two additional Argentinian urban settlements of the pampas, Sierra de la Ventana and Tandil, located 77 and 314 km linear distance from Bahia Blanca, respectively. Breeding habitats of the owls were classified as either rural or urban following the criteria in Carrete & Tella [3] and Reboloto-Ifran *et al.* [4]. ‘Urban nests’ were defined as those located in private and public gardens and along streets usually within 10–100 m of inhabited buildings. ‘Rural nests’ were those found outside the city border in grasslands and pastures of wide-ranging livestock where human presence and activities were minimal. For our study, we defined *a priori* seven sampling sites for the three urban–rural comparisons (figure 1): Bahia Blanca urban 1 and 2 (BB_{1urban}, BB_{2urban}), Bahia Blanca rural (BB_{rural}), Sierra de la Ventana urban (SV_{urban}) and rural (SV_{rural}), Tandil urban (TA_{urban}) and rural (TA_{rural}). From each of these sampling sites, we randomly selected 20 breeding individuals from 2012 to 2016, excluding first-degree relatives, except for SV_{rural} where we only sampled 17 individuals (total $n = 137$ blood samples). For the largest and more intensively monitored city (Bahia Blanca) we sampled 20 individuals from each of two spatially separated suburban areas (BB_{1urban} and BB_{2urban}) to test the robustness of demographic inference based on simulations of 20 individuals (see below). Both urban sites were matched with BB_{rural}. Below, we refer to each sample site as a ‘population’. For the reference genome, we used an additional blood sample from an adult male from the rural area around Bahia Blanca. All blood samples were stored in ethanol before analysis in the laboratory.

(b) Genome assembly and annotation

We extracted DNA from the reference male blood sample using a standard phenol–chloroform protocol. The sample was used to

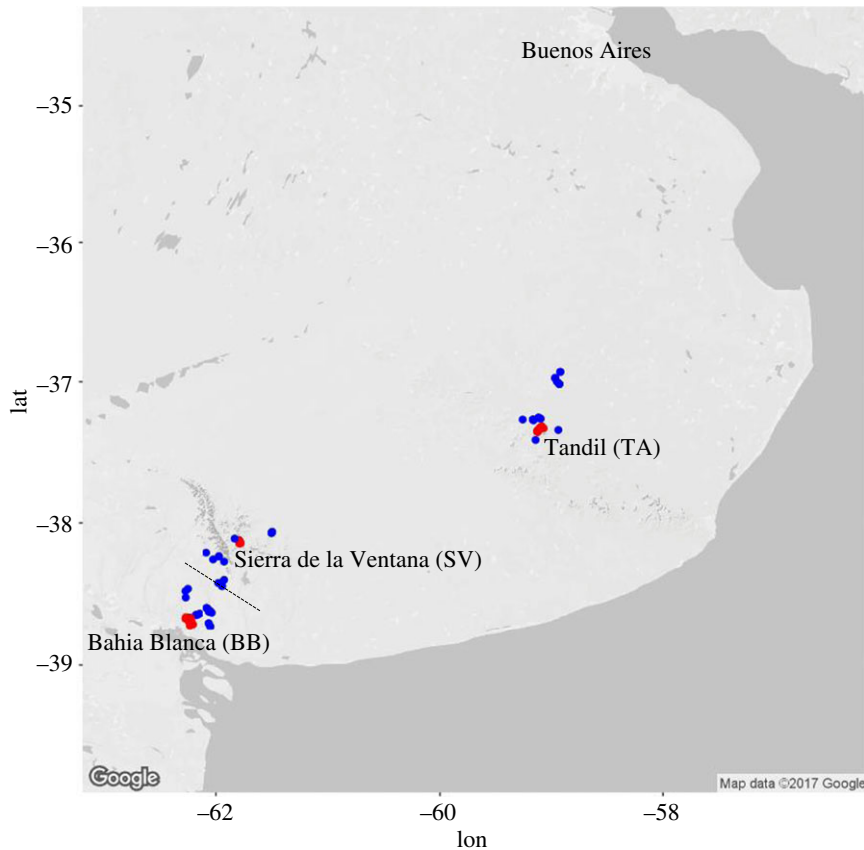


Figure 1. Sampling locations of urban sites (red) and rural sites (blue). The dotted line indicates the division between the two rural sampling sites BB_{rural} and SV_{rural} halfway between the cities.

construct a 500 bp insert Illumina Truseq2 paired-end sequencing library, a Nextera gel-free mate-pair library (insert size peak at 2500–3500 bp) and a 10 000 bp Nextera size-selected mate-pair library. DNA sequencing was performed using a 2×100 bp sequencing protocol on an Illumina HiSeq2500 system at the Sequencing Core Facility of the MPI for Molecular Genetics in Berlin.

After adaptor removal and quality clipping as well as removal of PCR-duplicated read pairs, we assembled the sequencing reads using the IDBA assembler [18] followed by the Newbler v. 3 assembler (Roche Diagnostics, Basel, Switzerland). This hybrid assembly strategy is described in more detail in the online electronic supplementary material, text S1. We obtained a total sequencing coverage of about 46-fold.

We annotated protein-coding sequences by alignment of all avian protein sequences of the NCBI protein database (date: 2015-09-22; 1 786 861 proteins) against the burrowing owl genome using SPALN v. 2.1.2 [19].

(c) Sequencing, reference mapping and single nucleotide polymorphism calling of urban and rural individuals

We extracted DNA from all blood samples from the urban and rural populations with the Blood QuickPure kit (Macherey-Nagel) applying a pre-digestion with Proteinase K in Digsol buffer. All 137 birds were individually sequenced with the Illumina HiSeq 2500 technique using a 200- to 300 bp insert paired-end library with 125 bp read length at the Sequencing Core Facility of the MPI for Molecular Genetics in Berlin.

For each individual, we mapped reads against the reference genome using BOWTIE2 [20]. We called variants using the GATK HaplotypeCaller in gvcf mode and assigned individual

genotypes by a joint genotype calling of all samples [21]. The single nucleotide polymorphisms (SNPs) were then quality-filtered following fixed rules from the GATK best practices recommendations [21]. Additionally, to avoid SNP calls from mis-assembled paralogous genome regions, SNPs were only included if read depth was smaller than the mean coverage plus five standard deviations across all SNPs. For subsequent analyses, we excluded Z-chromosomal SNPs, SNPs with minor allele count of one (singletons) and SNPs with more than 12 missing genotypes across the 137 individuals.

(d) Data analysis

For each individual, we calculated overall heterozygosity (% of all SNPs that are heterozygous) using vcfTools [22]. The same tool was used to count the total number of SNPs and to calculate allele frequencies in each population. The expected number of shared and non-shared SNPs for urban–urban population pairs under random sampling was estimated by permuting the individuals between the populations 20 times and averaging the resulting SNP numbers. We use these metrics to characterize the colonization history, in particular to assess founder effects.

To assess population structure, we calculated F_{ST} values [23] between all population pairs and performed a principal components analysis (PCA) on the genotypes of all individuals using the R package SNPRelate [24,25]. We used a subset of 2 292 644 SNPs, such that they showed a composite genotypic LD of less than 0.5 within windows of 50 kb to avoid the influence of linked SNP clusters on these analyses. We tested the significance of F_{ST} values by randomly permuting individuals between the populations 1000 times and comparing the observed F_{ST} value with the simulated F_{ST} values. The between-population genetic variance (as a proportion of the total variance) and its significance were estimated in an analysis of molecular variance

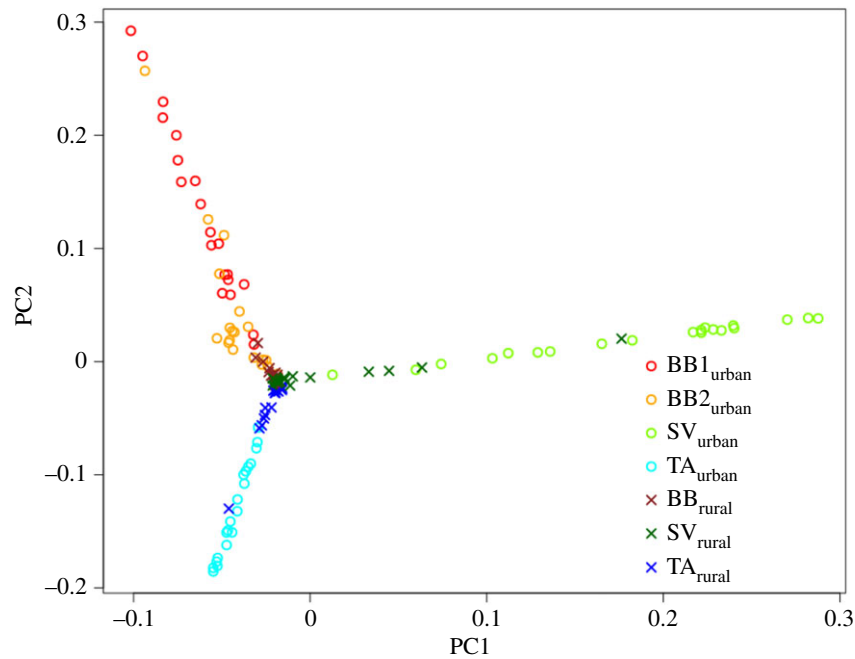


Figure 2. All individuals plotted on the first two principal components of a PCA on SNP genotypes (see Materials and methods). PC1 accounts for 1.6% and PC2 for 1.4% of the total variance.

(AMOVA) and a distance-based redundancy analysis (dbRDA) framework using the R packages *pegas* and *vegan*, respectively [26,27]. For both methods, we used the proportion of alleles that differ between two individuals as a measure of their genetic distance. The dbRDA analysis tests population differentiation after accounting for the effect of geographical distance (longitude and latitude effects). In addition, we explored population structure by a discriminant analysis of principal components (DAPC) using the R package *adegenet* [28]. To avoid overfitting with too many PCs, we determined the optimal number of PCs based on the difference between the probability of reclassification into the pre-specified populations and the probability of reclassification into randomly permuted clusters ('a-scores'; electronic supplementary material, figure S1). The optimal number (highest a-score) was 24 PCs, accounting for 26% of the total genetic variance. In the cluster analyses, individuals of a given population that are assigned to a neighbouring population indicate contemporary dispersal.

Within each population, we tested for 'isolation-by-distance' using Mantel tests between identity-by-state values (calculated using *SNPRelate*) and geodesic distances (calculated using the R package *geosphere*; [29]) implemented in the R package *ecodist* [30]. We further tested the combined longitude and latitude effect at different geographical scales in a dbRDA approach (see above). We also calculated the genetic distance of urban individuals to rural ones as the Euclidian distance from the position of the individual on the PCA plot (see above and figure 2) to the centre of all rural birds (defined as the median $PC1 = -0.019$ and the median $PC2 = -0.017$ of the rural individuals). We then plotted these genetic distances on the city map to assess—by visual inspection—whether the city area was sequentially colonized by founders.

We used an approximate Bayesian computation (ABC) method to estimate ancestral dynamics of effective population sizes (N_e) within each population. First, we simulated 200 000 datasets of 20 individuals using the software package *PopSizeABC* [13] and the coalescent-based simulator *scrm* [31]. We simulated 20 Mb-long sequences assuming a mutation rate of 4×10^{-9} and a recombination rate of 2×10^{-8} . We chose those values as representative for the unknown rates in the burrowing owl because they lie between the genome-wide average values for chicken and

passerines [32–35]. We allowed effective population size to change randomly by a factor of 10 between 32 and 316 228 individuals at 21 time points between 3 and 500 generations before the present.

For each simulated dataset, we then extracted the allele frequency spectrum (AFS) and average genotypic LD values of 20 distance bins ranging from 50 kb to 17 Mb, whereby we excluded SNPs with minor allele frequency less than 0.15. We included long-range LD values to estimate recent population sizes because theory predicts that LD between markers of more than 10 Mb distance on chromosomes with a recombination rate of 2 cM Mb^{-1} is affected by the population size 2.5 generations ago [13,36]. Second, we extracted the observed AFS and LD values from SNP data of the 16 scaffolds that were longer than 20 Mb, representing 79% of the assembled genome. Third, we compared the simulated summary statistics with the observed ones to identify the most similar simulations using the R package *abc* [37]. These simulations were selected with the simple rejection method and an acceptance rate of 0.00005. We plotted N_e over time assuming an average generation time of 2.5 years. Following the calculations of Boitard *et al.* [13], the prediction error for 2000 random samples of the 200 000 simulations was around 0.33 for all time intervals. This indicates that the average difference between true and estimated population sizes is three times smaller than if estimated with the prior distribution of population sizes, resulting in a reasonable power to distinguish demographic histories (electronic supplementary material, figure S2).

3. Results

(a) Genome assembly, individual sequencing and single nucleotide polymorphism calling

Our assembly of the burrowing owl (based on one adult male from the rural surrounding of Bahia Blanca) comprised 1144 Mb in 34 184 contigs with an N50 length of 64.1 kb. Scaffolding and splitting potential mis-assemblies resulted in scaffold N50 length of about 6.4 Mb (in total 1104 scaffolds,

Table 1. Number of SNPs, heterozygosity, geographical distance between individuals and tests for isolation-by-distance.

	no. SNPs	heterozygosity (mean \pm s.d.)	mean geographical distance (metre \pm s.d.)	Pearson correlation coefficient (95% CI) ^a
BB1 _{urban} ^b	7 336 788	0.110 \pm 0.013	1287 \pm 815	−0.315 (−0.428 to −0.234)
BB2 _{urban} ^b	7 605 854	0.111 \pm 0.009	1918 \pm 1218	−0.271 (−0.343 to −0.193)
SV _{urban}	6 561 678	0.114 \pm 0.004	1090 \pm 829	−0.119 (−0.245 to −0.012)
TA _{urban}	7 083 000	0.114 \pm 0.003	1991 \pm 1529	−0.280 (−0.348 to −0.212)
BB _{rural}	7 916 698	0.111 \pm 0.004	12 469 \pm 8408	−0.292 (−0.358 to −0.193)
SV _{rural}	7 478 491	0.116 \pm 0.002	28 435 \pm 20 168	0.050 (−0.037 to 0.132)
TA _{rural}	7 798 361	0.111 \pm 0.009	24 244 \pm 16 568	−0.312 (−0.357 to −0.271)

^aMantel test: correlation between identity-by-state values and geographical distances (see Materials and methods for details).

^bPearson correlation coefficient (95% confidence interval (CI)) of Mantel test for BB1_{urban} and BB2_{urban} combined: −0.308 (−0.349 to −0.276).

confirmed by consistently and uniquely mapped mate-pair coverage larger than 4-fold). After the final reference-assisted scaffolding step, the scaffolds were placed into 447 superscaffolds with an N50 length of 42.1 Mb. Ninety-nine per cent of the burrowing owl assembly (or 58 of the largest scaffolds) were assigned to *Gallus gallus* chromosomes or linkage groups. We annotated 17 858 protein-coding gene models in the genome assembly, which were on average 22.6 kb long and comprised 35% of the genome size (including introns). These gene models comprised 157 528 protein-coding exons covering 2.3% of the genome size. The burrowing owl genome browser can be found at <http://public-genomes-ngs.molgen.mpg.de> and is publicly available.

Sequencing coverage of the 137 burrowing owls ranged from 8.7-fold to 42.5-fold (median: 17.0-fold) and did not differ between urban and rural birds (*t*-test: $t_{131} = -0.34$, $p = 0.73$). After quality-control and singleton-filtering and after excluding Z-chromosomal SNPs, the total dataset contained 11 114 442 SNPs (on average 1 SNP per 100 bp).

(b) Population structure

Overall, there were fewer SNPs in the urban populations than in the nearby rural populations (paired *t*-test: $t_3 = -4.96$, $p = 0.016$; table 1). The number of SNPs in the urban populations of BB1, BB2, SV and TA respectively were 7%, 4%, 12% and 9% lower in comparison to the number of SNPs of their rural counterpart (table 1). Urban populations predominantly showed a lack of rare SNPs in comparison with their nearest rural population (electronic supplementary material, figure S3). Comparisons among the urban populations revealed that they differed in rare SNPs more than expected by random sampling (electronic supplementary material, figure S4). However, mean heterozygosity did not differ between urban and rural populations (paired *t*-test: $t_3 = 0.43$, $p = 0.70$; table 1).

F_{ST} values between populations were low, but significant ($p < 0.001$) for all pairwise comparisons (electronic supplementary material, table S1). We found the lowest F_{ST} values among the rural populations (mean $F_{ST} = 0.003$), intermediate values for the urban-rural pairs (mean $F_{ST} = 0.014$) and the highest values between the urban populations (mean $F_{ST} = 0.025$; *t*-tests among these three groups: all $p < 0.02$). The genetic variance between urban and rural habitats is small, but significant (dbRDA: 1.2%; AMOVA: 0.9%). The

genetic variance between rural populations is similar or somewhat higher (dbRDA: 3.7%; AMOVA: 0.7%), but the highest variance occurs between urban populations (dbRDA: 5.3%; AMOVA: 7%; electronic supplementary material, table S2).

The genetic population structure can be visualized by plotting all individuals on the first two PCs of the PCA (figure 2). Although the total variance explained by the first two PCs was low, figure 2 clearly distinguishes between the sampled populations and habitat affiliations. Whereas all three rural populations showed little differentiation and were clustered in the centre of the plot, the urban populations spread out in different directions. Individuals belonging to different cities are clearly separated, whereas individuals within cities cluster together on a single line. This is also true for the two urban sampling sites from Bahia Blanca BB1_{urban} and BB2_{urban}, although they show different clustering on the third PC (electronic supplementary material, figure S5). A few individuals from the rural populations lie further from the centre on the line of their respective urban population (figure 2). This indicates that there is some dispersal/gene flow back from the urban populations to the adjacent rural ones. The different urban-rural population structure was also corroborated by the DAPC analysis, in which the first two discriminant axes accounted for more than 20% of the genetic variation (electronic supplementary material, figure S6).

We further explored the spatial structure within urban and rural populations by testing isolation-by-distance for each population. As expected with some spatial structure, the correlation coefficients between identity-by-state values and geographical distance were negative in most populations (except SV_{rural}; table 1). All negative coefficients were in the same range, except for the weaker correlation in SV_{urban}. This indicates the same level of isolation-by-distance structure for all populations (except the SV populations), despite the strong difference in geographical scale (mean geographical distances among individuals) between urban and rural populations (table 1, electronic supplementary material, figure S7). The results of the dbRDA analysis (electronic supplementary material, table S2) are comparable to those of the Mantel tests (table 1): they indicate significant and similarly strong isolation-by-distance patterns within the urban populations (3.3% explained by longitude and latitude) and within the rural ones (3.7% explained; electronic supplementary material, table S2). This confirms that urban birds show substantial genetic variation over a small

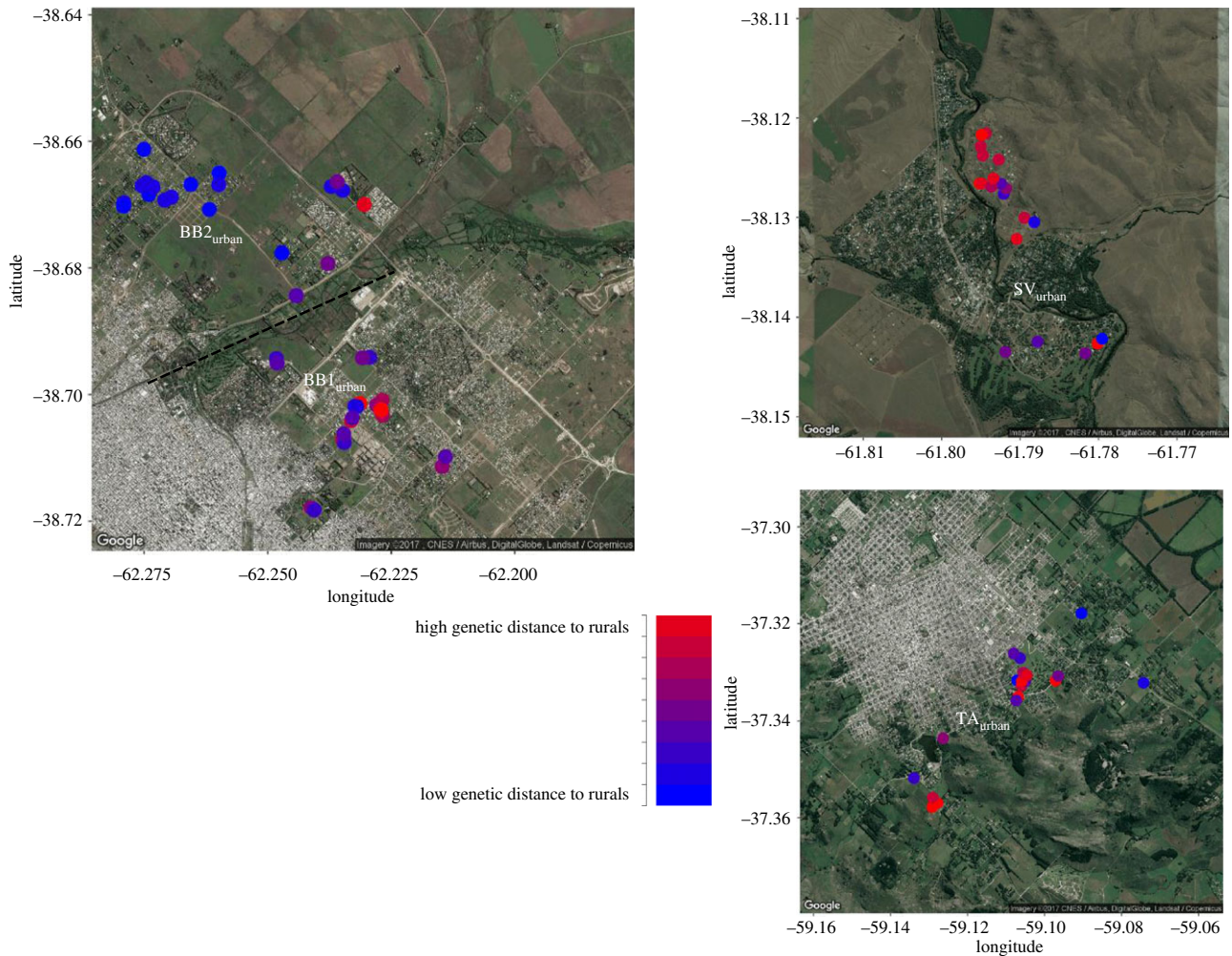


Figure 3. Maps showing the capture location of urban birds with dot colour reflecting the genetic distance to the rural populations. Colours range from blue (genetically closest to the rural centre, based on figure 2) to red (genetically most distant to the rural centre).

geographical scale (figure 3). Individuals with similar genetic distance to the rural birds are spatially clustered (figure 3), but individuals sampled closer to the city boundary do not show lower genetic distance than those sampled closer to the city centre (based on visual inspection of figure 3).

(c) Demographic history

Trajectories of estimated population sizes (N_e) over the last 1250 years (500 generations) show clear and consistent differences between urban and rural populations, although the credibility intervals still overlap given the limited number of simulations (electronic supplementary material, figure S8). Whereas urban population size estimates decreased from approximately 100 000 to approximately 100 over the last 100 years, the rural population size estimates decreased only little or not at all over the same period. We thus combined the accepted ABC simulations of all urban populations and all rural populations and plotted median and credible intervals for the pooled groups (figure 4). Urban and rural populations show a shared demographic history until about 50–75 years ago.

4. Discussion

Using genome-wide SNP data from 137 burrowing owls from three urban-rural population pairs, we found a weak but

significant population structure, whereby the three urban populations are genetically distinct from each other and from the rural populations (figure 2). The three widely distributed rural populations showed little differentiation (figure 2). The overall urban-rural population structure indicates that a limited number of founders from the surrounding rural area independently colonized the different cities and that there is no dispersal of individuals between cities. A similar colonization model has been described for the urbanization of the European blackbird [38]. The founder effect resulted in the random elimination of some rare SNPs, but it was too weak to affect the average heterozygosity of individuals in the urban populations. This confirms model predictions that founder events with subsequent restricted gene flow more often lead to loss of rare alleles than to a decrease in heterozygosity [39].

Among the urban birds, we found variation in their genetic distance from the cluster of rural birds (figure 2). On the other hand, some individuals from the rural populations did not belong to the rural cluster, i.e. they were more similar to individuals from the nearest urban population (figure 2). This indicates recent, but restricted gene flow between neighbouring urban and rural populations, whereby some urban birds recently emigrated to the rural population. Although ringing data of the Bahia Blanca population corroborate that there is limited gene flow between urban and rural sites, they suggest that rural birds also continue to move

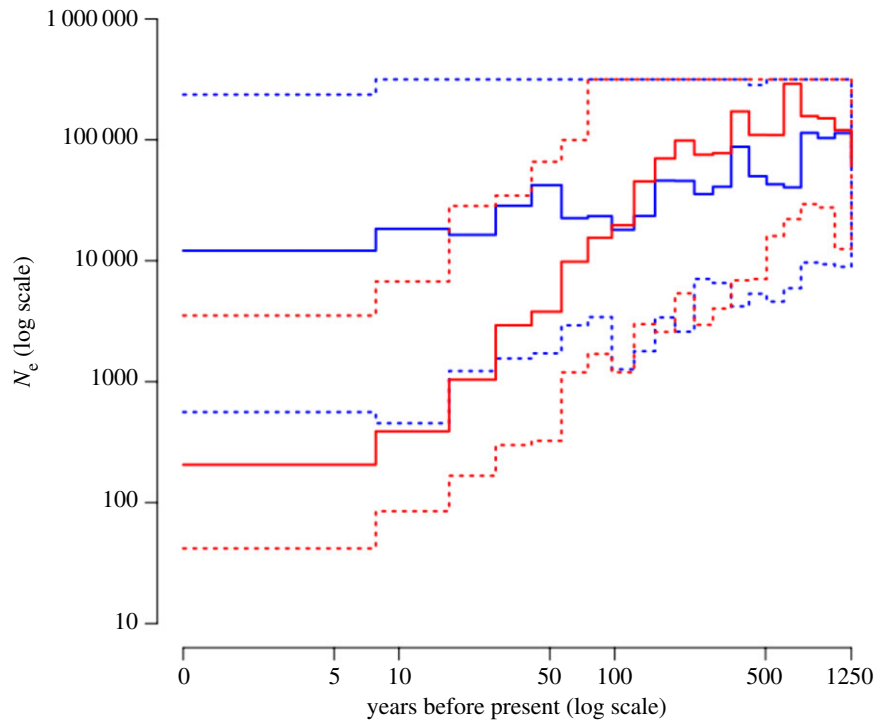


Figure 4. Estimated effective population size (N_e) over the last 1250 years (500 generations) for all urban (red) and all rural (blue) populations combined. Median (solid line) and 90% credible intervals (dotted lines) of the 40 and 30 accepted simulations of the urban and rural populations, respectively.

into the urban habitat: among 270 natal dispersal events, nine individuals (3%) ended up breeding in a habitat different than their natal one, whereby two moved from urban to rural, while seven moved from rural to urban habitat (our unpublished data).

Both rural and urban owl populations show signs of genetic isolation-by-distance at the individual level, indicating spatial restriction to gene flow even within the predefined populations. Note, however, that the spatial scale over which this isolation occurs differs: the strength of isolation-by-distance (as indicated by the correlation coefficients of the Mantel tests, table 1, and the proportion of genetic variance explained by the geographical positions of individuals within populations of the dBRDA analyses, electronic supplementary material, table S2) is comparable between the rural and urban birds, but the latter were sampled in a much more restricted area (figure 1 and table 1). This can be explained by more restricted gene flow in urban populations, where suitable habitat is more patchy and where barriers for moving between patches (e.g. streets, buildings) may exist even at small geographical scales. Such a pattern has been reported for several other species with lower mobility than birds, such as rodents [2,8]. Although unexpected given their high dispersal ability, weak but significant small-scale population structure related to urbanization has also been shown for other bird species, e.g. the house sparrow (*Passer domesticus*; [40,41]), the great tit (*Parus major*; [42]) and the Javan myna (*Acridotheres javanicus*; [43]). In our study model, reduced gene flow in the urban populations is more likely a consequence of a change in dispersal behaviour of urban individuals. Urban birds tend to be more philopatric and disperse shorter distances than rural individuals, and these differences in natal and breeding dispersal behaviour may be related to other differences in individual behaviour and to predation pressure (A. Luna *et al.* 2018, unpublished data). A similar difference in behaviour following

urbanization, namely increased sedentariness and reduced migratory behaviour, has also been reported for the European blackbird [44,45]. Note that the city with the lowest level of isolation-by-distance (Sierra de la Ventana) is also the smallest and youngest settlement. Thus, burrowing owls may have colonized this city more recently and in lower numbers, so that there was less time and more limited genetic variability for genetic differentiation among the inhabitable city patches to develop. Our demographic inferences of the Sierra de la Ventana urban population do not support an earlier timing of colonization, but indicate a lower final effective population size in comparison to the other urban populations (electronic supplementary material, figure S8). The number of SNPs was also lower in this urban population (table 1). Alternatively, the lower level of urbanization in this city may have created fewer barriers to dispersal. A relationship between genetic differentiation and urban development age and intensity has also been described for the wren tit (*Chamaea fasciata*; [46]) and the song sparrow (*Melospiza melodia*; [47]).

At the between-population level, our results suggest that the genetically different urban populations of burrowing owls evolved independently under random genetic drift processes following limited founder populations and limited subsequent immigration. If so, the effective population size of urban populations should decrease from the moment of colonization onwards. We showed that the ABC approach proposed by Boitard *et al.* [13] using LD values including long-range values up to 17 Mb distance can consistently infer effective population sizes only 2.5 generations ago (= 6.25 years ago, assuming a generation time of 2.5 years). Most methods, e.g. the ones based on the Sequentially Markovian Coalescent model [48], are limited in the resolution of recent population size [13,49]. The estimated population size dynamics of urban and rural populations differ consistently. Whereas rural population size estimates remain more or less constant at values greater than 10 000 or show a

moderate decline starting around 100 years ago, the estimated urban population sizes decrease consistently over the last 50–100 years to a current effective size between less than hundred to less than a thousand (electronic supplementary material, figure S8). The estimated start of the differentiation between urban and rural demographics lies around 50–75 years ago, which is consistent with the first observations of burrowing owls in Bahia Blanca and its suburbs more than 35 years ago (M. Carrete 2018, own observations).

Martinez *et al.* [14] hypothesized that burrowing owls started colonizing cities after they acquired the ability to dig their own burrows, which might have coincided with programmes to eradicate plains viscachas on agricultural land. Historically, burrowing owls typically used burrows of plains viscachas for breeding (hence the common Argentinian name of burrowing owls ‘lechucita de las vizcacheras’), which were still abundant at the end of the nineteenth century [50,51]. However, viscachas were declared a national pest in Argentina in 1907 and subjected to government control programmes. This species still is intensively persecuted through shooting, trapping, poisoning and fuming, and appreciated as bush meat in our study area. Although detailed data on the current distribution of the species is lacking, viscachas have long disappeared from most of the pampas [51]. The reduction in nest site availability at rural sites might have promoted the spread of the innovative digging behaviour of the burrowing owl which then served as pre-adaptation for the urban colonization.

Our data are consistent with the general pattern that urban populations are smaller and more genetically unique (owing to isolation with random genetic drift) than rural ones [2]. Genetic drift and isolation were not strong enough to decrease overall genetic diversity measured as heterozygosity, which is mostly influenced by common SNPs. However, the number of rare SNPs (singletons in the total dataset excluded) decreased by 4 to 12% in the urban populations in comparison to the neighbouring rural populations.

Thus, initial selection after urbanization potentially acting on rare standing variation might be limited and variable between cities. This leads to the following considerations when designing genomic studies searching for signals of selection. Selection studies addressing common variants will benefit from having multiple replicates (here multiple urban-rural pairs), which allows scanning for consistent selection signals across these replicates. By contrast, selection signals based on rare variants should mostly rely on information from single populations (e.g. sampling over different time periods during the urbanization process). Noticeably, the few molecular studies investigating selection in urban populations have reported allele frequency changes at both rare and common alleles [52,53,54], but more work is needed to understand how selection acts on standing variation [55].

Ethics. Fieldwork and procedures were conducted under permits from the Argentinean wildlife agency (22500-4102/09) in accordance with the approved guidelines of the Ethics Committee of CSIC (CEBA-EBD-11-28).

Data accessibility. The burrowing owl genome browser can be found at <http://public-genomes-ngs.molgen.mpg.de>. The raw sequences and the variant call format (VCF) file with all filtered SNPs and genotypes of all individuals are deposited at the NCBI archive under bioproject no. PRJNA431202.

Authors' contributions. M.C. and J.L.T. initiated and maintained the long-term study of urbanizing burrowing owls in Argentina. M.C., J.L.T., J.C.M. and B.K. contributed to study conception and design. H.K. assembled and annotated the owl genome. H.K. and S.B. collected the genomic variant data. J.C.M. analysed the SNP data. J.C.M., M.C., J.L.T., H.K. and B.K. drafted the manuscript. All other authors provided comments and approved the final manuscript.

Competing interests. We declare we have no competing interests.

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