



A genome-wide investigation of adaptive signatures in protein-coding genes related to tool behaviour in New Caledonian and Hawaiian crows

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Abstract

Very few animals habitually manufacture and use tools. It has been suggested that advanced tool behaviour co-evolves with a suite of behavioural, morphological and life history traits. In fact, there are indications for such an adaptive complex in tool-using crows (genus *Corvus* species). Here, we sequenced the genomes of two habitually tool-using and ten non-tool-using crow species to search for genomic signatures associated with a tool-using lifestyle. Using comparative genomic and population genetic approaches, we screened for signals of selection in protein-coding genes in the tool-using New Caledonian and Hawaiian crows. While we detected signals of recent selection in New Caledonian crows near genes associated with bill morphology, our data indicate that genetic changes in these two lineages are surprisingly subtle, with little evidence at present for convergence. We explore the biological explanations for these findings, such as the relative roles of gene regulation and protein-coding changes, as well as the possibility that statistical power to detect selection in recently diverged lineages may have been insufficient. Our study

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contributes to a growing body of literature aiming to decipher the genetic basis of recently evolved complex behaviour.

KEYWORDS

corvids, genomics, selection, tool use

1 | INTRODUCTION

Humans' extraordinary ability to make and use tools is believed to have co-evolved with a suite of unusual traits, including a large brain, advanced cognitive capacities, language, bipedalism, opposable thumbs, an extended developmental period, extreme sociality and an ability to culturally transmit and accumulate knowledge (Henrich, 2015; Kaplan et al., 2009; Sprevak, 2014; Sterelny, 2012). Inferring causal inter-relationships between these traits is extremely challenging, not least because some of them have reached degrees of sophistication or specialization not found in any other species (Gibson et al., 1994). But perhaps other tool users have evolved comparable tool-use-related traits? If so, what might their underlying genetic architectures be and can these be identified using genomic approaches? Addressing this challenging topic requires comparisons between multiple tool-using and non-tool-using species, ideally from a nonprimate system (Rutz et al., 2016). Given the rarity of animal tool behaviour (Biro et al., 2013; Hunt et al., 2013; Shumaker et al., 2011), the genus *Corvus*, which comprises over 40 species of crows and ravens (Haring et al., 2012), including at least two habitual tool users (Rutz et al., 2016), offers an exceptional opportunity for such replicated analyses.

The New Caledonian crow (*Corvus moneduloides*), from the South Pacific archipelago of New Caledonia, is one of the most accomplished nonhuman tool users (Hunt, 1996; Hunt & Gray, 2002, 2003). The species is able to forage with, as well as manufacture, a diverse repertoire of tools (Hunt, 1996; Hunt & Gray, 2002, 2003; Rutz & St Clair, 2012; St Clair et al., 2018) and exhibits a range of traits that appear to be related to its tool-using lifestyle (Hunt & Uomini, 2016). These include (a) a genus-atypical bill morphology that aids dexterous tool handling (Matsui et al., 2016; Troscianko et al., 2012); (b) large, mobile eyes and an exceptionally wide field of binocular vision facilitating visual feedback and motor coordination during tool manipulation (Matsui et al., 2016; Troscianko et al., 2012); (c) genetic predispositions that enable the ontogenetic development of basic tool skills (Kenward et al., 2005, 2006); (d) a prolonged juvenile dependency period providing opportunities for juveniles to hone their technical skills and learn from proficient adults (Bluff et al., 2010; Holzhaider et al., 2011; Hunt et al., 2012); and (e) a highly dynamic social system that may aid the social transmission of tool-related skills within and between generations (Holzhaider et al., 2011; St Clair et al., 2015).

It has also been reported that New Caledonian crows have unusually large brains (Cnotka et al., 2008) with relatively enlarged associative forebrain regions (Mehlhorn et al., 2010), but

these results could not be replicated with a larger sample of birds (Medina, 2013). While a number of studies have argued that the species possesses impressive problem-solving abilities (Gruber et al., 2019; Taylor et al., 2010), some claims have been contested (for a recent review, see Rutz & Hunt, 2020) and evidence that New Caledonian crows' cognitive abilities exceed those of other corvids remains equivocal (see Taylor & Gray, 2014). Indeed, very few studies have been carried out to date that compare the cognitive performance of New Caledonian crows to that of non-tool-using congeners, using tasks that do not require object manipulation (but see Teschke et al. (2013)).

While some non-tool-using crow species can learn to use tools in captivity, usually after some training or facilitation (Bird & Emery, 2009; Gallot & Gruber, 2019; Kanai et al., 2014; Powell & Kelly, 1977), it was long thought that the New Caledonian crow is the only natural tool user within the genus. Recent work revealed, however, that the critically endangered Hawaiian crow (*C. hawaiiensis*), from Hawai'i Island in the North Pacific, is also highly skilled at making and using tools (Klump et al., 2018; Rutz et al., 2016). Two lines of evidence suggest that tool use is part of the Hawaiian crow's natural behavioural repertoire (Rutz et al., 2016): naive juveniles spontaneously develop functional tool use (i.e. without demonstrations or training), and tool use is a species-wide capacity (adults use tools in a highly dexterous manner, without facilitation). Furthermore, there are striking similarities between Hawaiian and New Caledonian crows in terms of craniofacial morphology (Rutz et al., 2016) and prolonged juvenile dependency (Banko et al., 2002). Importantly, New Caledonian and Hawaiian crows are not closely related (Jønsson et al., 2012), suggesting that their tool behaviour arose convergently, in response to similar ecological conditions prevailing on their tropical home islands (Rutz et al., 2016).

High-throughput genome sequencing has greatly aided the identification of genomic regions under selection and has thus improved our understanding of the molecular basis of adaptive evolution. Several approaches have been developed to quantify selection pressures acting on the genome. One of the best-known methods is to test for deviations from neutral evolution in protein-coding regions, using the ratio of nonsynonymous to synonymous substitutions—the dN/dS ratio where a ratio larger than one indicates positive selection and a ratio smaller than one, purifying selection (Kimura, 1977; Yang & Bielawski, 2000). This approach has been used widely to examine gene family evolution in several lineages, including *Drosophila* (Hahn et al., 2007), mammals (Agaba et al., 2016; Park et al., 2015) and birds (Almén et al., 2016; Sackton et al., 2019). Strong positive selection

acting on a locus will also leave a signature in neighbouring genomic regions. When a beneficial mutation increases in frequency and becomes fixed in the population, genetic variation in the vicinity of the advantageous mutation can be reduced or eliminated in a 'selective sweep' (Smith & Haigh, 1974). Selective sweeps have been detected in the patterns of genetic variation in the vicinity of genes associated with pigmentation, olfaction and immunity in humans (Williamson et al., 2007). Similarly, great tit (*Parus major*) genomes show evidence for selective sweeps in regions containing genes related to cognition and neuronal function (with one such gene (ERG1) also exhibiting a high dN/dS ratio indicative of positive selection; Laine et al., 2016), and selective sweeps are also implicated in the evolution of cognitive abilities in wasps (Miller et al., 2020). However, dN/dS may not be suitable for detecting selection in recently diverged species where sufficient numbers of substitutions may not have accumulated yet (Wolf et al., 2009) and where polymorphism may bias its estimation (Mugal et al., 2020). Moreover, the dN/dS ratio can only be estimated for protein-coding regions. In nonmodel organisms with limited 'omics' resources, genome scans for selective sweeps are a useful method to identify candidate genome regions for positive selection. Therefore, using both dN/dS and selective sweep detection approaches may better explore footprints of selection in closely related nonmodel organisms.

Here, we use a comparative genomic approach to search for genetic signatures of selection associated with traits facilitating tool use, by comparing the tool-using New Caledonian and Hawaiian crows to a sample of ten non-tool-using congeners. Specifically, we undertook de novo whole-genome sequencing and assembly of *C. moneduloides* and whole-genome resequencing of multiple individuals from our set of *Corvus* species to (a) establish a new genomically informed phylogeny; (b) explore the phylogenetic relationship between tool-using and non-tool-using crows; (c) identify signatures of positive selection in New Caledonian and Hawaiian crows using phylogenetic and population genetic approaches, as well as possible signatures of convergent molecular evolution; and (d) contrast the population genomics of tool-using New Caledonian crows with those of a closely related and ecologically matched non-tool-using species, the white-billed crow (*C. woodfordi*), which is endemic to the tropical Solomon Islands, north of New Caledonia. Our findings suggest that relatively subtle genetic changes can contribute to the evolution of traits facilitating tool use, including highly unusual craniofacial morphology.

2 | MATERIALS AND METHODS

2.1 | Sampling and genome sequencing

We collated and generated data for a total of 12 crow species (see Appendix S1; Tables S1 and S2). Short read data are deposited at ENA (<https://www.ebi.ac.uk/ena>; ENA project Accession Numbers PRJEB33755 (umbrella project), PRJEB33706 and PRJEB33707), and metadata are available in Table S2.

2.2 | Reference genomes and annotation

We used a published reference assembly and its annotation for *C. (corone) cornix* (NCBI assembly Accession Number GCF_000738735.1; scaffold N50 = 16.4 Mb; Poelstra et al., 2014). For the purpose of this study, we also generated a de novo genome assembly of *C. moneduloides* (NCBI assembly Accession Number: GCA_009650515.1) using ALLPATHS v47402 (Butler et al., 2008) as described in the Appendix S1. We then annotated this assembly using the MAKER2 v2.31.7 annotation pipeline (Holt & Yandell, 2011), using a data set of 1,300 manually curated *C. (c.) cornix* proteins, a transcriptome data set for *C. woodfordi* (<https://www.ebi.ac.uk/ena>; ENA project Accession Numbers PRJEB33755 (umbrella project) and PRJNA577979) and ab initio gene predictions. The annotation is available on Dryad (<https://doi.org/10.5061/dryad.w0vt4b8m9>).

We assessed the quality of the assembly and annotation of the two reference genomes using the BUSCO v1.22 (Simão et al., 2015) pipeline and the 'vertebrata' data set (631 genes). We also identified orthologous coding sequences of the two annotations using ORTHOGOGUE v1.0.3 (Ekseth et al., 2014). Specifically, we identified orthologs, paralogs and co-orthologs as described in Ekseth et al. (2014) (see Appendix S1).

2.3 | Short reads processing and protein-coding gene sets generation

We trimmed adapters and mapped the newly sequenced and available short reads for the 12 crow species to both the *C. (c.) cornix* and *C. moneduloides* assemblies. We marked duplicates and realigned reads around indels (see Appendix S1). Next, we generated consensus genomes for each of the 12 species from the resulting bam files, and following Mugal et al. (2020), masked polymorphic sites with 'N', thereby only considering fixed sites for tests of positive selection (PAML, McDonald-Kreitman tests). For all downstream analyses, we only retained protein-coding sequences with at least 80% completeness (i.e. containing no more than 20% 'N' relative to the gene in the respective annotation) in order to avoid potential bias when calculating indices of selection. Because of varying data quality among resequenced genomes, not all consensus genomes had the same number of genes with $\geq 80\%$ completeness. Therefore, in order to maximize the number of genes with $\geq 80\%$ completeness, while also maintaining adequate sample sizes and statistical power, we generated data sets for 5, 7 and 8 species (see Appendix S1).

2.4 | Phylogenetic tree reconstruction

We extracted sequences of 631 core vertebrate genes present in all species ('vertebrata' data set from BUSCO; Simão et al., 2015) and aligned them in PRANK v100802 (Loytynoja & Goldman, 2005). We

then used RAXML v8 (Stamatakis, 2014) to perform a maximum-likelihood analysis, assuming a GTR + gamma model of sequence evolution including four rate categories for each codon position and using 1,000 bootstrap iterations. *Taeniopygia guttata* was specified as the outgroup (see Appendix S1).

2.5 | Tests of positive selection

We used two approaches to identify signatures of positive selection between habitually tool-using and non-tool-using species. First, we used codeml from the PAML package v4.9 (Yang, 2007) to test for different rates of evolution between crow lineages (Appendix S1, Table S3). PAML estimates dN/dS (ω), which compares the rate of substitutions at synonymous sites (dS), which are presumed neutral, to the rate of substitutions at nonsynonymous sites (dN), which are under selection. A dN/dS > 1 is thus taken to imply the action of positive selection on a protein-coding gene, whereas a dN/dS < 1 indicates purifying selection. We used a branch model and considered a 'null model' assuming one ω value across the entire tree, and an 'alternative model' assuming one separate ω for some branches and another ω for the remainder of the tree. Null and alternative models were compared using a likelihood ratio test (LRT) with 1 degree of freedom. False discovery rate (FDR) for multiple testing corrections was applied (Benjamini et al., 2009), using the 'qvalue' R package (Storey et al., 2019) at a FDR threshold of 0.05. We tested the hypothesis that a sequence evolved at different rates in the tool-using *C. moneduloides* or *C. hawaiiensis* lineages compared

with the rest of our *Corvus* phylogeny. We ran these tests labelling only the *C. moneduloides* branch or labelling both *C. moneduloides* and *C. hawaiiensis* to have a different ω from the rest of the tree (Table S3). For the latter model, we tested (a) a different ω for each species and (b) the same ω for both species, thereby testing for a signal of convergent positive selection in the two species (Yang, 2007; Yang & Bielawski, 2000; see Appendix S1). In order to assess the effects of the varying quality of the assemblies and their annotation on our results, these tests were run twice, using genes extracted either from the *C. moneduloides* reference genome or from the *C. (c.) cornix* reference genome. This approach also enabled us to look for evidence of genetic novelties arising in *C. moneduloides* vs. *C. (c.) cornix* that might correlate with tool use. For each of the two reference genome assemblies, we compiled three different species data sets that used comparisons among 5, 7 or 8 species of the genus *Corvus* together with an outgroup, the zebra finch (*T. guttata*). Compiling these three subset of our data allowed us to (a) maximize the number of genes with 80% completeness and maintain adequate sample sizes and statistical power (Table S3; see above and Appendix S1); and (b) minimize the discovery of false positives associated with ancestral and lineage-specific polymorphisms (Mugal et al., 2014, 2020) by excluding *C. woodfordi*, the closest related species of *C. moneduloides*, from these analyses (Figures 1 and S1). To ensure that analyses using different reference genomes produced similar results, we compared ω values obtained under the null model from analyses using different reference genomes for individual genes. We also compared the average ω of genes within Gene Ontology (GO) terms (see Appendix S1). Finally, we compared ω values obtained under the

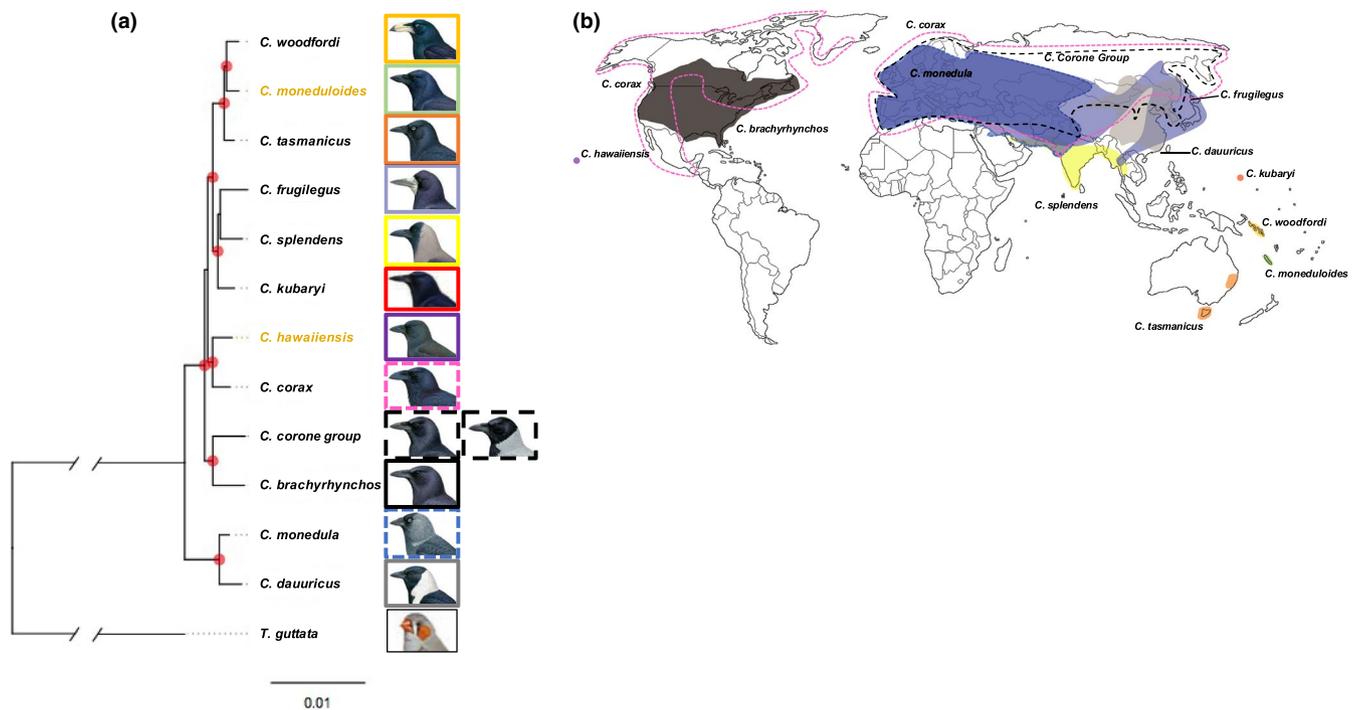


FIGURE 1 Phylogeny and worldwide distributions of the *Corvus* species investigated. (a) Maximum-likelihood phylogeny based on 631 core eukaryotic, single-copy genes. Red points at nodes indicate $\geq 95\%$ bootstrap support. Note that the branch to *Taeniopygia guttata* has been truncated to 30% of its actual length for clearer visualization. (b) Contemporary geographical distribution of crow species used in this study

alternative model using different reference genomes for the *C. moneduloides* lineage and for the background lineages.

As a second approach to identify positive selection, we applied the McDonald–Kreitman framework (McDonald & Kreitman, 1991; Mugal et al., 2014) to test for evidence of selection in *C. moneduloides*, contrasting divergence with polymorphism data, based on the *C. moneduloides* genome assembly and annotation. Variant discovery and genotyping were performed using the GATK pipeline v3.4.0 (DePristo et al., 2011; Van der Auwera et al., 2013) from processed bam files as described in the Appendix S1. The VCF file was annotated using SnpEff v4.2 (Cingolani et al., 2012). Counts of synonymous (pS) and nonsynonymous (pN) polymorphic changes for each gene were extracted from the VCF file and merged with counts of synonymous (dS) and nonsynonymous (dN) substitutions for the branch leading to *C. moneduloides* in different PAML runs (5, 7 or 8 species; as described above). We tested for significant deviations from neutrality for each gene by performing Fisher's exact tests in R v3.4.2 (R Core Team, 2019). FDR corrections were applied with a threshold of 0.05. Further, we calculated the neutrality index $NI = (pN/dN)/(pS/dS)$. In the case of neutral evolution, the ratio of nonsynonymous to synonymous substitutions and polymorphisms should be represented at equal proportions resulting in $NI = 1$. Conversely, for genes under positive selection and indicating an excess of nonsynonymous fixed differences, this index will result in a value of $NI < 1$ (Rand & Kann, 1996). For further details, see Appendix S1.

2.6 | Pathway and biological function analysis

To examine the functional implications of our results, we explored Gene Ontology (GO) and performed a statistical over-representation test of biological processes in PANTHER (Mi et al., 2013). We used as input all candidate genes indicative of positive selection identified with PAML and the McDonald–Kreitman tests in *C. moneduloides* or *C. hawaiiensis*. We used Fisher's exact test with multiple FDR correction and a FDR threshold of 0.05.

2.7 | Population genomic analyses in *Corvus moneduloides* and *Corvus woodfordi*

Corvus moneduloides and *Corvus woodfordi* are closely related and inhabit ecologically similar tropical islands, but only the former is known to use tools for extractive foraging (Jönsson et al., 2012). A comparison of genome-wide diversity in coding and noncoding regions within these species, which experience comparable levels of mutational load (Kutschera et al., 2020), may thus reveal evidence of more recent selection that is unique to *C. moneduloides*. Selective sweeps should leave a signature of locally reduced diversity. Such reductions in diversity that are unique to *C. moneduloides* (and do not appear in *C. woodfordi*) would point to selection pressures other than those associated with living on tropical islands, possibly including selection on tool-use-related traits. Therefore, we examined low-diversity genomic regions from processed bam files using ANGSD

v0.917 (Korneliusson et al., 2014) and calculated genome-wide diversity indices for *C. moneduloides* and *C. woodfordi* (see Appendix S1). To polarize the site frequency spectrum (SFS), we reconstructed an 'ancestral' consensus genome using all the available data from the *C. corone* species group, *C. frugilegus* and *C. dauuricus*. This ancestral consensus genome was assembled as for the other species (see Appendix S1). We then estimated Tajima's *D*, and Fay and Wu's *H* in overlapping windows of 50 kb with a step size of 10 kb based on this polarized SFS. We used a threshold for Tajima's *D* of -1.51 based on population genetic simulations (see Appendix S1). To check for evidence of population structure, we ran a PCA with PLINK v1.9 (Chang et al., 2015).

3 | RESULTS

3.1 | Comparison of reference genome assemblies and annotations

The de novo assembled genome of the New Caledonian crow (*C. moneduloides*) had a total size of 1.01 Gb, a contig N50 of 331 kb and a scaffold N50 of 4.5 Mb (SI Materials and Methods). Overall, the reference genome annotations contained 14,149 and 18,649 protein-coding gene models for *C. (c.) cornix* and *C. moneduloides*, respectively. Mean gene model length is 1,416 bp for *C. moneduloides* and 1,759 bp for *C. (c.) cornix*. We examined homology between protein-coding sequences from the two reference genomes with orthoAgogue v1.0.3 (Ekseth et al., 2014) resulting in 12,100 orthologs. Out of these, 8,489, 3,714 and 1,942 were unique orthologs, paralogs and co-orthologs, respectively (see Appendix S1).

3.2 | Phylogenetic relationships

The topology of our phylogenetic tree based on 631 core vertebrate genes was broadly consistent with earlier phylogenetic reconstructions based on fewer molecular markers (Figures 1 and S1; Haring et al., 2012; Jönsson et al., 2012; Rutz et al., 2016). However, there are some notable differences; for example, in our phylogeny *C. hawaiiensis* groups with *C. corax*, rather than with *C. frugilegus* (Figures 1 and S1).

3.3 | Phylogeny-based tests of positive selection

Next, we screened for genes with evidence of positive selection using comparative genomic analyses. We mapped resequencing data from 12 *Corvus* species to either the *C. (c.) cornix* or the *C. moneduloides* reference genome and extracted all protein-coding sequences. Using the *C. moneduloides* reference genome, for which we generated an annotation of 18,649 protein-coding genes, we recovered 17,967, 17,487 and 17,155 genes with $\geq 80\%$ completeness for the 5-, 7- and 8-species data sets, respectively. With the *C. (c.) cornix*

reference genome, we recovered 10,138, 10,096 and 10,070 genes with $\geq 80\%$ completeness for the 5-, 7- and 8-species data sets, respectively (Table S3).

Using these data sets and branch models of codon substitution rates, we tested for the evidence of positive selection on branches leading to *C. moneduloides* and *C. hawaiiensis* as well as for convergent evolution between them. Overall, we found evidence of positive selection in *C. moneduloides* in 12 genes: five genes when using *C. moneduloides* as the reference genome and seven genes when using *C. (c.) cornix* as the reference genome (Table 1). Among the five genes identified using the *C. moneduloides* reference genome, we found two genes (CAPN15 and CAMLG), one gene (TPBGL) and two genes (SPSB1 and CIITA) under putative positive selection ($\omega > 1$) in the 5-, 7- and 8-species data sets, respectively (Table 1). We found only one gene (CIITA) under putative positive selection in *C. moneduloides* and *C. hawaiiensis* when assuming the same substitution rate for both species (Table 1).

Among the seven genes identified using the *C. (c.) cornix* reference genome, we found three (LHX1, ZC2HC1A and DTNBP1), two (HTRA2 and TBC1D10A) and two genes (NPRL2 and SLC6A20) with $\omega > 1$ as candidates for positive selection in *C. moneduloides* using the 5-species, 7-species and 8-species data set, respectively (Table 1). It is worth noting that several other genes have unreasonably high ω values, indicative of the low number of synonymous changes in crows reducing the denominator in dN/dS to near zero (Table 1), which can occur when comparing closely related species (Wolf et al., 2009).

No candidate genes were shared among the analyses using the two different reference genomes. This lack of overlap may result from a genuine absence of these genes due to varying quality of the

respective annotations, or it may simply be explained by the fact that there were only 12,100 orthologs in common between the two annotations. Additionally, the lack of overlap may be caused by incomplete lengths of gene models in both genomes' annotations. We therefore tested whether there was any correlation in the estimates of ω under the null model (a single common ω for the entire tree) between analyses using two different reference genomes. Correlations were strong for all species data sets (Figure S2). Strong correlations were also evident when averaging ω values of individual genes across GO terms (Spearman's rank correlations between 0.80 and 0.81 across all data sets; Figure S2). In contrast, the correlations for p - and q -values of individual genes were much weaker (Spearman's rank correlations between 0.20 and 0.57 across all data sets). Correlations of ω estimates for the *C. moneduloides* lineage in alternative models across analyses using different reference genomes were also much lower (~ 0.5 ; Figure S3). Moreover, in data sets using the *C. (c.) cornix* reference genome, pairwise correlations of ω estimates for the *C. moneduloides* lineage from three separate software runs were high but not perfect (~ 0.8), while correlations of ω estimates for the background lineages were much better (~ 0.9 ; Table S4).

3.4 | McDonald-Kreitman tests

We contrasted between-species substitutions on the *C. moneduloides* branch obtained from the PAML analyses with within-species polymorphism based on the *C. moneduloides* reference genome. Across three different data sets, we found a total of 14 candidate genes with NI smaller than one (Rand & Kann, 1996)

TABLE 1 Candidate genes under putative positive selection when comparing *Corvus moneduloides* and/or *Corvus hawaiiensis* to other crow species

Reference genome	Data set	Gene name	Full gene name	ω	Species with $\omega > 1$
<i>C. moneduloides</i>	5 sp.	CAPN15	Calpain-15—cysteine Peptidases	1.01	<i>C. moneduloides</i>
<i>C. moneduloides</i>	5 sp.	CAMLG	Calcium signal-modulating cyclophilin ligand—transporter	18.57	<i>C. moneduloides</i>
<i>C. moneduloides</i>	7 sp.	TPBGL	Trophoblast glycoprotein-like	1.79	<i>C. moneduloides</i>
<i>C. moneduloides</i>	8 sp. same rates	CIITA	Class II major histocompatibility complex transactivator	1.05	<i>C. moneduloides</i> and <i>C. hawaiiensis</i>
<i>C. moneduloides</i>	8 sp. diff. rates	SPSB1	sp1A/ryanodine receptor domain and SOCS box-containing 1	1.46	<i>C. moneduloides</i>
<i>C. cornix</i>	5 sp.	LHX1	LIM homeobox 1	13.27	<i>C. moneduloides</i>
<i>C. cornix</i>	5 sp.	ZC2HC1A	Zinc finger C2HC-type containing 1A	5.41	<i>C. moneduloides</i>
<i>C. cornix</i>	5 sp.	DTNBP1	Dystrobrevin-binding protein 1	1.78	<i>C. moneduloides</i>
<i>C. cornix</i>	7 sp.	HTRA2	HtrA serine peptidase 2	9.78	<i>C. moneduloides</i>
<i>C. cornix</i>	7 sp.	TBC1D10A	TBC1 domain family member 10A	7.99	<i>C. moneduloides</i>
<i>C. cornix</i>	8 sp. diff. rates	NPRL2	NPR2-like, GATOR1 complex subunit	2.48	<i>C. moneduloides</i>
<i>C. cornix</i>	8 sp. diff. rates	SLC6A20	Solute carrier family 6 member 20	1.02	<i>C. moneduloides</i>

Abbreviation: sp., species.

at $p < .05$ (Fisher's exact test) (Table S5). Of these, 11 genes were present in the 5-species data set (17,967 genes) and one gene (LOC100232337) was present in the 7-species data set (17,487 genes). This same gene also formed part of the results from the 8-species data set (17,096 genes) based on the model with *C. moneduloides* and *C. hawaiiensis* with different substitution rates, along with two more genes (NCOR2 and PTPN9) with $NI < 1$ and $p < .05$ (Fisher's exact test) (Table S5). After applying the false discovery rate (FDR) correction for multiple testing ($q = 0.05$), no gene with $NI < 1$ remained significant for any of the data sets. None of the 14 candidate genes identified in the McDonald–Kreitman test showed a signal for positive selection in the phylogeny-based analyses using PAML.

3.5 | GO term over-representation analysis

Over-representation analysis based on gene function (gene ontology biological processes) showed that genes with elevated ω (mostly in *C. moneduloides*; Table 1) and with an excess of non-synonymous fixed differences (McDonald–Kreitman tests; Table S5) were associated with cell differentiation, growth and development, brain and nervous system, and retinal development (e.g. LHX1; Table S6).

3.6 | Comparative population genomics in a tool-using and a non-tool-using crow species

We calculated population genetic diversity statistics for *C. moneduloides* and *C. woodfordi* in 50-kb sliding windows with 10 kb overlap. Overall, genetic diversity (π) was lower in *C. woodfordi* (mean and 95% CI, autosomes: 0.00036 [0.000356, 0.000359], Z chromosome: 0.00026 [0.000256, 0.000268]) than in *C. moneduloides* (A: 0.0011 [0.00105, 0.00106], Z: 0.00081 [0.000803, 0.000822]). The relationship between genetic diversity and chromosome length was strongly negative in both species (*C. moneduloides*: $\rho = -0.73$, $p < .001$; *C. woodfordi*: $\rho = -0.9$, $p < .001$). As in other avian lineages (Dutoit et al., 2017; Ellegren, 2013; Weissensteiner et al., 2017), larger chromosomes have lower diversity, on average, than smaller chromosomes. At the same time, Tajima's D was on average slightly lower in *C. woodfordi* (autosomes: 0.180 [0.175, 0.184], Z chr.: -0.046 [-0.0623, -0.0341]) than in *C. moneduloides* (autosomes: 0.182 [0.179, 0.185], Z chr.: 0.32 [0.304, 0.334]). In both species, mean Tajima's D was consistently greater than zero (Figure 2). Fay and Wu's H was on average higher than zero in *C. moneduloides* (except on the Z chromosome), while in *C. woodfordi* values were consistently lower than zero (Figure S4).

In *C. moneduloides*, we found 81 genomic windows with Tajima's D lower than what would be expected for neutrally evolving regions based on population genetic simulations (see Methods; Figure S5). PCA did not reveal any obvious patterns of population structure in *C. moneduloides* (Figure S6a) despite individual samples originating

from different islands and different sampling years. In *C. woodfordi*, samples were differentiated along the first PC axis according to sampling location (Figure S6b). Undetected population admixture would increase values of Tajima's D (Huber & Lohmueller, 2016; Tajima, 1993), although this would make the simulation-based threshold conservative. Extracting all candidate windows with Tajima's $D < -1.51$ in *C. moneduloides* as potentially indicating a selective sweep, as well as 1 Mb up- and downstream, and then merging all overlapping windows into contiguous regions, we obtained 11 wider regions spanning an average of ~2 Mb (Figure 2b). In several of these windows, Tajima's D was only reduced in *C. moneduloides* (highlighted in grey in Figure 2b), and in these same regions, Fay and Wu's H was also markedly reduced only in *C. moneduloides*. The 11 wider regions contained a total of 350 genes (Table S7), among which three genes have previously been associated with craniofacial or bill morphology evolution in avian lineages (CALM1, PPP4R4 and DKK2; Abzhanov et al., 2006) and two genes with the mouse 'small maxilla' GO term (TRPS1, Suemoto et al., 2007; CHST11; Klüppel et al., 2005; Figure 2b). Over-representation analysis (GO) of biological processes of these 350 genes revealed an over-representation of genes related to glycosylation (Table S1). However, none of these 350 genes showed evidence of positive, divergent selection in our PAML analyses or the McDonald–Kreitman tests (see above).

4 | DISCUSSION

There are over 40 species of crows and ravens worldwide (Haring et al., 2012). While this taxonomic group exhibits surprisingly conserved morphology and behaviour, habitual tool use seems to have evolved in only two island species: the New Caledonian crow and the Hawaiian crow (Hunt, 1996; Rutz et al., 2016). Here, we sequenced the genomes of 12 crow species, established a phylogeny from these data and used comparative genomic approaches to search for genomic signatures of a tool-using lifestyle in coding sequences. While we detected signals of positive selection near genes associated with bill morphology (as expected from earlier work; Matsui et al., 2016; Troscianko et al., 2012), genetic changes associated with tool behaviour in crows appear subtle. Perhaps, key adaptations do not require extensive changes in protein-coding regions but are rather underpinned by several genes of small effect or differences in gene regulation. Finally, the lack of concordance among our analyses using different reference genomes, which vary in quality for mapping resequencing data from different species, illustrates the limitations of using a single reference assembly for tests of positive selection and offers an important cautionary note to interpretations made using these unidirectional comparisons.

Phylogenetic reconstruction based on substitutions in 631 genes confirmed that *C. moneduloides* and *C. hawaiiensis* are distantly related, suggesting that their tool behaviour evolved convergently (Rutz et al., 2016). The interspecific relationships identified within the genus differ slightly compared with earlier phylogenies based on a few nuclear and mitochondrial markers (Haring et al., 2007; Jønsson et al., 2012).

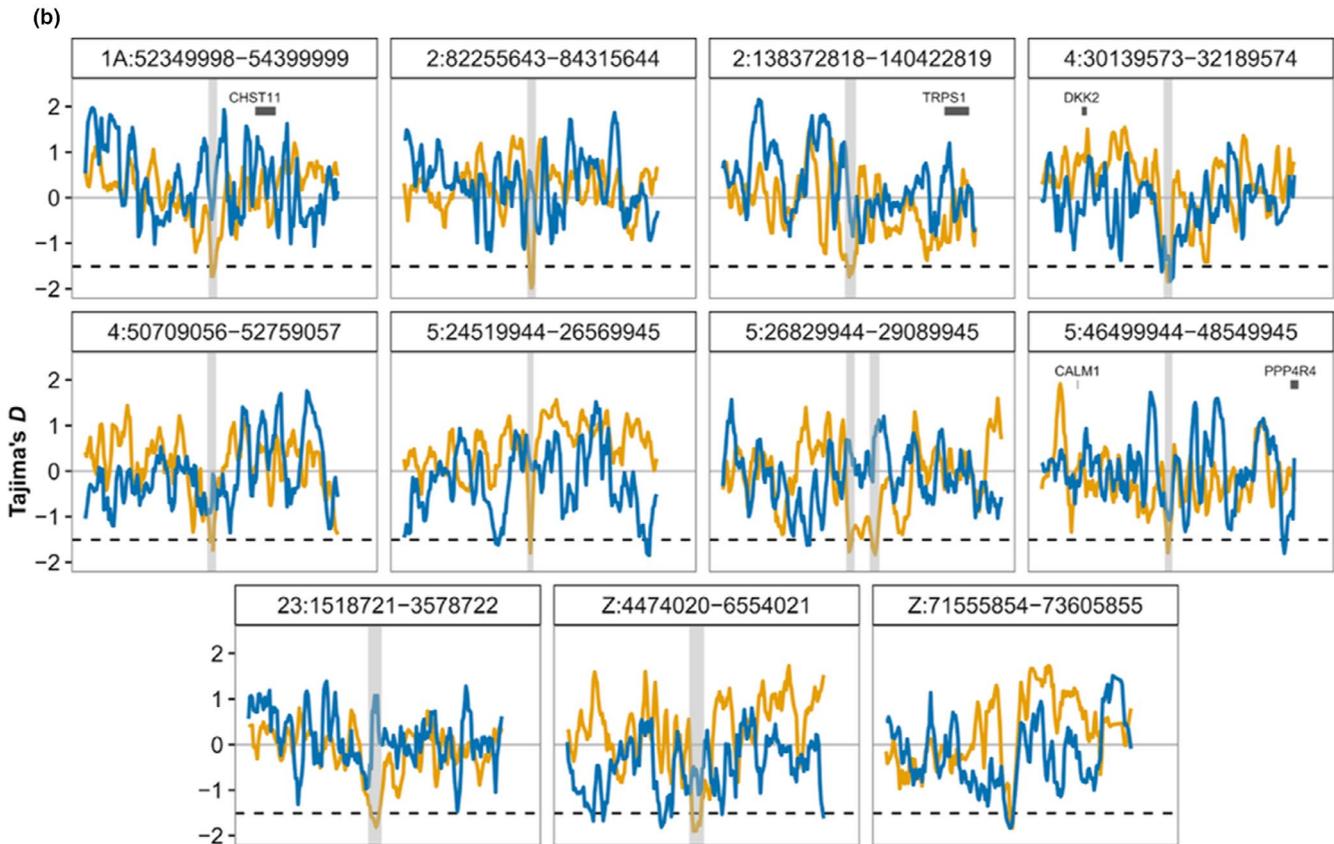
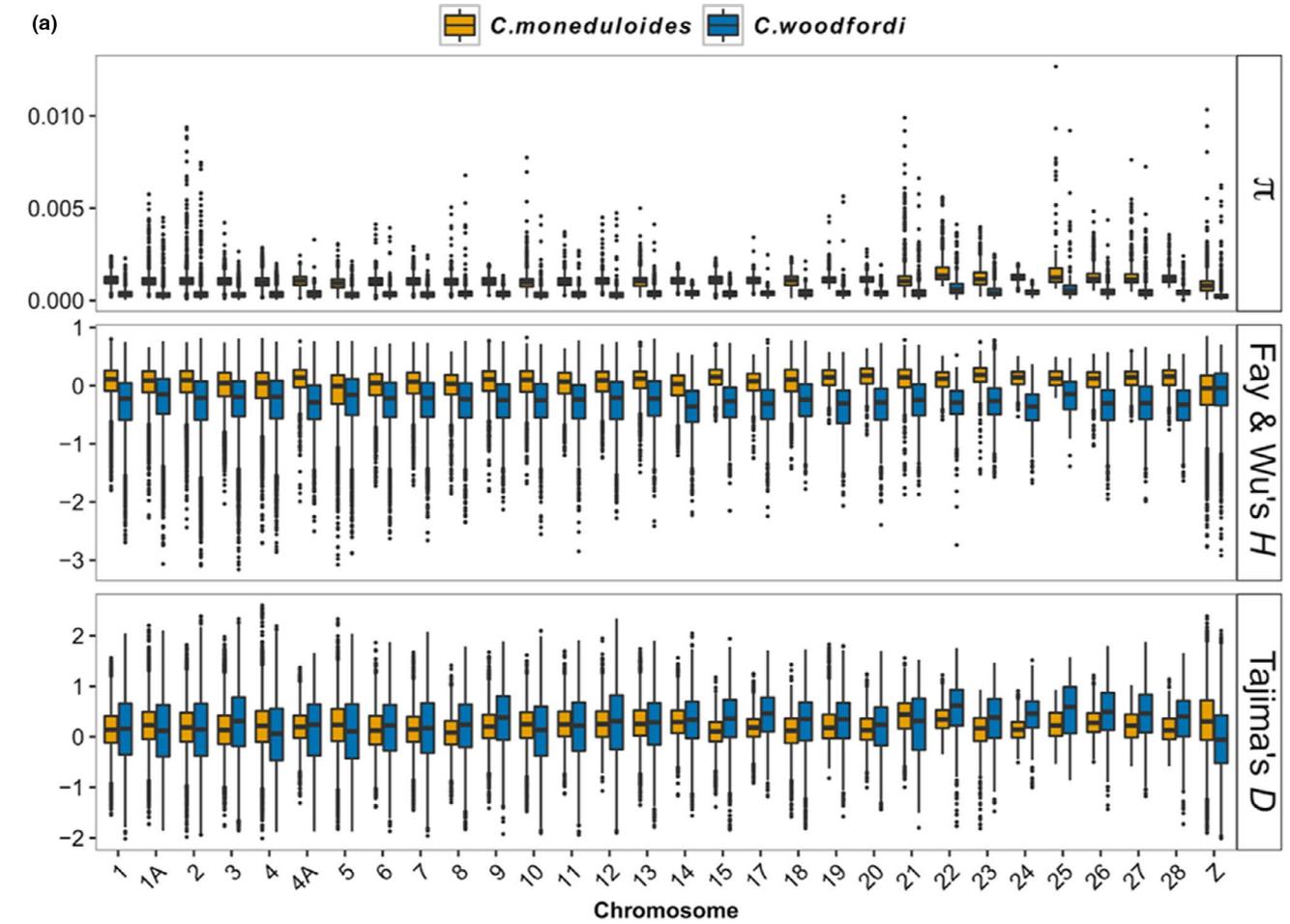


FIGURE 2 Genome-wide diversity in *Corvus moneduloides*. (a) Nucleotide diversity (π) and tests of neutrality summary statistics (Fay and Wu's H , and Tajima's D) in windows across all *C. (c.) cornix* scaffolds, placed on in silico chromosomes from Weissensteiner et al. (2017). (b) Tajima's D statistics in the 11 regions identified as candidates for positive selection and the locations of five genes with a known association to development of bill morphology in birds (depicted with black horizontal bars). Regions highlighted by vertical grey regions show where Tajima's D is below the theoretical threshold of -1.51 (dashed horizontal lines) in *C. moneduloides* but not in *C. woodfordi*.

Across all species comparisons, we identified candidate signals of positive selection in 12 genes associated with cell differentiation, growth and development, and involved in brain, nervous system and eye development. Positive selection was identified mostly in *C. moneduloides*, while only one gene coding for class II major histocompatibility complex transactivator (CIITA) showed weak but convergent signals for positive selection in *C. moneduloides* and *C. hawaiiensis*. We further investigated population genomic signals of selection in *C. moneduloides* and *C. woodfordi*, an ecologically matched non-tool-using sister species. These analyses identified genomic regions with low genetic diversity (i.e. low Tajima's D and Fay and Wu's H) in *C. moneduloides*, proximal to genes associated with bill morphology, potentially as a result of recent selection. This could be indicative of selective sweeps (Fay & Wu, 2000; Kim & Stephan, 2002; Smith & Haigh, 1974; Stephan, 2016) that occurred as a result of selection on genes underlying variation in bill morphology that enhances tool manipulation skills (Matsui et al., 2016; Troscianko et al., 2012). The overall positive values of Tajima's D and negative Fay and Wu's H on a genome-wide level suggest that we may have sampled structured populations in both species with unequal representation (Huber & Lohmueller, 2016; Tajima, 1993). In fact, an earlier study found significant local structuring of *C. moneduloides* populations (Rutz et al., 2012), although island-scale patterns appeared weaker (Abdelkrim et al., 2012). No data on population structure are available for *C. woodfordi*, but significant structuring has recently been reported for another crow species inhabiting a remote tropical island, the Mariana crow (*C. kubaryi*; Cortes-Rodriguez et al., 2019). Curiously, Tajima's D is negative on the Z chromosome in *C. woodfordi*, which might be due to sex-biased dispersal or strong purifying selection. A biased sampling of heterogametic females bearing on diversity estimates is not a likely cause for this negative Tajima's D since four out of five *C. woodfordi* were males. A complete description of population structure and gene flow in these species will require more systematic sampling of more individuals, which was outside the scope of the current study.

The subtle genetic changes identified for tool-using New Caledonian and Hawaiian crows are consistent with the observation that crows in general have large brains compared with other birds when corrected for body size, and exhibit notable behavioural plasticity and innovation potential (Emery & Clayton, 2004). As noted in the introduction, some crow species that do not routinely use tools in the wild, such as rooks (*C. frugilegus*), can use stick-type tools under laboratory conditions, usually following some facilitation (e.g. Bird & Emery, 2009). Thus, the cognitive ability for basic tool use probably arose in the common ancestor of *Corvus* (Lefebvre et al., 2002). We found evidence for positive

selection and selective sweeps near genes that control bill morphology and development, but not near genes associated with brain function. Bill shape is one of the most striking differences between habitually tool-using and non-tool-using crows (Matsui et al., 2016; Rutz et al., 2016; Troscianko et al., 2012; Figure 1). Several lines of evidence suggest that straight bills and highly mobile (and large) eyes facilitate the handling of stick-type tools (Matsui et al., 2016; Troscianko et al., 2012). Indeed, non-tool-using rooks are not as dexterous as *C. moneduloides* and *C. hawaiiensis* at using tools, presumably partly because they lack enabling bill features (Bird & Emery, 2009). At present, it is unclear whether selection for specialized craniofacial features preceded (e.g. to enable woodpecker-like chiselling of deadwood; for Rutz & St Clair, 2012), and/or followed (Hunt & Gray, 2007; Matsui et al., 2016), the emergence of tool behaviour (Troscianko et al., 2012). In any case, while morphological change seems a necessary component for the early evolution of habitual dexterous tool behaviour, more subtle changes affecting ontogenetic programmes and cognitive capacities may also occur, but remained undetected in our present analyses.

There is high conservation in gene sequence and chromosomal synteny in birds (Zhang et al., 2014), and the crow lineage diverged relatively recently (~17.5 mya), with the last common ancestor of *C. moneduloides* and *C. hawaiiensis* dated to the mid-Miocene (~11 mya; Jönsson et al., 2012). It seems probable, therefore, that the relatively short evolutionary time frames since their divergence may have limited the possibility for repeated changes in coding regions, and thus resulted in the low number of overall substitutions among the crow lineages, leading to low statistical power in some of our tests. This is consistent with the lack of a strong signal for positive selection we observed using dN/dS analyses and the McDonald–Kreitman tests. Moreover, our results indicate that, while single estimates of ω were robust to the reference genome under the null model, these estimates varied substantially according to the chosen reference genome for the alternative models. This may further explain the lack of overlap in the identified candidate genes from our analyses using two different reference genomes and further indicates that our dN/dS analyses may be limited in resolution and power. Importantly, the lack of overlap in candidate genes between dN/dS analyses illustrates the limitations associated with using a single assembly for tests of positive selection. Because using one or the other assembly led to inconsistent results, different interpretations and conclusions on the link between genomic changes and a trait could have been drawn. However, mapping resequenced data to two different reference genomes and performing reciprocal dN/dS analyses enabled us to determine whether the signals of positive selection

in coding genes observed have a robust biological basis or instead result from mapping or analysis bias. We thus caution against the use of a single reference genome and strongly recommend that reciprocal tests be performed whenever possible, especially when several assemblies of varying qualities (i.e. contiguity, coverage) are available. Ideally, reference genomes should be assembled for each species under consideration along with population genomic data to also account for within-species variation.

It is possible that genomic changes underlying recent adaptations across this phenotypically conserved group of birds may not be reflected in extensive coding sequence divergence but instead in regulatory regions (Mack & Nachman, 2017; Wittkopp & Kalay, 2011). This, too, is consistent with our findings of signatures of selective sweeps up- and downstream of candidate genes and a mixed signal within coding sequences, although this interpretation should be treated cautiously due to low sample sizes. Analysis of regulatory motifs, such as conserved nonexonic elements (CNEEs), would enable more refined examination of the genomic adaptations to tool behaviour in crows. However, the need for large sample sizes, high-quality assemblies extending to noncoding elements for all crow species, as well as high-quality gene annotations, means a robust analysis of such CNEEs is beyond the scope of the present study.

The importance of regulatory changes in driving phenotypic differences (King & Wilson, 1975) has become increasingly obvious as relevant genomic data have become available. Work in humans, rodents, flies and fish indicates that regulatory variants have broad influence on the transcriptome and the proteome, sexual dimorphism, skin colour, behaviour, disease susceptibility and cognition (Albert & Kruglyak, 2015; Enoch et al., 1998; Mank, 2017; Miller et al., 2007, 2020; Wray, 2007). A recent study examining the loss of flight in ratites, for example, adds to a growing body of evidence suggesting that changes in regulatory regions (e.g., CNEEs) are frequently more important than changes in protein-coding genes (Sackton et al., 2019). While coding sequence variation is important in some classes of genetic divergence (e.g. immune function; Blais et al., 2007), and the relative importance of coding and noncoding divergence has been debated, regulatory changes may be of primary importance for phenotype evolution in very recently diverged species (Mack & Nachman, 2017; Wittkopp & Kalay, 2011).

One challenge for studies on the genetic basis of complex traits, such as tool behaviour, which may not only be associated with specialized morphology but also with developmental, cognitive and other behavioural adaptations, is that such traits are likely polygenic and not underpinned by strong divergent selection on only one or a few genes (Nagel et al., 2018; Savage et al., 2018). This implies that changes in the frequency of advantageous alleles may be subtle and thus hard to detect (Pritchard et al., 2010; Stephan, 2016). Moreover, epigenetic processes are known to regulate genes associated with a wide range of traits, including some associated with cognition (Goldberg et al., 2007). Methylation patterns, one form of epigenetic regulation, have been shown to correlate with higher expression of neuronal genes in humans (Lister et al., 2009). Great tits

(*Parus major*), for example, a species that is a useful model for cognitive studies (Laine et al., 2016), have reduced CpG and non-CpG methylation signatures similar to those found in the neuronal tissues of mammals (Guo et al., 2014; Laine et al., 2016). Consequently, further investigation of the molecular basis of adaptations associated with the tool-using and tool-making abilities of New Caledonian and Hawaiian crows would likely benefit from the examination of both genetic and epigenetic changes in coding and regulatory regions.

Taken together, our results indicate that the genetic changes associated with habitual tool-related behaviour in crows are surprisingly subtle, perhaps reflecting, in part, the difficulty in identifying signatures of selection in recently diverged lineages, and the fact that crows, in general, share a common capacity for behavioural innovation. However, at least one of our findings is consistent with a potential adaptation to tool behaviour in New Caledonian and Hawaiian crows—an unusually straight bill. Investigating the genetic basis of traits that can facilitate seemingly sophisticated skills such as advanced tool behaviour is challenging. In fact, traits such as the unusual bill shape of New Caledonian crows and (to a lesser extent) Hawaiian crows are very likely to be underpinned by numerous genes of small effect and not by a few genes of large effect, as has been documented for speech (Atkinson et al., 2018; Krause et al., 2007), intelligence and personality (Nagel et al., 2018; Savage et al., 2018). Furthermore, with the realization that changes in regulatory regions can be associated with developmental pathways (Sackton et al., 2019), the exploration of genetic and epigenetic changes in regulatory regions will be instrumental in understanding the evolution and genetic basis of a variety of traits that may not be obvious based on the examination of protein-coding regions alone.

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AUTHOR CONTRIBUTIONS

G.R.H., R.D.G., M.G.R., C.R., J.B.W.W. and N.J.G. conceived the project, and M.G.R., C.R., J.B.W.W. and N.J.G. coordinated and ran the work programme. G.R.H., H.A., R.F., C.R. and N.J.G. contributed samples and/or assisted in sample preparation and permitting. N.D., V.E.K., R.A.W.W., D.P. and K.R. performed the bioinformatic analyses, under supervision from M.G.R., J.B.W.W. and N.J.G.. N.D., V.E.K., R.A.W.W., G.R.H., C.R. and N.J.G. contributed to writing the main body of the manuscript with input from all other authors. N.D., V.E.K. and R.A.W.W. wrote the supplementary documentation and R.D.G., R.F., M.G.R., C.R., J.B.W.W. and N.J.G. contributed to the interpretation and presentation of results in the main manuscript and supplementary documents.

DATA AVAILABILITY STATEMENT

Corvus moneduloides de novo assembly: NCBI Accession Number: VRT000000000; BioProject ID: PRJNA557728. *C. moneduloides* annotation: Data Dryad (<https://doi.org/10.5061/dryad.w0vt4b8m9>). *C. woodfordi* RNAseq data: BioProject ID: PRJNA577979—SRA submission SUB6432980. Umbrella Project ID: PRJEB33755. Short read data: PRJEB33706 and PRJEB33707.

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SUPPORTING INFORMATION

Additional supporting information may be found online in the Supporting Information section.

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