



Mixed ancestry and admixture in Kauai's feral chickens: invasion of domestic genes into ancient Red Junglefowl reservoirs

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Introduction

Humans have dispersed over most of the Earth's surface, and we have not made these journeys alone. Our migrating ancestors were accompanied by both accidental stowaway species (Mack *et al.* 2000; Lockwood *et al.* 2005; Estoup & Guillemaud 2010) and domesticated taxa that were utilized for food, labour or companionship (Larson *et al.* 2007, 2012). Subsequent to anthropogenic dispersal, many domesticated species have escaped cultivation and colonized new habitats, a process termed feralization. It can be helpful to think about feralization as 'domestication in reverse', as it involves the removal of direct anthropogenic control over natural and sexual selection regimes (Price 1984). Thus, feral population persistence requires survival and reproduction within novel social and ecological contexts. While there has been extensive research into what facilitates or hinders invasions of nondomesticated species (e.g. standing genetic and phenotypic variation), the process of feralization is less well understood. Progress in this area will help advance our basic understanding of biodiversification and can help mitigate feral species' impacts on native ecosystems and competitors (Loope 1999).

Feral habitats can potentially exert strong selection on several components of fitness in the wild (e.g. mate acquisition, foraging success, predator avoidance and disease resistance). Evolutionary responses to these selection pressures will depend upon both the genetic variability of feral populations and the genetic architecture of fitness-related traits (Goodwin 2007; Zohary *et al.* 2012). These properties of feral populations result from combined histories of domestication and feralization, each of which can be complex (Verardi *et al.* 2006; Stephens 2011; Feulner *et al.* 2013; McTavish *et al.* 2013; Nussberger *et al.* 2013). By characterizing genetic and phenotypic variation in feral taxa, we can therefore make progress towards the interrelated goals of understanding feral populations' origins and ascertaining their capacities to respond to current and future selection. To date, very few studies have jointly examined genetic and phenotypic variation in feral species using modern tools (although see Hampton *et al.* 2004; Randi 2008).

Here, we examine genotypic and phenotypic variation in feral chickens (*Gallus gallus*) on the Hawaiian island of Kauai. The origins of these birds are presently unclear; they have been alternatively described as either escaped farm pests ('feral domestic fowl') or as a 'legacy species' introduced by Polynesian colonists (i.e. Red Junglefowl), the chicken's closest free-living ancestor (Eriksson *et al.* 2008; see Box 1). Broad-scale studies of Pacific 'chicken' biogeography (using MtDNA markers) have also drawn conflicting conclusions as to whether contemporary populations are of ancient origin (Polynesian Red Junglefowl) or are descended from domestic breeds that originated more recently in Europe (Storey *et al.* 2012; Larson *et al.* 2014; Thomson *et al.* 2014). These uncertainties complicate efforts to use *G. gallus* biogeography to reconstruct Polynesian expansion into the Pacific and, possibly, South America (Storey *et al.* 2007, 2012; Beavan 2014; Bryant 2014; Thomson *et al.* 2014). They also raise important questions about best practices for feral population management. Although chickens and Red Junglefowl (RJF) can interbreed, applied biologists regard the two lineages very differently. Domestic chickens are a globally critical food resource, vectors of highly lethal pathogens and our planet's most abundant bird (for example, see http://www.uspoultry.org/economic_data/). In contrast, RJF are poorly suited to commercial food production, are threatened or endangered in their native range and merit stringent conservation effort (Peterson & Brisbin 1998). Thus, ascertaining the history of Kauai's chickens will have important implications for invasion biology, cultural anthropology, and *G. gallus* conservation and management.

Our aim in this study was to characterize the demography, genetics and phenotypes of *G. gallus* on Kauai and thereby elucidate their origins and capacity for evolutionary responses to feral selection pressures. We assessed population substructure and phylogeny using whole-genome sequencing (WGS) of modern samples taken from disparate Kauai sampling localities. We then determined relationships among sampled individuals' nuclear and mitochondrial genomes, including previously published data sets from (i) both ancient (pre-European contact) and modern samples from the Pacific, (ii) RJF and (iii) modern domestic chicken breeds. We also measured

Box 1. Biogeographic history of Hawaiian *Gallus gallus*

Potential sources of Kauai's *Gallus gallus*

Archaeological evidence indicates that chickens were first introduced to the Hawaiian island chain by AD1200 (including Kauai, see Fig. 1a) via human migration into the eastern Pacific (Wilmshurst *et al.* 2011; Thomson *et al.* 2014). Their sources were most likely Red Junglefowl (RJF) transported from the western Pacific by Polynesian settlers (Thomson *et al.* 2014). An additional 857 Pacific RJF were introduced to Kauai in 1939 in a state-sponsored effort to maintain game bird populations in the islands (Pyle & Pyle 2009). Therefore, it is possible that wild RJF persisted on these islands for over 1000 years, although this reservoir population may also be more recently derived (most likely from other Polynesian-dispersed sources in the Pacific). In this manuscript, we consider *G. gallus* from both ancient and historic (1939) RJF introductions as 'heritage' animals because (i) both were dispersed from their native range without experiencing modern, artificial selection for food production, and (ii) modern and ancient samples from Kauai share MtDNA genotypes (see Results); thus, if RJF re-introductions contributed to feral gene pools, then both ancient and historic introductions originated from closely related source populations. In the light of anecdotal claims from Kauai residents that contemporary *G. gallus* originated within the last few decades, it is also possible that RJF were extirpated from Hawaii and/or have been replaced by escaped domestics.

In the recent past, multiple European-derived, modern breeds have been cultivated in Hawaii for food production and cockfighting (personal communication from Kauai residents to D. Wright and E. Gering; and online sales from Asagi hatchery, Oahu, see <http://www.asagihatchery.com/>). In the 1980s and 1990, Tropical storm Iwa and Hurricane Iniki destroyed many of the coops containing Kauai's domestic birds, released their occupants into local forests and potentially spurred large-scale species invasions. Consistent with this possibility, our analysis of *G. gallus* point counts revealed marked increases in population densities during the last few decades (see Fig. 1). Nonetheless, this expansion of domestic genes into Polynesian-derived reservoirs may have been preceded by earlier episodes of introgression, as morphological analyses of five skins that were sampled on Kauai in 1895 also showed evidence of 'genetic pollution' from domesticated chickens (Peterson & Brisbin 2005).

In summary, the gene pool of feral Kauai's *G. gallus* may descend from ancient Polynesian RJF introductions, from historic (1930s) RJF re-introductions and/or from domestic chickens of recent European origins.

History of Pacific *G. gallus*

The domestication of the chicken is believed to have occurred up to 8000 years ago in China, South Asia and South-East Asia (West & Zhou 1988). Much more recently, domestic breeds have undergone a range of phenotypic and genotypic changes. Domestic breeds show a loss of nuclear genetic diversity (Muir *et al.* 2008) yet still exhibit a high degree of structure and variability in mitochondrial (Mt) sequences (Fumihito *et al.* 1996; Kanginakudru *et al.* 2008; Silva *et al.* 2009; Thomson *et al.* 2014), with nine major Mt clusters identified worldwide (Liu *et al.* 2006). MtDNA sequences from several ancient Hawaiian specimens fall solely within haplogroup D, a clade restricted to Asia-Pacific areas (Thomson *et al.* 2014; but see also Beavan 2014; Bryant 2014; Storey *et al.* 2007). In contrast, a small modern sample (n = 10) taken from the Koke'e region of Kauai was solely comprised of haplogroup E (Thomson *et al.* 2014). The E haplogroup currently occurs worldwide and, together with haplogroups A and B, is the source of European-derived domestic food production breeds (Liu *et al.* 2006). Both D and E clades have been found within modern Pacific samples, with the majority of samples outside of Hawaii being haplogroup D (Thomson *et al.* 2014; see Fig. 1).

phenotypic traits that are known to differ between domesticated chickens and RJF (rooster vocalizations, leg colours and plumage; see Box 2) among free-living *G. gallus* on Kauai. We used these data together to determine (i) whether Kauai's feral chickens are of mixed, Polynesian or European origin, (ii) whether there is evidence of interbreeding between feral lineages and (iii) whether co-ancestry and admixture on Kauai is associated with enhanced phenotypic variation.

Discussion

*Evidence of mixed ancestry in Kauai's feral *G. gallus**

We discovered several intriguing patterns of genetic variation within Kauai's feral chickens. First, our analyses of whole Mt genomes revealed that two divergent Mt lineages co-occur on the island (clades 'E' and 'D'). The E haplogroup includes sequences found in modern European breeds that are cultivated worldwide for food. In contrast, the D haplogroup is overwhelmingly restricted to Asia and the Pacific and (based on ancient DNA sequences) was already present on Kauai nearly 1000 years ago. Ancient and modern sequences from other Pacific Islands suggest that this lineage was dispersed by Polynesian settlers long before European exploration. Thus, clade D either persisted on Kauai into the present day or was subsequently repopulated from a closely related source population.

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Within Kauai, the historic displacement of clade D by clade E may have accompanied the feralization of domestic animals, a possibility that is supported by evidence of a rapid increase in *G. gallus* density within Kauai's recent past (Fig. 1C). Among Kauai residents, this change is typically attributed to the damage of island infrastructure following tropical storms Iwa and Iniki, which potentially released farm birds into local forests. Alternatively (or additionally), increased tourist activity since the 1970s may have contributed to the feralization of Kauai domestics by providing habitat, food or other key resources to escaped animals (Pyle & Pyle 2009). Further study is needed to ascertain the contributions of these biotic, abiotic and anthropogenic facilitators of invasion and to assess their potential role(s) in the recent expansion of clade E.

*Evidence of admixture from Pacific *G. gallus**

This is the first study to jointly examine Mt and nuclear genotypes from Pacific feral chickens. Our nuclear (PCA) analyses reveal that some genotypes found in Kauai are distinct from other populations, although they are similar to European samples (see Fig. 3 and Fig. S2, Supporting information). ADMIXTURE analyses of nuclear data indicated mixed ancestry of Kauai individuals, which share source populations with candidate European and RJF founders (Fig. 5A,B), although more RJF samples are required to verify this pattern. STRUCTURE analyses of Kauai birds indicated that (i) population substructure exists within Kauai,

(ii) admixed genotypes occur within some Kauai individuals (Fig. 5C), and (iii) the subpopulations delimited by STRUCTURE (using nuclear genotypes) are not restricted to individuals with either 'D' or 'E' mitotypes. Our nuclear genetic analyses are thus consistent with the hypothesis that the descendants of Polynesian-introduced birds (RJF) and feral domestics are interbreeding within the Pacific, although they cannot rule out alternative hypotheses without additional (Mt and phenotypic) evidence.

*Phenotypic variation among feral *G. gallus**

Despite extensive knowledge of the genetic underpinnings of *G. gallus* phenotypes, very few studies have measured both genetic and phenotypic variation in non-captive populations of this species. Our analyses of coloration (plumage) and behaviour (vocalizations) of Kauai chickens give insight to their history and evolutionary potential as follows: (i) 'classic' RJF traits (plumage, call characters) are prevalent within modern Kauai. (ii) Phenotypes on Kauai are both intermediate between, and more variable than, those of RJF and domestics (see Figs 2 and 4). In fact, the minima and maxima of the calls of Kauai birds are more extreme than the RJF or domestic birds sampled and also display greater variation. (c) Coloration and behaviour phenotypes are apparently correlated within

Box 2. Phenotypic signatures of *Gallus gallus* domestication

Domestication has induced a multitude of heritable changes in *G. gallus* phenotypes, including changes in behavioural, reproductive and physiological traits (Wright *et al.* 2006, 2008, 2010; Johnsson *et al.* 2012, 2014). Perhaps some of the most striking alterations are in the plumage, with the classic red, black and green feather pattern of the RJF giving way to far more variable coloration in domestic and fancy chicken breeds. Broiler and layer birds (selected for meat and egg production, respectively) have been bred to display a range of coloration, although the vast majority of broiler breeds are white (of the Aviagen, Cobb and Grimaud breeds available, only the Rowan Ranger, Cobb Sasso and Hubbard Color breeds are brown or black, see www.aviagen.com, www.cobb-vantress.com, www.hubbardbreeders.com). Most commercial layer breeds are either white or reddish brown (e.g. the Hy-Line W36, CV22, Silver-Brown, Brown and White Leghorn breeds), while heritage breeds of layer chickens tend to exhibit far greater plumage diversity (see www.hpbba.com).

The genetics of plumage colour is fairly well understood in the chicken. For example, the major locus causing white coloration in the chicken is the *Dominant White* mutation, occurring at the *PMEL17* gene (Kerje *et al.* 2004); other color mutations at *MC1R* are also known (Kerje *et al.* 2003). Yellow legs are another characteristic that distinguished many domestic chickens from RJF (which are fixed for grey legs); the locus controlling this polymorphism has also been previously identified (Eriksson *et al.* 2008).

The extensive variation in plumage and coloration introduced by domestication can be helpful in determining whether an RJF gene pool has been 'contaminated' by the introgression of domesticated alleles (e.g. Brisbin & Peterson 2007). However, captive intercross studies also show that it is difficult to infer the degree of introgression within individuals based on plumage or other phenotypic characters (Condon 2012). This is perhaps unsurprising, given that poultry breeders have long understood the inheritance of most *G. gallus* phenotypes (including plumage traits) to be subject to epistasis.

While RJF and domestic chickens bear many similarities in vocal repertoires, they are reported to differ consistently in the length of the last syllable of the rooster crow (Collias 1987), a trait that is considered diagnostic of domestic vs. RJF ancestry (Miller 1978). Evidence of genetic effects on call phenotypes is further supported by enhanced call variation following hybridization between domestic *G. gallus* breeds (Marler *et al.* 1962). To our knowledge, the present study is the first to compare vocalizations from numerous chicken breeds and from individuals sampled in multiple (worldwide) localities. It therefore offers new insights into the relative roles of genes and environments in *G. gallus* vocalizations. Our results confirm a significant difference between calls recorded from chickens and RJF (see Results). Thus, plumage colour, skin colour and vocalizations of Kauai birds comprise three genetically controlled traits that can be compared with *G. gallus*' ancestral (RJF) and derived (domesticated) states.

individuals (i.e. individuals exhibiting colour phenotypes associated with domestic genes had domestic-like calls; see Fig. 4), although this result is largely driven by four individuals in the domestic-like Kauai group.

Both increased population density and transitions to feral habitats are likely to involve radical changes in social and natural selection regimes. The phenotypic and genetic variabilities we report suggest the potential for evolutionary responses, but these may be constrained by antagonistic pleiotropy and/or epistatic

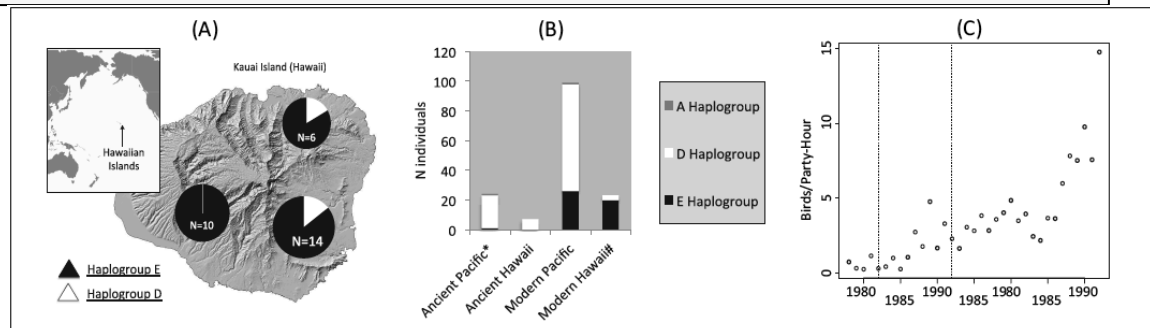


Fig. 1 (A) Map of Kauai showing MtDNA haplogroup frequencies from sampling localities in the western, central and northern areas of the island (details provided in Table S1, Supporting information). (B) Data from modern and ancient MtDNA sequences show a recent increase in frequency of clade E, which is associated with domestic chickens of European origin, which are now farmed worldwide. Data shown consist of western and eastern Polynesian samples taken from Thomson *et al.* (2014) and Dancause *et al.* (2011). *E haplogroup samples that are disputed as potential contamination (see text), #Hawaii samples from the current study only. (C) Data from Christmas bird counts in Kapa'a and Waimea (Kauai). Increased densities of feral *G. gallus* coincided with two major storm events (indicated by dashed lines) that damaged island infrastructure and may have facilitated the fertilization of escaped livestock



Fig. 2 Sample *G. gallus* phenotypes from Kauai. Panes A–C depict the standard Red Junglefowl (RJF) plumage. Panes D–F illustrate white coloration (D, E, F) and yellow legs (D, E), two genetically regulated traits that do not occur in native RJF.

interactions between the loci that control selected traits. It is hoped that future studies of these possibilities (including analysis of genetic and phenotypic data from a single pool of individuals) can help determine whether or not observed trait

correlations are indicative of evolutionary constraint.

In combination, our findings suggest that Pacific feral chickens present excellent opportunities for studies of postinvasive evolution. ADMIXTURE and STRUCTURE results potentially indicated that the Kauai population is distinct from other standard breeds of chicken and resembles RJF. However, the number of RJF samples was very low in this study, and the Kauai samples also overlapped with certain European samples in the ADMIXTURE results.

Very few individuals exhibited mitotypes associated with RJF dispersed by early Polynesians. In contrast, despite evidence of a recent population expansion (causing a tripling in the population size since 1992; see Fig. 1C), the plumage of individuals closely resembled the classic RJF phenotype. This is unusual given that RJF phenotypes are not typically observed following hybridization between RJF and domestic layers (personal observations of RJF x White Leghorn hybrids by D. Wright, but see Condon

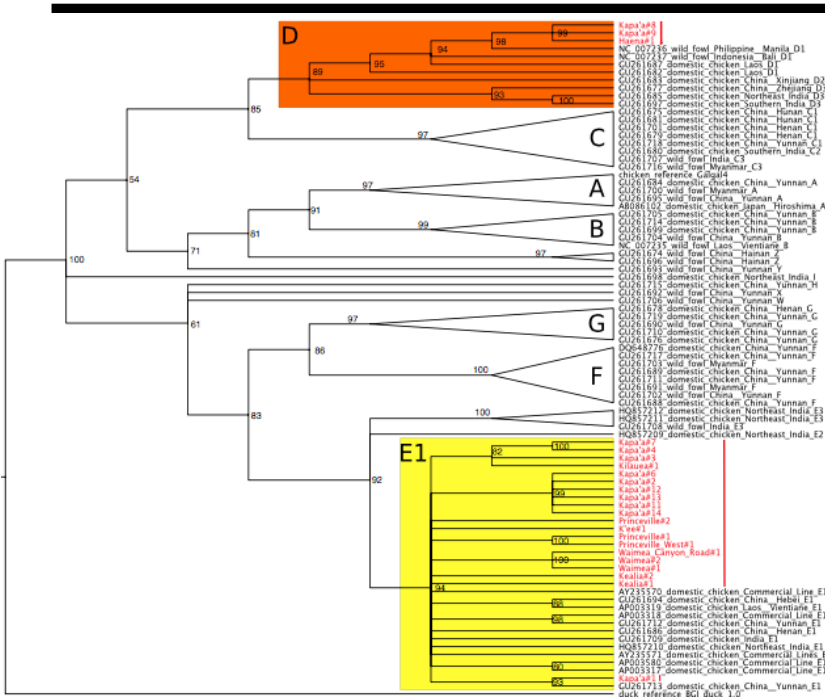


Fig. 3 Bayesian whole MtDNA genome phylogeny for birds from Kauai in relation to domestic chickens and RJF. Subtrees representing haplogroups other than D and E have been collapsed. Posterior probabilities (expressed as percentages) are indicated at nodes. Kauai samples are highlighted with red brackets.

2012). The contrast between both the nuclear and phenotypic data and the Mt sequence variation implies that natural or sexual selection may favour ancestral, RJF-like traits. Additional studies of the Kauai population should therefore test or genomic signatures of feralization in the form of selective sweeps (Storz 2005) and could reveal, for the first time, the types of genetic changes that occur with feralization. Further studies from both RJF and other Polynesian islands would increase the power of such analyses while providing more definitive insight into *G. gallus* invasion(s) of the Pacific.

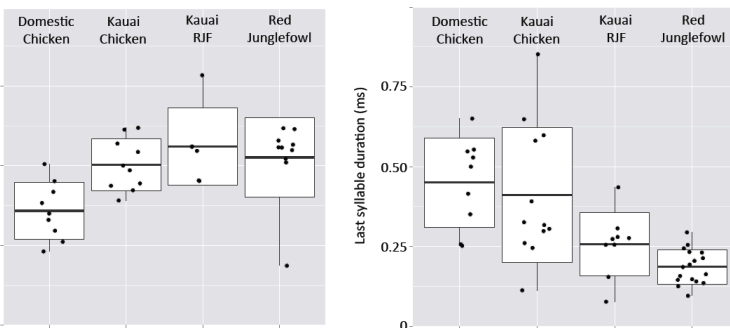


Fig. 4 Durations of third and fourth syllables of rooster crows sampled in the field (Kauai) and mined from public databases and literature (worldwide). For sampling details, see Table S2 (Supporting information).

Conservation implications

Our findings complicate management priorities for Kauai's feral flocks, which defy simple classification as RJFs (which are considered threatened) or as domestic chickens (the world's most abundant bird). A morphological study of RJF suggested that they are threatened by genetic pollution (i.e. domestic introgression) throughout their native range (Peterson & Brisbin 1998). Our genetic data indicate the possibilities

of mixed and admixed ancestry on Kauai, confirming the threat admixture poses to native RJF. At the same time, our study highlights the potential of feral birds as reservoirs of genetic variation that might one day abet RJF conservation. Hawaii State law currently protects 'wild chickens' found in natural areas. State agencies also sponsor efforts to eradicate 'free-flying domestic chickens' found in developed areas, which are considered alien pests. Based on the small sample presented here, these conservation and control efforts appear to target a common gene pool derived from both 'heritage' (Polynesian RJF) and feralized *G. gallus* founders. Ecological effects of Hawaiian *G. gallus* have not been studied but probably include deleterious impacts on the islands' natives and endemics. Thus, genetic, cultural and environmental considerations present both ethical and applied challenges for feral chicken management.

The variation we report from Kauai could also contribute to the future sustainability of chickens, a globally critical food resource. There is evidence of losses of genetic diversity during *G. gallus* domestication (Muir et al. 2008), which may limit its resilience to future environmental challenges (e.g. pathogens, extreme temperatures, drought). Our case study corroborates the idea that selective and neutral processes might promote genetic variation in feral taxa, which could therefore (theoretically) assist evolutionary rescues of genetically depleted domestic populations (Price 1984).

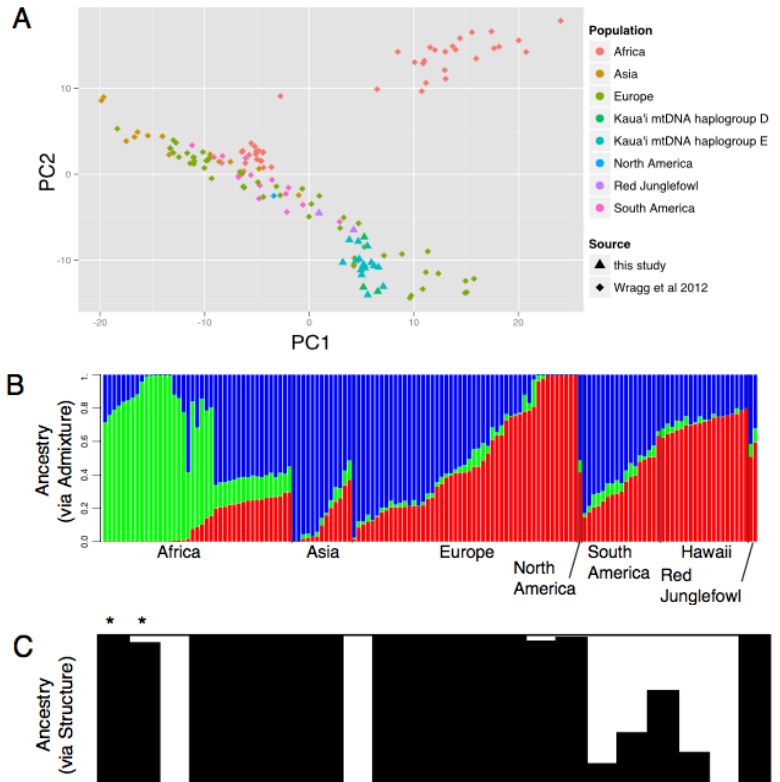


Fig. 5 (A) PCA plot of genetic data showing PC1 vs. PC2 for samples from Kauai in relation to various other chicken breeds (taken from Wragg et al. 2012). (B) ADMIXTURE plot showing probable ancestry of Kauai samples in relation to other chicken breeds (using data from Wragg et al. 2012). (C) STRUCTURE plot indicating assignment proportions for individuals sampled on Kauai. *Individuals with Dclade mitochondrial sequences. RJF = Red Junglefowl sequences sampled from a captive population (see Table S1, Supporting information).

Regardless of whether Kauai's feral *G. gallus* merit conservation or eradication, they offer a valuable but potentially fleeting opportunity to study evolution in action. Feral chickens are far less abundant on all other Hawaiian Islands, perhaps owing to the presence of natural predators (e.g. mongoose) outside of Kauai. Mongoose became extremely abundant on other islands following deliberate introduction to Hawaii for rodent biocontrol (Mooney & Drake 1986). Considering the success of many other exotic and biocontrol species in interisland colonization, mongoose may soon arrive on Kauai. Given the potential for future population decline or extirpation, we advocate further study of the island's feral chickens. This work will both further document standing diversity and provide baseline data for assessing the impacts of mongoose or other invasions.

Further studies of Pacific feral chickens can help to illuminate how the genetics of colonizing species (e.g. admixture and recombination) can promote biotic invasions (e.g. Hovick & Whitney 2014). Prior work on feral *G. gallus* has principally focused on reconstructing human migration into the Pacific (e.g. Storey *et al.* 2007). As a result, little is presently known about the distribution or consequences of ancestral and derived (domesticated) traits within feral populations. Because domestication commonly involves the elaboration of key life history traits such as growth and fecundity, we might expect the introgression of domesticated alleles into ancestral reservoirs to facilitate population expansion and persistence. Recent work indicates that such introgression has occurred within diverse taxa (e.g. Grossen *et al.* 2014), but its ecological and evolutionary

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consequences are presently unclear. A rich literature on the domestication process makes studies of 'reverse domestication' well poised to enhance our understanding of colonizing species' genetics, which has remained an active area of biological research over the last 50 years (e.g. other articles in this issue, Whitney & Gering 2015).

Conclusions

In summary, the chickens present on Kauai represent an incredibly valuable resource for conservation and scientific study, allowing examinations of causes and consequences of admixture and feralization. We have shown that birds inhabiting Kauai today exhibit characteristics of both original RJF founders and more recently derived European domestics; these characteristics may be involved in adaptation to feral environments. Changes in social and ecological environments attending feralization are likely to promote evolutionary changes, offering exciting possibilities to study adaptation under complex selection regimes. From a conservation perspective, Kauai's *G. gallus* now present something of a conundrum, as they exhibit genetic and phenotypic signatures of RJF ancestry, reflecting possible 'heritage' origins, as well as traits and alleles from invasive domesticated breeds. This complexity presents many challenges and possibilities for further evolutionary studies of 'reverse-domestication' processes.

For full article: Gering, E., et al. "Mixed ancestry and admixture in Kauai's feral chickens: invasion of domestic genes into ancient Red Junglefowl reservoirs." *Molecular Ecology* (2015) 24, 2112-2124. Published by John Wiley & Sons Ltd., March 6, 2015

[A link to the full article will be made available on our website](#)

HAS Celebrated International Migratory Bird Day on Kona Coast.

By Lance Tanino

On Saturday, May 9, 2015, four Big Island residents from Waimea, Kailua-Kona, and Pahoa participated in a Hawaii Audubon Society field trip along the Kona coast. We celebrated International Migratory Bird Day as well as eBird's Global Big Day by birding along the Kona coastline.

We encountered 21 species at three locations (Keahole Point, Kealahou Wastewater Treatment Plant (WWTP), and Kaloko-Honokohau National Historical Park) during our three-hour birding trip. The highlights included:

-Franklin's Gull (*Leucophaeus pipixcan*) - There were four adults in breeding plumage foraging and resting at Kealahou WWTP. April and May is the only time of year to encounter adult breeding plumaged gulls in the islands and is always Franklin's Gull. The arrival of Franklin's Gulls is one of the few signs of spring migration in the Hawaiian Islands, as they will continue their journey to their breeding grounds in the prairie regions of interior western North America. Interestingly, the gulls were very vocal, not usually the case with other gull species that show up in the islands.

-Hawaiian Coot (*Fulica alai*) - There were 28 present at Kealahou WWTP and there were a number of active nests and nests under construction. It was very disturbing to notice closely through my spotting scope man-made materials flushed down toilets being used as nest material by our endemic and endangered Hawaiian Coots.

-Shorebirds - Although most winter resident shorebirds left the islands last month, over 30 of them were still present in the second week of May during our trip: Pacific Golden-Plover (7), Ruddy Turnstone (6), and Wandering Tattler (15). A few of them were in breeding plumage but most were in non-breeding plumage and will more than likely over-summer.

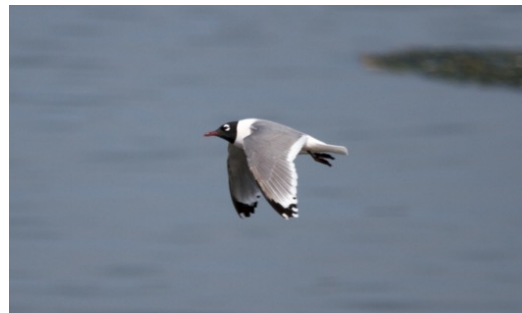


Photo taken by Sherman Wing



(left to right) Fred Lindsey (Kailua-Kona), John Lynch (Kailua-Kona), and Sherman Wing (Pahoa)

Upcoming Field Trips, Volunteer Opportunities & Events

Please RSVP with name and contact information to
Hawai'i Audubon Society at 808-528-1432 or hiaudsoc@pixi.com unless otherwise specified

Kawainui Marsh Restoration Saturday, August 1st from 9am – noon

Volunteer at the monthly Kawainui Volunteer Day led by DLNR/DOFAW. HAS has adopted ponds #10 and 11. Support some of Hawaii's most endangered waterbirds and contribute to the success of the new restoration ponds behind Castle Medical Center in Kailua (at the end of Ulukahiki St.)



Photo Nate Yuen

Tour of the Red-footed Booby Colony on Marine Corps Base Hawaii Kaneohe Friday July 10th: Check in at 8am, Tour 9-11am Must RSVP by June 24th. Limited to 20 people

The Red-footed Booby colony located in the heart of an active training range on Marine Corps Base Hawaii is one of only two large booby colonies in the Main Hawaiian Islands; the other is managed by the Fish & Wildlife Service on Kauai. Approximately 2500 Boobies loaf or nest in the Ulupa'u Crater Wildlife Management Area. The Boobies have become quite acclimated to the sound of weapons fire and explosions on the Range. The Red-footed Booby is white with brown wings, has a blue bill and red feet. It is currently the Booby nesting season, so you will see young chicks in the nests that look like white cotton balls with black leathery bills. Red-footed boobies feed at sea, but nest on land in coastal trees and low growing shrubs; they are the only tree dwelling Booby in Hawaii and are the smallest of more than half a dozen booby species. At the colony on MCB Hawaii, you can get quite close to them and their nests, but please stay at least 10 feet away so as not to cause stress to the adults or chicks. Pictures are permitted.

Nature Hike to Kahuku Point and Wetlands at Turtle Bay Saturday, July 18th; 9am-12pm

Meet outside the Helipad @ 8:45am

Be prepared to see Hawaiian monk seals, turtle nest sites, endangered and endemic plants, rare Hawaiian bee nesting areas, shore birds, sea birds, endangered water birds, possibly nene and who knows what else. Folks can either join us

for the 2 mile walk to Kahuku Point (4 miles total) 1.5 hours or do the 5 mile loop which would include seeing the waterbirds, 3 hours. Kids welcome. Some kind of backpack carrier for little ones recommended. 80% of the terrain is dirt path, the rest is beach. Bring sunscreen, water, cameras, binoculars and wear a swimsuit under your clothes for a dip in the Keiki Cove on the way back if you fancy doing that.

Bathrooms are adjacent to Ola Restaurant.

RSVP ahuntemer@aol.com or 808-224-3101 with the number in your party and cell phone numbers. More details emailed a few days before.

Paiko Lagoon Welcome Home Shorebirds Saturday, August 29th 8:30am

Check out birds, limu, and sea creatures that may be at Paiko Lagoon! Remember to wear protective shoes, clothing and sunblock. Meet at Kuli'ou'ou Road.

Please RSVP to Alice with your name and phone number at 808-864-8122

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The Hawai'i Audubon Society offers grants for research in Hawaiian or Pacific natural history. Awards are oriented toward small-scale projects and generally do not exceed \$500.00.

Proposals are reviewed semi-annually, with the next deadline falling on **OCTOBER 1ST**. Email hiaudsoc@pixi.com for an application or visit the "Programs & Projects" section of our website at www.hawaiiiaudubon.org.

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Shorebird Farewell at Paikō Lagoon Wildlife Sanctuary

by Alice P S Roberts



Photo Roberta Chun

Low-Tide Reef-Walk: Saturday, April 18th, 2015, 8-10:00 am

As seven of us gathered on Kuli'ou'ou Road at 8:00, we observed many mixed ducks: light brown to classic Mallard, some with obvious white Eastern Duck in them. Most looked like a cross of Mallard X Koloa. We did not see any of the expected black ducks, until you looked closely at the beautiful iridescent blue-green feathers. We saw no babies and only a few young. Of course, throughout the two hours we saw and heard many urban birds such as mynas, finches, zebra doves, and a Red-Vented Bulbul.

As we walked out, we spoke about many plants: Milo, a hibiscus relative with a gorgeous carving wood; Coconut Palm; Ironwood, *Casuarina equisetifolia* with both male and female parts active. I've been told machetes chip when cutting this species.

Pickleweed, 'Ākulikuli-Kai; 'Ākulikuli with beautiful little pink star flowers, and 'Aki'aki grass. Though much of the Kiawe has been removed, some small trees with thorns can still be found.

Once down to the beach we saw many male ghost crab holes with their advertising pyramids and a couple of babies scurrying to the water. Surprisingly we saw only a few shorebirds. We expected to see many fattening up for their flights north. We did see two Kōlea, my favorite "PGPs" or Pacific Golden-Plovers (*Pluvialis fulva*). One Wandering Tattler ('Ūlili, *Heteroscelus incanus*) flew into view calling its Hawaiian name: ulili-ulili-ulili-ulili. We saw no Ruddy Turnstones ('Akeke/Keke, *Arenaria interpres*) doing their stone-flipping. High up in the sky, we saw a Frigatebird ('Iwa, *Fregata minor palmerstoni*) but could not determine its sex. This is the first 'iwa I've seen in the past couple trips, after years of seeing at least one every trip. Several White Terns (Manu-O-Kū, *Gygis alba*) were visible, and several Cattle Egrets (*Bubulcus ibis*) with their s-shaped necks and legs out behind. We did not see the usual Black-Crowned Night-Heron ('Auku'u, *Nycticorax nycticorax hoactli*). We heard and then saw two Black-Necked Stilts (Ae'o/Kukuluae'o, *Himantopus mexicanus knudseni*) fly over us.

In the -0.4ft low water we saw a couple schools of little Mullet/'ama'ama and lots of tiny Gobies, a family of fish interesting for their use of pelvic fins as suction cups for jumping waterfalls on their spawning return to freshwater streams of their birth. We found a whole crab molt and a box crab carapace. We usually see many crabs.

During our walk we threw many clumps of leathery mudweed, an invasive seaweed/algae, up above the high tide line to dry out and die, but saw very few other seaweeds. It looked surprisingly barren. There was a noticeable lack of any Hypnea, Acanthophora or Padina. We talked about many conservation issues, flora and fauna, and the geology of the area. As always, as we returned to our starting point, we collected several bags of trash.

For those of you that have been to Paikō with me before, we found 2 "tongues", but NO "sand balls".

Will I see you Saturday, the 29th of August 2015, on Kuli'ou'ou Road at 8:30am? Call me (808) 864-8122.



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Nature Hike to Kahuku Point and Wetlands at Turtle Bay
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Paiko Welcome Home Shorebirds
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