

## FIRST NORTH AMERICAN RECORD OF THE COMMON MOORHEN (*GALLINULA CHLOROPUS*) CONFIRMED BY MOLECULAR ANALYSIS

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On 12 October 2010 Schwitters briefly observed a gallinule or moorhen in a small interior wetland on Shemya Island, Alaska (52° 43' N, 174° 07' E). In spite of considerable effort, he could not find the bird again until the evening of 14 October 2010, when it was relocated foraging in another interior wetland (Figure 1) and was collected (University of Alaska Museum [UAM] 27369). The bird likely arrived on Shemya with a decaying typhoon (Malakah) that passed just north of the island on 27 September 2010 but went undetected in the intervening time because of its secretive behavior. The specimen is a juvenile male with the following characteristics: mass 269 g, trace amounts of fat, left testis 4 × 2 mm, wing chord 169 mm, tail 62 mm, tarsus 50.1 mm, bill (from anterior edge of nares) 14.5 mm, bill height (at same point) 8.8 mm, bill width 5.2 mm, feet/legs yellow-green (Figure 2).

The American Ornithologists' Union's checklist committee (Chesser et al. 2011) recently split the Old and New World populations of *Gallinula chloropus* into two species, the New World Common Gallinule (*G. galeata*) and the Old World Common Moorhen (*G. chloropus*), on the basis of differences in vocalizations (Constantine et al. 2006) and mitochondrial DNA (Groenenberg et al. 2008).

In North America, *G. galeata* ranges primarily in the eastern and southern regions, occurring locally from southeastern Minnesota, central Wisconsin, the northern lower peninsula of Michigan, southern Ontario, extreme southern Quebec, eastern New Brunswick, and western Nova Scotia south to Costa Rica and the coast of the Gulf of Mexico, as well as on Bermuda and throughout the West Indies. West of the Great Plains it is local in New Mexico, Utah, Arizona, Nevada, and California. Northern populations are migratory, while the localized western populations are largely sedentary (Bannon and Kiviat 2002). North of California there are few records: 10 from Oregon (two in winter, one in April, and seven in May, all but one of single birds—H. B. Nehls, Oregon Bird Records Committee, in litt., October 2011), none from Washington (see Wahl et al. 2005), and one in extreme southwestern British Columbia (one, May–June 1981, Campbell et al. 1990).

In the Old World, *G. chloropus* is widely distributed, breeding in the Azores, northern Africa, and the greater part of Eurasia (Vaurie 1965, Cramp and Simmons 1980), east to Japan (Hokkaido) and the southern Kuril Islands (OSJ 2000). North and east of the Kuriles, there have been three extralimital records in the Russian Far East: two in southern Kamchatka (Bolshaya River, in October 1974, and Nalicheva River, 29 October 1981; Artyukhin et al. 2000) and one in the Commander Islands (Bering Island, 24 April 1956; Marakov 1962, Artyukhin et al. 2000). More northerly populations are migratory (Vaurie 1965), with most birds leaving northern Japan by mid-October (Brazil 1991).

With over a dozen described subspecies, geographic variation in the former *G. chloropus* is considerable, although it is mostly clinal within each hemisphere (Cramp and Simmons 1980, del Hoyo et al. 1996). The birds of eastern Asia, sometimes separated as subspecies *indica* (Vaurie 1965), average smaller than birds from elsewhere in the Old World—all of which average smaller than New World birds. Measurements of Old World and New World birds overlap considerably (see Ridgway and Friedmann 1941, Cramp and Simmons 1980, Pyle 2008), however, and they

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could not be used to indicate the origin of the Shemya bird. Similarly, the age of the Shemya bird prevents use of several important defining characters useful in identifying adult specimens, e.g., size, coloration, and shape of the bill and ornamental shield. Determining the origin of the Shemya bird therefore required a molecular comparison.

To provide a molecular framework for comparison, we obtained 17 sequences of cytochrome oxidase subunit I from GenBank, and we sequenced this gene in a sample of one additional Old World bird at UAM. These sequences represented eight specimens of Old World *G. chloropus* and 10 of New World *G. galeata* for comparison with the Shemya bird (Table 1).

We extracted DNA from frozen tissues with a DNeasy tissue kit (Qiagen, Valencia, CA) by following the manufacturer's protocol. To amplify the DNA by the polymerase chain reaction (PCR) we followed the protocols of Kerr et al. (2007). The High-Throughput Genomics Unit of the University of Washington, Seattle, cleaned the product of the PCR by an ExoSAP process, cycle-sequenced the DNA with BigDye (Applied Biosystems, Foster City, CA), using an internal forward primer (AGGCTTTG-GCAACTGACTAGTACC) and an internal reverse primer (AGATGGCTAGGTC-TACTGAAGCAC), and sequenced it on a high-throughput capillary sequencer. We aligned and edited the sequences with Sequencher 4.7 (Gene Codes, Ann Arbor, MI) and archived them in GenBank with accession numbers JN982467 and JN982468.

We sequenced 416 base pairs of cytochrome oxidase subunit I from the Shemya bird. Comparison of homologous sections of the 18 reference sequences obtained from GenBank and UAM tissue holdings revealed 15 positions with fixed differences between Old and New World specimens and two sites with variations that the Old and New World clades shared. At all 15 of these positions the Shemya bird had the bases characteristic of Old World specimens, indicating it was probably of Old World origin (Table 1). Similarly, a parsimony analysis with 1000 bootstrap replicates (run in PAUP version 4.0b10; Swofford 2003) of the cytochrome oxidase subunit I data from the 19 gallinules and moorhens and five sequences from four close relatives (Table 2) clearly placed the Shemya bird with other Old World birds (Figure 3).

Rails as a group are known for their propensity to appear far from their normal ranges (Ripley 1977, Taylor 1998), and moorhens/gallinules in particular are adept at colonizing remote islands (Olson 1973). They have been recorded as vagrants in Greenland, where all records are of the North American *G. g. cachinnans* (Boertmann 1994). Nominata *G. c. chloropus* has been recorded from Iceland and Spitsbergen (AOU 1998); Taylor (1998:499) misread AOU (1983) in attributing *cachinnans* to the Commander Islands. Given the distribution of *Gallinula* in Eurasia and North America and the Asian origins of most migrant birds reaching the western Aleutian Islands (Gibson and Byrd 2007), it is not surprising that the Shemya bird came from Asia.

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**Table 1** The 17 Variable Positions in the 416 Base Pairs of Cytochrome Oxidase Subunit I<sup>a</sup>

GenBank accession number	Location	Variable sites
<i>Gallinula chloropus</i>		
JN982467	Germany	TACAGCCCTGCTTCCTT
JF498859	Japan	TACAGCCCTGCTTCCTT
HQ896036	Old World	TACAGCCCTGCTACCTT
EF515779	S. Korea	TACAGCCCTGCTTCCTT
GQ481956	Russia	TACAGCCCTGCTTCCTT
GU571907	Sweden	TACAGCCCTGCTTCCTC
GU571906	Sweden	TACAGCCCTGCTTCCTT
GU571413	Norway	TACAGCCCTGCTTCCTT
JN982468	Shemya	TACAGCCCTGCTTCCTT
<i>Gallinula galeata</i>		
DQ433655	Quebec	CCTGCTTTCATATTTCT
DQ433657	Quebec	CCTGCTTTCATATTTCT
DQ434600	Ontario	CCTGCTTTCATATTTCT
DQ433656	Ontario	CCTGCTTTCATATTTCC
DQ433654	Ontario	CCTGCTTTCATATTTCT
FJ027610	Argentina	CCTGCTTTCATATTTCT
FJ027609	Argentina	CCTGCTTTCATATTTCT
FJ027608	Argentina	CCTGCTTTCATATTTCT
DQ432936	Florida	CCTGCTTTCATATTTCT
JF498856	Hawaii	CCTGCTTTCATATTTCT

<sup>a</sup>Of these, 15 are fixed in the New World or Old World populations; the Shemya bird has all of the fixed Old World variants. Sites correspond to positions 6904, 6958, 6967, 7000, 7003, 7108, 7150, 7159, 7165, 7198, 7207, 7216, 7236, 7240, 7243, 7279, and 7300, respectively, in the mtDNA genome of the chicken.

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Figure 1. The Shemya Common Moorhen (*Gallinula chloropus*) in life on 14 October 2010.

Photo by Michael T. Schwitters



Figure 2. Prepared specimen of the Common Moorhen collected 14 October 2010 on Shemya Island, Alaska.

Photo by Jack J. Withrow

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**Table 2** GenBank Accession Number, Source, and Vouchers Numbers of Specimens Used in Molecular Comparisons

Species and location	Genbank accession	Source	Voucher
<i>Gallinula chloropus</i>			
Shemya	JN982468	this study	UAM 27369
Germany	JN9824677	this study	UAM 18775
Russia: Tyumen` region	GQ481956	Kerr et al. 2009	ZMMU RYA 1902
Norway: Rogaland, Utsira	GU571413	Johnsen et al. 2010	NHMO-BC46
Sweden: Skane	GU571907	Johnsen et al. 2010	BISE-Aves92
Sweden: Oland	GU571906	Johnsen et al. 2010	BISE-Aves413
South Korea	EF515779	Yoo et al. 2006	KRIBB2684
Old World	HQ896036	Kan and Li unpubl. data	?
Japan: Chugoku	JF499135	Kerr and Dove unpubl. data	USNM 641876
<i>Gallinula galeata</i>			
Argentina: Entre Rios	FJ027610	Kerr et al. 2009	MACN-Or-ct 1946
Argentina: Corrientes	FJ027609	Kerr et al. 2009	MACN-Or-ct 1788
Argentina: Corrientes	FJ027608	Kerr et al. 2009	MACN-Or-ct 1414
Canada: Quebec	DQ433655	Kerr et al. 2007	CWS42847
Canada: Ontario	DQ434600	Kerr et al. 2007	LMA865-05699
Canada: Quebec	DQ433657	Kerr et al. 2007	CWS42846
Canada: Ontario	DQ433656	Kerr et al. 2007	AXBS003
Canada: Ontario	DQ433654	Kerr et al. 2007	CWS42845
USA: Florida	DQ432936	Kerr et al. 2007	USNM 622527
USA: Hawaii	JF498859	Kerr and Dove unpubl. data	USNM 643457
<i>Gallinula melanops</i> (Spot-flanked Gallinule)			
Argentina: Corrientes	FJ027612	Kerr et al. 2009	MACN-Or-ct 3055
Argentina: Corrientes	FJ027611	Kerr et al. 2009	MACN-Or-ct 1692
<i>Fulica atra</i> (Eurasian Coot)			
Japan: Chugoku	JF499133	Kerr and Dove unpubl. data	USNM 641834
<i>Fulica alai</i> (Hawaiian Coot)			
USA: Hawaii	JF498858	Kerr and Dove unpubl. data	USNM 643398
<i>Fulica americana</i> (American Coot)			
Canada: Ontario	DG434598	Kerr et al. 2007	LMA1046-29312

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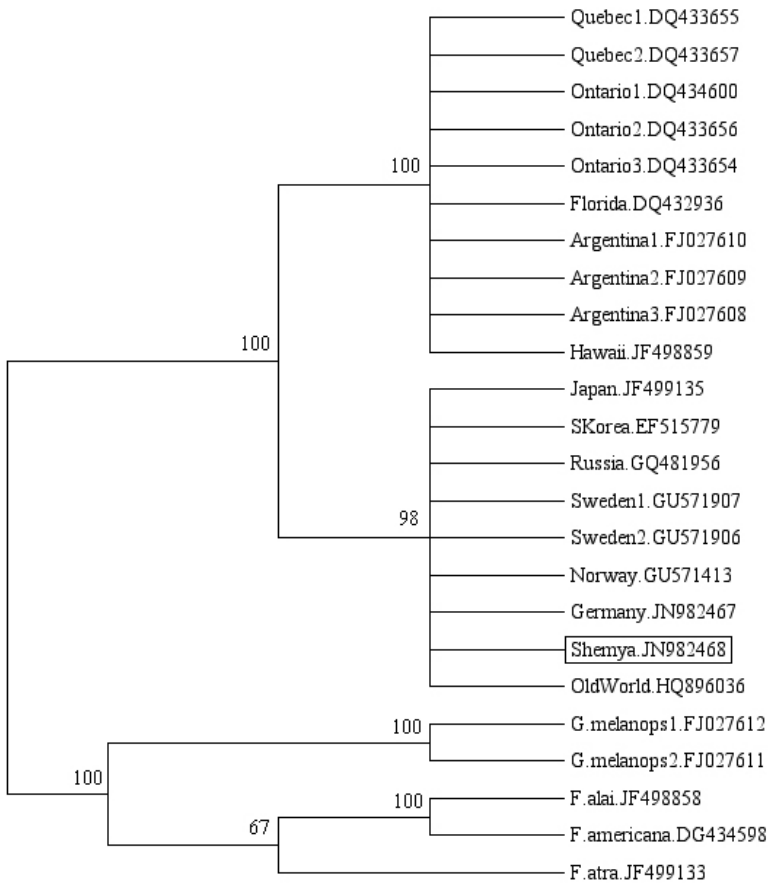


Figure 3. Parsimony analysis of 416 base pairs of cytochrome oxidase subunit I, in which sequences of the Old World Common Moorhen (*Gallinula chloropus*), the New World Common Gallinule (*G. galeata*), and outgroups (*G. melanops*, *Fulica alai*, *F. americana*, and *F. atra*) cluster by species. The Shemya bird (boxed) groups with the Old World birds. Numbers above nodes are the percentage of 1000 bootstrap replicates in which the node appeared. Letters and numbers after location (for moorhens and gallinules) or taxon name (for outgroups) are GenBank accession numbers.

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After 13 years as associate and assistant editor, Kathy Molina stepped down this year. It's with much regret I make this announcement, as Kathy has played a critical role in sustaining the scientific quality of *Western Birds* since 1999. As the person coordinating the reviews of manuscripts with our associate editors, and recruiting many reviewers, reviewing many manuscripts, and providing feedback to many authors herself, Kathy has made a monumental and lasting contribution to WFO and to ornithology. Her leadership in developing the scientific content of *Western Birds* has been central to our success, and I cannot thank her enough for lending her expertise, diligence, and valuable time to our journal.

At the same time, I'm delighted to announce that Daniel D. Gibson is stepping into the role of assistant editor. Dan Gibson has played many key roles in WFO for many years—associate editor, board member, vice-president, reviewer, indexer, author, and tireless promoter—and his commitment to *Western Birds* is something for which we should all be thankful. Dan spearheaded the festschrift in honor of Bob Dickerman that constitutes this issue. It's with much fondness as well as gratitude that I call both Kathy and Dan colleagues and friends.

*Philip Unitt*