

COMMENTARY

DEMOGRAPHY, GENETICS, AND THE VALUE OF MIXED MESSAGES

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Abstract. Iverson et al. (2004) used estimates of the homing rate for molting adult Harlequin Ducks (*Histrionicus histrionicus*) in Alaska to draw inferences about population structure. Homing rates, defined as one minus the ratio of birds recaptured elsewhere to those recaptured at the original banding site, were high (0.95–1.00) for males and females. Iverson et al. (2004) concluded that these high rates of homing are indicative of demographic independence among molting groups separated by small distances (tens to hundreds of kilometers) and that conservation efforts should recognize this fine-scale population structure. We re-examined their use of the homing rate, because their assumption of equal detection probability across a wide sampling area could have led to an upward bias in their estimates of site fidelity. As a result, we are hesitant to agree with their conclusion of high adult homing to molting areas and that molt-site fidelity is evidence for demographic independence. Our hesitancy stems from the fact that little is known about juvenile and adult movements within and among years, breeding area origins, and the variation of demographic parameters (e.g., survival and productivity) among molting groups. Furthermore, population genetic data of these molting groups suggest gene flow at both nuclear and mitochondrial loci. Such mixed messages between demographic (i.e., banding) and genetic data are increasingly common in ornithological studies and offer unique opportunities to reassess predictions and make more robust inferences about population structure across broad temporal and spatial scales. Thus, we stress that it is this broader scale perspective, which combines both demography and genetics, that biologists should seek to quantify and conservation efforts should seek to recognize.

Key words: Harlequin Duck, *Histrionicus histrionicus*, homing rate, population structure, winter philopatry.