Abstract  We studied the population structure of a high arctic breeding wader bird species, the White-rumped Sandpiper *Calidris fuscicollis*. Breeding adults, chicks and juveniles were sampled at seven localities throughout the species’ breeding range in arctic Canada in 1999. The mitochondrial control region was analysed by DNA sequencing, feathers were analysed for carbon isotope ratios (C\(^{13}/\)C\(^{12}\)) by isotope ratio mass spectrometry, and morphological measurements were analysed using principal component analyses, taking the effect of sex into account (identified by molecular genetic methods). In general, our results support the notion that the White-rumped Sandpiper is a monotypic species with no subspecies, and most of the morphological and genetic variation occurs within sites. Nevertheless, some differences between sites were found. Birds from the two northernmost sites (Ellesmere and Devon Islands) had relatively longer bill and wing and shorter tarsus than birds sampled further south, possibly reflecting genetic differences between populations. The carbon isotope ratios were higher at the easternmost site (Baffin Island), revealing differences in the isotope content of the food. The mtDNA sequences showed no significant differentiation between sites and no pattern of isolation-by-distance was found. Based on the mtDNA variation, the species was estimated to have a long-term effective population size of approximately 9,000 females. The species shows no clear evidence of any population expansion or decline. Our results indicate that carbon isotope ratios, and possibly also certain mtDNA haplotypes, may be useful as tools for identifying the breeding origin of White-rumped Sandpipers on migration and wintering sites.

Keywords  mtDNA sequencing · Phylogeography · Population genetics · Principal component analysis · Stable isotopes analysis

Introduction

The development of population markers that can be used to recognise birds from different breeding populations makes it possible to follow bird populations throughout their annual cycle. Thereby, many new aspects of bird migration patterns can be studied, as well as adaptations to the different environments that the birds encounter during different parts of the year. Various types of population markers have been applied on migrating birds, including morphological characters, genetic markers and stable isotopes (Engelmoer and Roselaar 1998; Haig et al. 1997; Hobson 1999). For example, in the Willow Warbler *Phylloscopus trochilus*, wing length was used to distinguish between populations from northern and southern Sweden (Lindström et al. 1996). Genetic analysis of mitochondrial DNA was used to reveal the breeding origins of Dunlin *Calidris alpina* on migration stop-over and wintering sites (Wenink and Baker 1996; Wennerberg 2001a), and analyses of stable isotopes ratios in feathers have been used to identify natal origin and moulting sites of several passerine species (Chamberlain et al. 1997, 2000; Hobson and Wassenaar 1997; Hobson et al. 2001).

We have studied the White-rumped Sandpiper, *Calidris fuscicollis*, one of the worlds’ most extreme long-distance migrant birds. It breeds on the high arctic tundra of northern Canada and Alaska, and makes extraordinary flights over the Atlantic Ocean to winter in southern South America (Parmelee 1992). No population differentiation has been described in the species and it is generally considered to be a monotypic species (del Hoyo et al. 1996; Parmelee 1992). The only study of the genetic variation of the White-rumped Sandpiper, a study of
allozymes by Baker et al. (1985), was carried out outside the breeding range. It showed no genetic differentiation between individuals from James Bay (Canada) and Camarones (Argentina). Yet, the breeding origins of these birds were unknown, making it unclear whether the result also reflects genetic similarity between breeding populations. Thus, the conclusion that the White-rumped Sandpiper is monotypic requires further investigation.

In this paper, we examine various aspects of the population structure of the White-rumped Sandpiper. We (1) describe the genetic structure of the species, using mitochondrial DNA sequences, and (2) look for parameters (mtDNA, morphology and stable isotope ratios) that could potentially be used to distinguish populations outside their breeding area. Population markers would be valuable tools in studies of bird migration. The genetic structure of the species gives information about, e.g. breeding site-fidelity and dispersal rates, and can be used as a way to acquire insight into the species history, as well as being important for conservation issues.

Using various techniques and samples from geographically divergent areas throughout the species’ breeding range, we describe the intraspecific variation in the White-rumped Sandpiper today. We also discuss the evolutionary history of the species leading up to its present geographic pattern, and use genetic data to test some possible factors involved.

**Materials and methods**

The field work was carried out during a ship-borne expedition to the Canadian Arctic in summer 1999 (“Tundra North West 1999”; Grönlund 2000). At 18 different sites, we spent 24–48 h ashore, trapping shorebirds. White-rumped Sandpipers were caught at seven localities throughout the species breeding range (Fig. 1). Adults birds were caught in walk-in traps on their nests and chicks were trapped by hand (sites 3, 6). Fledged juveniles were trapped in mist-nets or walk-in traps at feeding sites along rivers, lakes and the seashore (sites 11, 12, 15–17; Lindström et al. 2002). The birds were ringed and measured, after which small samples of feathers and blood were collected (see below) and the birds were released.

Our analyses are based on the assumption that independent juveniles originated from breeding areas close to the sampling locality, because (1) the sampling sites were situated in or near suitable breeding habitat within the species’ breeding range and (2) it is unlikely that birds from one sampling site would pass the other sites on migration (Fig. 1). All White-rumped Sandpipers seem to head for main stopover areas in southeastern Canada (Harrington et al. 1991) and radar studies from Canada show that arctic waders on autumn migration prefer to fly along great circle routes (Alerstam et al. 2001; Fig. 1). Thus mixing of birds from western and eastern sites is unlikely, but mixing of birds from nearby sites can not be excluded by these criteria (but see also Results).

We analysed the intraspecific variation in a number of characters, investigating both genetic and phenotypic variation. Three types of data from the same individuals were combined: morphological measurements, mitochondrial DNA sequences and stable isotope ratios, revealing different aspects of population structuring.