Typology Revisited: Historical Taxa of the Bean Goose - Pink-Footed Goose Complex

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Typology revisited: historical taxa of the bean goose – pink-footed goose complex

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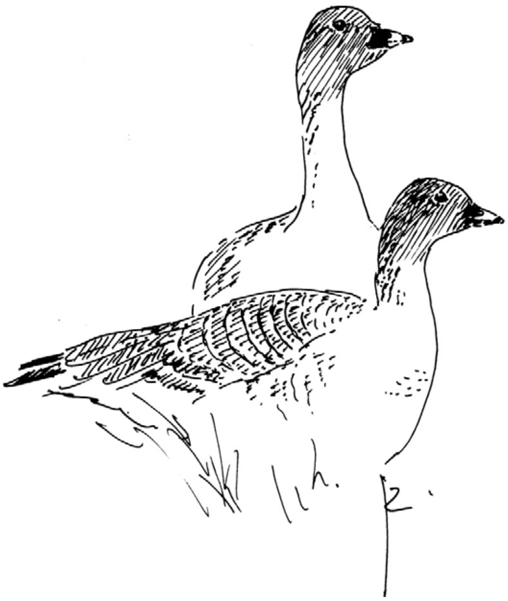

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Taxonomic practices change over time and this affects the number of taxonomical units recognized. In late 19th and early 20th centuries the number of species increased as a consequence of typological thinking, i.e. classifying all aberrant individuals to a separate species. During this period, several species or subspecies of the bean goose complex were described, and currently their status is either considered not valid or is not agreed upon. We studied individuals from five of the historical taxa, *Anser neglectus*, *A. mentalis*, *A. oatesi*, *A. fabalis johanseni* and *A. fabalis curtus*, by using mitochondrial DNA and morphological measurements to clarify their taxonomical status. Overall, we did not find support for additional taxa other than those currently recognized.

Key words: Bean Goose, *Anser fabalis*, Middendorff's Goose *Anser middendorffii*, *oatesi*, *mentalis*, *johanseni*, *neglectus*, *curtus*

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As the number of taxa depends on the criteria used to define them, changes in taxonomic practices can be followed by looking at the number of genera, species and subspecies through time (Bock & Farrand 1980). Taxonomy of the Bean Goose *Anser fabalis* and Pink-footed Goose *A. brachyrhynchus* species complex has been subject to numerous changes in species and subspecies assignments through time. Since Naumann (1842) published the first taxonomic view with three species included, the number of species suggested has varied between one and six, with up to eight subspecies (Table 1). Until the late 19th century typological thinking (e.g. Mayr 1970), essentially rejecting intra-specific variation and regarding (morphologically) definable types as separate species, was prevailing. Concordant with the trends in the contemporary taxonomical practices, Alpheraky (1905) and Buturlin (1935) listed six and four species, respectively, even though they both included also subspecies within the species (Table 1). One of the species included by both of them was *A. neglectus* Sushkin, 1897, listed also by Hartert (1921), who was one of the strongest proponents of the polytypic species concept in Europe (Haffer 2001), although in his opinion, more material from the breeding areas would be required to confirm the status. This taxon was still listed by Johansen (1945, Table 1), but as a subspecies, although later authors as well as Johansen (1962) himself have considered its morphological characteristics as variation within a species. Alpheraky (1905) included *A. mentalis* Oates, 1899, as one of the species, whereas later Buturlin (1935) and Johansen (1945) considered this taxon as a subspecies. During the period of typological thinking two additional species were described: *A. oatesi* Rickett, 1901, and *A. curtus* Lönnberg, 1923. From these *oatesi* has received little attention and has not been considered valid by later authors (e.g. Buturlin 1935), but *curtus* was listed as a subspecies by Johansen (1959). Thus, it seems that many of the species described during the typological period were maintained in taxonomy even after the typological thinking was abandoned, although in that case their status was downgraded to the subspecies level. Also other species were described during the period of typological thinking (e.g. *A. carneirostris* Buturlin, 1901, Table 1), but they are outside the focus of this paper (see below) and hence not discussed here.

From the mid-20th century onwards, i.e. after the establishment of population thinking accepting the presence of individual differences within a population

(Mayr 1970), the bean goose – pink-footed goose complex was suggested to include either one or two species with up to eight subspecies (Johansen 1945, Delacour 1951, Dementiev & Gladkov 1952, Johansen 1959, Vaurie 1965, Bauer & Glutz von Blotzheim 1968, Cramp & Simmons 1977, Stepanyan 1990; Table 1). During this period the main controversy has concerned the specific or subspecific status of the taxa, significance of separation between the tundra and taiga breeding birds and validity of yet another subspecies, *A. fabalis johanseni* Delacour, 1951. According to Sangster & Oreel (1996), the number of species was again raised to three (Table 1): the Pink-footed Goose *A. brachyrhynchus* breeding in Greenland, Iceland and Svalbard, the Taiga Bean Goose *A. fabalis* breeding in the taiga zone and the Tundra Bean Goose *A. serrirostris* breeding in the tundra zone of the Palearctic, all species being monotypic. Similarly, a recent molecular phylogeny recognized three species, although different, based on mitochondrial (mt)DNA supported by morphometrics and ecological data (Ruokonen *et al.* 2008).

However, the species' borders and breeding ranges suggested by the latter study differ from previous descriptions. In addition to the Pink-footed Goose *A. brachyrhynchus*, the Bean Goose *A. fabalis*, breeding in the tundra and western taiga zone, and the Middendorff's Goose *A. middendorffii* breeding in the eastern taiga zone of the Palearctic were supported (Ruokonen *et al.* 2008). Three subspecies, *A. fabalis fabalis*, *A. f. rossicus* and *A. f. serrirostris* were further recognised within the Bean Goose, which was based on not sharing mtDNA haplotypes (with the exception of haplotype SER1 shared by *rossicus* and *serrirostris*), being almost monophyletic in the phylogenetic tree, the fact that they inhabit separate breeding areas and probably separate wintering areas as well (Ruokonen *et al.* 2008).

In this paper we have analysed the affinities of five historical and currently abandoned or otherwise controversial bean goose taxa relative to the phylogenetic data on the individuals collected from breeding areas (published in Ruokonen *et al.* 2008). Three of the taxa studied here were originally described as species, *A. neglectus* Sushkin, 1897, *A. mentalis* Oates, 1899, and *A. oatesi* Rickett, 1901, and two as subspecies, *A. fabalis curtus* Lönnberg, 1923, and *A. fabalis johanseni* Delacour, 1951. Some of these taxa are still considered valid by some authors.

METHODS

Sampled individuals are given in Table 2. Total DNA was isolated from museum feathers or skin using proteinase-K digestion followed by ethanol precipitation (Sambrook & Russell 2001).The 5' region of the mitochondrial control region (CRI) was amplified using PCR conditions and primers L180 and H466 as described elsewhere (Ruokonen *et al.* 2000a, b). Double-stranded sequencing of PCR products was carried out by using BigDye 3.1 and ABI PRISM 377 according to manufacturer's instructions. PCR primers were used for sequencing. Haplotype sequences have been submitted to GenBank with accession numbers HM567317–HM567332. The sequences were aligned manually. A neighbour-joining tree with 1000 bootstrap replicates was constructed in MEGA3.1 (Kumar *et al.* 2004) using Kimura's 2-parameter distances. Bayesian analysis was performed with MrBayes v3.0 (Huelsenbeck & Ronquist, 2001). The search was run with four incrementally heated MCMC chains for 10^6 generations using a GTR + gamma model of substitution and default priors. Sampling frequency was set to 100, and the first 1000 trees were discarded as burn-in, yielding a total of 9001 trees for constructing the consensus tree. The primary task of this study was to identify the haplotypes of the historical taxa, and not to construct a phylogeny. Because some of the museum samples were more than 100 years old, a 221 base pairs (bp) fragment of the mtDNA control region was sequenced only. Despite being short, this fragment of the control region includes almost half of the variable sites in the complete control region (29 variable sites in the 1164 bp fragment vs. 13 variable sites in the 221 bp fragment in the Ruokonen *et al.* 2008 data). Further, because of the existence of nuclear copies of mtDNA, the primer design is problematic: there are only a few nucleotide positions that separate the nuclear copy and mtDNA sequence. Not enough nucleotide variation was obtained to construct a robust phylogenetic tree (Fig. 1), and we refer to the original taxonomical paper by Ruokonen *et al.* (2008) for this.

Morphological measurements were taken and analysed as in Ruokonen *et al.* (2008). Bill length, bill nail length and grinning patch (measured from the middle on the visible ridge on the upper mandible to the visible ridge on the lower, in the most wide area) were used in the discriminant function analysis (Stepwise, Wilks' Lambda) to predict the (sub)species memberships for the historical taxa. Bill height was included originally, but was rejected during the analysis since it did not contribute to the model. Wing length was not used since the reference specimens in Ruokonen *et al.* (2008) were collected during the breeding period with at least 32% of the specimens in visible moult. All historical taxa were included to the analysis independently from the previously studied individuals. Means are given ± SE.

RESULTS

A neighbour-joining tree including individuals from the breeding areas (from Ruokonen *et al.* 2008) together with *neglectus*, *mentalis*, *oatesi*, *curtus* and *johanseni* individuals is shown in Figure 1. A Bayesian tree was also constructed with an essentially identical topology, and the posterior probabilities for the branches are shown in Figure 1.

Results of the discriminant function analysis based on bill measurements are shown in Figure 2. The discriminant function analysis of the reference material (included in Ruokonen *et al.* 2008, excluding the historical taxa) classified (Box's M = 29.105, $P = 0.387$) 90.3% of the individuals correctly (*brachyrhynchus* 100% ($n = 25$), *fabalis* 88.2% ($n = 17$), *middendorffii* 100% ($n = 8$), *rossicus* 87.5% ($n = 8$), *serrirostris* 71.4% ($n = 14$)).

***Anser neglectus* Sushkin, 1897**. Description of *A. neglectus* was based on eight birds collected in 1891 in the government of Ufa, Russia, on their autumn migration (Sushkin 1897). The feet and the middle portion of the bill were flesh-coloured, or rosy in some of the birds, whereas in typical bean geese these parts are deep orange. In body dimensions and plumage *A. neglectus* was described to be closer to *rossicus* type bean geese than to pink-footed geese. In later taxonomical lists (Table 1) *neglectus* was maintained as a species until Johansen (1945) downgraded it to a subspecies and later even he considered it merely as a colour phase (Johansen 1962).

Five specimens labelled as *neglectus* were analysed, four of them from the western Palearctic and one from China (Table 2). The *neglectus* individuals were very diverse both in respect of mtDNA and morphology. They carried four different mtDNA haplotypes (Table 2, Fig. 1). Three of the haplotypes have previously been found from *fabalis*, *middendorffii*, *rossicus* and *serrirostris* individuals. One of the individuals, *neglectus* 5, carried a new haplotype. *Neglectus* 2 was a second calendar year bird and could not be assigned to any of the subspecies based on morphology, because the reference material consists of adults only. The others were

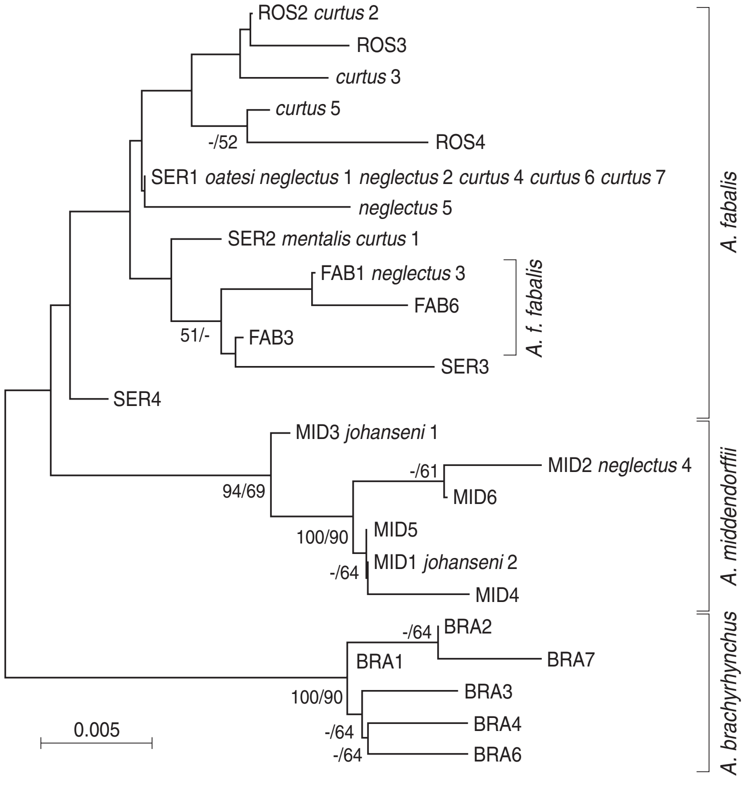

Figure 1. A neighbour-joining tree of mtDNA haplotypes found in the breeding areas and in the historical taxa studied. For each node posterior probabilities (Bayesian analysis)/bootstrap support (neighbour-joining method) above 50% are shown. The scale is based on Kimura's 2-parameter distances in the neighbour-joining analysis. Haplotype names refer to taxa (FAB, *Anser fabalis fabalis*; SER, *A. f. serrirostris*; ROS, *A. f. rossicus*; MID, *A. middendorffii*; BRA, *A. brachyrhynchus*) with the exception of haplotype SER1, which is shared by *rossicus* and *serrirostris*.

Table 1. Taxonomical representations of the bean goose – pink-footed goose by different authors.

Reference	Number of		Species	Subspecies
	species	subspecies		
Naumann (1842)	3	0	*arvensis*[1]	
			segetum[2]	
			brachyrhynchus	
Alpheraky (1905)	6	4	*arvensis*[1]	*arvensis*
				sibiricus
			segetum[2]	*segetum*
				serrirostris
			neglectus	
			carneirostris	
			mentalis	
			brachyrhynchus	
Hartert (1921)	3	3	*fabalis*	*fabalis*
				serrirostris
				sibiricus[3]
			neglectus[3]	
			brachyrhynchus	
Buturlin (1935)	4	7	*fabalis*[4]	*fabalis*
				sibiricus
			serrirostris[5]	*serrirostris*
				rossicus
				carneirostris
				mentalis
				anadyrensis
			neglectus	
			brachyrhynchus	
Johansen (1945)	1	8	*fabalis*	*fabalis*
				middendorffii
				sibiricus
				rossicus
				serrirostris
				neglectus
				mentalis
				brachyrhynchus
Delacour (1951)	1	6	*fabalis*	*fabalis*
				johanseni
				middendorffii
				rossicus
				serrirostris
				brachyrhynchus

Table continued on next page.

assigned to *rossicus* or *fabalis* (Fig. 2, Table 2). For two individuals the mtDNA haplotype and subspecies based on morphology did not agree. *Neglectus* 3 carried a *fabalis* haplotype, but was assigned to *rossicus* based on the bill measurements. *Neglectus* 4 had a *middendorffii* haplotype, but grouped with *fabalis* based on morphology. However, both individuals were very close in their measurements to the subspecies indicated by their mtDNAs (Fig. 2).

***Anser mentalis* Oates, 1899**. In going through the Seebohm collection, Oates (1899) paid attention to one of the specimens originating from Yokohama, Japan. The bird resembled the common bean goose in plumage, except that the chin was white. Additionally, the bill was described as massive. This one individual was enough to convince Oates that a previously overlooked species, *A. mentalis*, occurred in Japan and probably in China and Burma (presently Myanmar).

Table 1. Continued.

Reference	Number of		Species	Subspecies
	species	subspecies		
Dementiev & Gladkov (1952)	1	4	*fabalis*	*fabalis* *serrirostris* *sibiricus* *brachyrhynchus*
Johansen (1959)	2	5	*fabalis*	*fabalis* *johanseni* *middendorffii* *rossicus* *serrirostris*
			brachyrhynchus	
Vaurie (1965)	1	6	*fabalis*	*fabalis* *johanseni* *middendorffii* *rossicus* *serrirostris* *brachyrhynchus*
Bauer & Glutz von Blotzheim (1968), Cramp & Simmons (1977)	2	5	*fabalis*	*fabalis* *johanseni* *middendorffii* *rossicus* *serrirostris*
			brachyrhynchus	
Stepanyan (1990)	1	4	*fabalis*	*fabalis* *middendorffii* *serrirostris* *brachyrhynchus*
Sangster & Oreel (1996)	3	0	*fabalis* *serrirostris* *brachyrhynchus*	
Ruokonen *et al.* (2008)	3	3	*fabalis*	*fabalis* *rossicus* *serrirostris*
			middendorffii *brachyrhynchus*	

[1] *arvensis* refers to taiga-breeding birds.
[2] *segetum* refers to tundra-breeding birds.
[3] Hartert (1921) makes a comment that more material from the breeding areas is required to confirm the status.
[4] In Buturlin's classification *A. fabalis* includes the taiga-breeding subspecies only.
[5] In Buturlin's classification *A. serrirostris* includes all the tundra-breeding subspecies.

Alpheraky (1905) maintained the species status for *mentalis*, but later authors listed it as a subspecies (Table 1) or considered it as a synonym to *A. f. serrirostris* (Hartert 1921, Delacour 1951).

The type specimen collected from Japan (Table 2) was analysed. The mtDNA haplotype of *mentalis* was identical to the haplotype SER2 found in *serrirostris* birds (Fig. 1). Based on morphology this individual was assigned to *middendorffii* (Table 2), but the individual is clearly an outlier (Fig. 2). Based on function 1 it seems to be a typical *middendorffii*, but based on function 2 it is more like the tundra breeding subspecies of the Bean Goose and closer to *serrirostris* than to *rossicus*.

Anser oatesi **Rickett, 1901**. Description of *A. oatesi* is based on a single specimen collected in Fohkien Province, China. The bird was described similar to *brachyrhynchus*, but having a much larger bill and a

Table 2. Sampled individuals, sampling locality and year, mtDNA haplotypes and predicted groups of the individuals based on morphological measurements (given in mm). Posterior probabilities (*pp*) for the best group predictions are given for each individual, except *neglectus* 2, a second calendar year (2cy) bird for which no prediction could be obtained.

Taxon	No	Museum code[a]	Sampling locality	Sampling year	mtDNA	Predicted group	*pp*	Bill length	Bill height	Nail length	Grinning patch	Age
johanseni	1	ZMUC 30.022	Tomsk, Russia	1907	MID3	*middendorffii*	0.765	68.2	33	14.8	6.97	Ad
johanseni	2	ZMUC 30.024	Tomsk, Russia	1907	MID1	*middendorffii*	0.502	70.2	33.5	18.9	7.57	Ad
neglectus	1	ZMUC 60.858	Novaya Zemlya, Russia	1903	SER1	*rossicus*	0.662	58	29.7	17.3	8.4	Ad
neglectus	2	ZMMU R24956	Novaya Zemlya, Russia	?	SER1	-	-	54.8	-	14.9	-	2cy
neglectus	3	ZMUC 65.173	Sønderjylland, Denmark	1920	FAB1	*rossicus*	0.770	56.7	31.4	15.7	6.68	Ad
neglectus	4	NRM 570752	C. Kansu, China	1921	MID2	*fabalis*	0.895	69	28.9	17	4.65	Ad
neglectus	5	ZMMU R49186	Samara, Russia	1906	FAB7, NEW	*fabalis*	0.994	59.6	27	15	3.04	Ad
curtus	1	NRM 570746	Shansi Province, China	1920	SER2	*fabalis*	0.951	60.1	33.5	17.2	2.75	Ad
curtus	2	NRM 570747	Shansi Province, China	1920	ROS2	*rossicus*	0.615	53	28.6	17.2	3.86	Ad
curtus	3[b]	NRM 569905	Shansi Province, China	1921	ROS5, NEW	*rossicus*	0.795	55	28.5	18.3	5.55	Ad
curtus	4[b]	NRM 569903	Shensi Province, China	1922	SER1	*rossicus*	0.735	57.3	30.5	17.3	6.87	Ad
curtus	5[b]	NRM 569904	Shensi Province, China	1922	ROS6, NEW	*rossicus*	0.911	53.7	29.4	17.4	6.18	Ad
curtus	6	NRM 570749	Gobi, Mongolia	1929	SER1	*serrirostris*	0.572	59.4	30	18.3	6.47	Ad
curtus	7	NRM 570748	Gobi, Mongolia	1929	SER1	*rossicus*	0.737	56.7	29.2	17.7	6.19	Ad
oatesi		BMNH 1902.8.5.365	Fohkien Province, China	1890	SER1	*serrirostris*	0.823	62.1	34.5	18.2	8.84	Ad
*mentalis**		BMNH 1894.8.12.11	Yokohama, Japan	?	SER2	*middendorffii*	0.979	72.3	38.6	20	11.05	Ad

[a] ZMUC, Zoological Museum of Copenhagen University; ZMMU, Zoological Museum of Moscow State University; NRM, Swedish Museum of Natural History in Stockholm; BMNH, British Museum of Natural History, Tring.

*Type specimen. [b] Paralectotype.

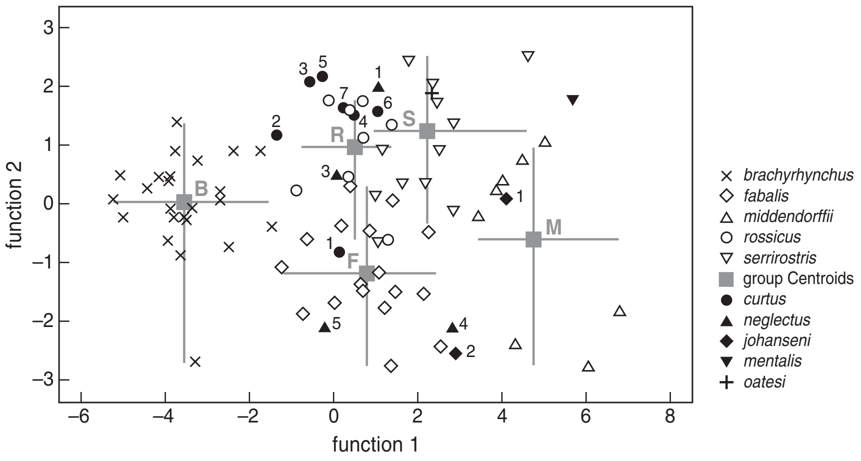

Figure 2. Discriminant function analysis of morphological measurements in bean goose and pink-footed goose. Plotted are the scores of 15 historical taxa (identification numbers refer to Table 2). As a reference, the scores for five established taxa with group centroids and sample space (x- and y-directions) are shown.

white chin (Rickett 1901). Later authors have not considered *oatesi* as a valid taxon (Table 1).

Unfortunately, the type specimen did not amplify in PCR, but one specimen of *oatesi* also collected by Rickett was studied. This individual had the haplotype SER1, which is widespread in the tundra zone of Russia (from Kola Peninsula to Kamchatka) and thus it is shared by subspecies *serrirostris* and *rossicus* (Fig. 1). Based on morphology, *oatesi* grouped with *serrirostris* (Fig. 2, Table 2).

***Anser fabalis curtus* Lönnberg, 1923**. The description of the subspecies *curtus* is based on a type specimen from Shensi Province, China, from 1922 (Lönnberg 1923, see also Gyldenstolpe 1926). Compared to typical characteristics of *fabalis*, the bill is said to be shorter and the nail of the bill larger. Also coloration of the plumage in the head differs from the uniformly brown colour of the European bean geese: top of the head and nape are darker brown (sepia) and a still darker large patch at the base of the upper mandible in front of the eye was usually found. Johansen (1959) has been the only author to list *curtus* as a subspecies in the recent literature (Table 1), but it is still recognized e.g. in Japan (Brazil & Yabuuchi 1991).

The seven specimens studied here are from China and Mongolia (Table 2). All of them had haplotypes typical for or closely related to *serrirostris* and *rossicus* (Fig. 1). Based on bill measurements four individuals from China and one from Mongolia were assigned to *rossicus* (Fig. 2, Table 2). One individual from China grouped with *fabalis* and one from Mongolia with *serrirostris* (Fig. 2, Table 2). On average, the bill is shorter than but overlapping with *fabalis* and similar to *rossicus* (*curtus* 56.7 ± 2.7 vs. *rossicus* 57.4 ± 2.4 vs. *fabalis* 60.8 ± 3.7). When compared to *rossicus* and *serrirostris* the nail length of *curtus* is in-between (*rossicus* 16.4 ± 0.8 vs. *curtus* 17.6 ± 0.5 vs. *serrirostris* 18.2 ± 1.8), and indeed larger than in *fabalis* (15.1 ± 0.9).

***Anser fabalis johanseni* Delacour, 1951**. Based on the original data by Johansen, Delacour (1951) described *johanseni* similar to *fabalis*, but larger in size, with longer bill showing more black and less yellow. The type specimen was collected in NW China together with 15 other specimens. *Johanseni* was said to interbreed with *rossicus* in the north, and to intergrade with *fabalis* in the west and with *middendorffii* in the east (Delacour 1951). The subspecific status of *johanseni* has been accepted by many recent authors (Table 1; van den Bergh 2003), but its validity has also been questioned (Roselaar 1977, Burgers *et al.* 1991, Sangster & Oreel 1996).

Two individuals collected from central Russia labelled as *johanseni* (Table 2) were analysed, and both had haplotypes typical for *middendorffii* (Fig. 1). Both individuals grouped with *middendorffii* also based on morphology (Fig. 2, Table 2).

DISCUSSION

The mtDNA tree of the bean goose – pink-footed goose complex (Ruokonen *et al.* 2008) supported three main clades: the Pink-footed Goose *A. brachyrhynchus*, the

Middendorff's Goose *A. middendorffii* and the Bean Goose *A. fabalis*. *A. brachyrhynchus* and *A. middendorffii* show little intraspecific variation and are well supported in the tree, whereas *A. fabalis* is a more diverse group with three subspecies (Ruokonen *et al.* 2008). In this study, altogether ten mtDNA haplotypes were found from *neglectus*, *mentalis*, *oatesi*, *curtus* and *johanseni*. None of these taxa showed phylogenetic evidence for a species status based on mtDNA. One of the indications for this would have been the formation of monophyletic groups in the neighbour-joining tree or a clear grouping based on morphology (compare to *brachyrhynchus* and *middendorffii* in Fig. 1 and 2). This was not observed for any of the taxa with more than one individual analyzed. Instead, the haplotypes found were either identical with the haplotypes that have been found earlier or very closely related to them. Also, *mentalis* and *oatesi*, which were represented by a single specimen each, carried mtDNA haplotypes that were identical with haplotypes common in the breeding areas of the Bean Goose *A. fabalis* or the Middendorff's Goose *A. middendorffii*. Overall, a higher level of variation would have been desirable for making the conclusion stronger.

In recent literature *neglectus* has not been considered a valid taxon, and the flesh-coloured (instead of orange) bare parts have been explained by individual variation or a mutation causing loss of yellow carotenoid pigment (Delacour 1951, Dementiev & Gladkov 1952, Johansen 1959, Bauer & Glutz von Blotzheim 1968, Cramp & Simmons 1977, Sangster & Oreel 1996). It has been suggested that these birds belong to *A. fabalis fabalis* or *A. f. rossicus*, or possibly this colour variation is found in all taxa (Cramp & Simmons 1977). The latter suggestion is supported by our results: mtDNA haplotypes typical for *A. middendorffii* and *A. fabalis*, including at least two of the three subspecies of the latter, were found among the individuals studied. Also, morphology of the individuals supported this finding. Thus, it can be concluded that the colour of the bill and the feet are not taxonomically valid traits in bean geese (see also Burgers *et al.* 1991). It is probable that the same concerns *A. carneirostris* Buturlin, 1901 with flesh-coloured bill but orange legs, although this taxon was not included in our study due to lack of material.

The descriptions of *A. oatesi* and *mentalis* were based on single individuals with the most prominent difference compared to the other taxa being the white patch in the chin. However, white feathering is not uncommon across top and down sides of base in upper mandible or at the chin in bean geese (von Wright & Palmen 1873, Cramp & Simmons 1977, Svensson *et al.* 2010), and as early as 1905 Alpheraky dismissed this character for subspecies identification. Buturlin (1935) later synonymized *oatesi* with *serrirostris* and this is supported by the mtDNA haplotype, bill morphology and the locality of collecting of the specimen. Similarly, also *mentalis* was considered as a synonym of *serrirostris* in later taxonomical papers (Hartert 1921, Delacour 1951). Haplotype SER2 carried by *mentalis* has previously been found in *serrirostris* individuals in Kamchatka (Ruokonen *et al.* 2008). It is known that *serrirostris* birds from Kamchatka overwinter in Japan (Miyabayashi *et al.* 1994) where also *mentalis* was sampled, and thus it is probable that this individual is indeed *serrirostris*. However, the individual differed considerably in bill morphology from both *serrirostris* and *middendorffii* that both exist in Japan (Fig. 2).

The status of *johanseni* has continued to be controversial up until now. Originally Delacour (1951) described *johanseni* as an intermediate form intergrading with *fabalis* in the west and with *middendorffii* in the east. However, the two *johanseni* individuals studied in this paper belong most likely to *middendorffii*, as they carried mitochondrial haplotypes typical for the species and also their morphology supported this. In recent years *johanseni* has also been reported from Europe (van den Bergh 2003), but we have not found any individuals with *middendorffii* haplotypes from either breeding or wintering areas in the western Palearctic (Ruokonen *et al.* 2008 and unpubl. data; more than 150 individuals studied). This would be expected if *johanseni* is a separate taxon with similar or identical mtDNA with *middendorffii*, as did the two individuals studied here. In fact, Tomsk in Russia, where the two *johanseni* were sampled, is the westernmost locality where *middendorffii* haplotypes have been found so far (four additional individuals; Ruokonen *et al.* 2008). However, a greater number of individuals claimed to be *johanseni* analysed would have been desirable.

Delacour (1951) surmised that *curtus* in the tundra zone may be an equivalent of taiga-breeding *johanseni*: an intermediate form intergrading with *rossicus* and serrirostris, although this was not the original description of Lönnberg (1923). Because *rossicus* and *serrirostris* share at least one very common mtDNA haplotype in the breeding areas (SER1, Fig. 1), the taxonomical status of *curtus* is not easy to interpret. Out of the five haplotypes found in *curtus* individuals, one is identical to *serrirostris* haplotypes (SER2), one has been found from both *serrirostris* and *rossicus* (SER1), one has been found in *rossicus* (ROS2) and two haplotypes are closely related to a *rossicus* haplotype (ROS5, ROS6; Fig. 1). The localities where individuals were collected, China and Mongolia, are within the non-breeding range of serrirostris, but based on the molecular evidence it is thus not possible to exclude the possibility that *curtus* would represent e.g a hybrid population. Another explanation could be that some of the (easternmost breeding) *rossicus* take a migration route to China and would seem strikingly different compared to *serrirostris* individuals wintering there. Some of the *curtus* individuals are very small even when compared to *rossicus* (*curtus* 2, 3, 5; Fig. 2), although the sample size for *rossicus* sampled from the breeding areas used for comparison is admittedly small. However, it is not known where these individuals breed or whether they even come from the same area.

By examining many of the historical taxa, we did not find conclusive evidence of additional species or subspecies of the Bean Goose or Middendorff's Goose. Affected by typological thinking, many aberrant-looking individuals were classified as separate taxa in late 19th and early 20th centuries. Because these individuals were morphologically outliers and therefore caught the attention of the ornithologists, it was also challenging for us to assign the subspecies of some of the individuals based on bill measurements.

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SAMENVATTING

Ideeën over het onderscheiden van soorten veranderen in de loop van de tijd. Als gevolg daarvan kan de taxonomische status van organismen aan verandering onderhevig zijn. Aan het eind van de negentiende en het begin van de twintigste eeuw had men de gewoonte om vogels die een iets afwijkend verenkleed vertoonden, tot (onder)soort te verheffen. In die tijd werd een aantal soorten en ondersoorten van het rietgans complex beschreven waarvan tegenwoordig de status niet meer erkend wordt of waarvan de status omstreden is. Om duidelijkheid te brengen in de taxonomie van deze groep werden vijf van deze historische taxa onderworpen aan een analyse op grond van genetische verwantschap (door middel van mitochondriaal DNA) en overeenkomsten in lichaamsmaten. Het betrof de Sushkins Rietgans *Anser neglectus*, de West-Siberische Taigagans *A. fabalis johanseni* en verder *A. mentalis*, *A. oatesi* en A. *fabalis curtus*. Er werden geen aanwijzingen gevonden die het onderscheid van deze soorten of ondersoorten rechtvaardigt. Elk van de vijf werd ingedeeld bij een van de huidige soorten en ondersoorten van de groep van rietganzen. (JP)

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