INTRODUCTION

This report includes taxonomic and nomenclatural changes adopted by the Dutch committee for avian systematics (Commissie Systematiek Nederlandse Avifauna, CSNA) since Sangster et al. (2003). We review newly published evidence affecting the scientific names and sequence of taxa on the Dutch List. The committee consists of four members (year of election between parentheses): Arnoud B. van den Berg (1995), André J. van Loon (2002), C.S. Roselaar (1995) and George Sangster (Secretary, 1996). The committee’s approach towards the recognition of species and higher taxa was described by Sangster et al. (1999). Unless otherwise stated, the sequence of species on the Dutch List remains unchanged.

TAXONOMIC CHANGES

Flamingos and grebes

Phylogenetic analyses based on DNA–DNA hybridization data (van Tuinen et al. 2001), mitochondrial and nuclear DNA sequences (van Tuinen et al. 2001, Chubb...
Recent phylogenetic studies indicate that the species currently included in *Hieraaetus* and *Aquila* do not form separate monophyletic groups (Wink & Seibold 1996, Wink et al. 1998, Wink 2000, Wink & Sauer-Gürth 2000, Roulin & Wink 2004, Wink & Sauer-Gürth 2004, Bunce et al. 2005, Helbig et al. 2005, Lerner & Mindell 2005). The CSNA has considered two alternative taxonomic rearrangements: (i) include all species of *Hieraaetus* and *Aquila* in a single genus (Wink & Sauer-Gürth 2004) or (ii) recognise three genera (Helbig et al. 2005). In view of the incongruence among studies in the placement of some eagle taxa and the lack of support for some internal nodes, we feel that recognition of three genera is not sufficiently supported. Therefore, we place the species traditionally included in *Hieraaetus* in *Aquila* (cf. Sangster et al. 2005). The sequence and nomenclature of the eagles on the Dutch List becomes as follows:

- Greater Spotted Eagle *Aquila clanga*
- Lesser Spotted Eagle *Aquila pomarina*
- Booted Eagle *Aquila pennata*
- Golden Eagle *Aquila chrysaetos*
- Bonelli’s Eagle *Aquila fasciata*
- Steppe Eagle *Aquila nipalensis*
- Eastern Imperial Eagle *Aquila heliaca*

**Generic limits of gulls**

Two studies, one based on morphology (Chu 1998) and another based on mitochondrial DNA sequences (Pons et al. 2005) have examined phylogenetic relationships of the entire gull clade. Both studies indicate that the genus *Larus*, as currently defined (e.g. Voous 1977, Cramp & Simmons 1983), is not monophyletic.

The results of the two studies show several differences but there are also some important points of agreement. Both Chu (1998) and Pons et al. (2005) indicate a separate position of Swallow-tailed Gull *Creagrus furcatus*, the kitiwakes *Rissa*, Sabine’s Gull *Xema sabini* and Ivory Gull *Pagophila eburnea* from all other gulls, supporting the continued recognition of these genera. Both studies indicate that the ‘masked gulls’ (which include Slender-billed Gull, Bonaparte’s Gull and Black-headed Gull) are not part of the main clade of gulls. Both studies further indicate a sister-group relationship of Little Gull and Ross’ Gull and a separate position of these two species from the main clade of gulls.

We have considered five alternative rearrangements, including those proposed by Chu (1998) and Pons et al. (2005). These proposals range from including all species of gulls in a single genus (Chu 1998) to recognising 10 genera, including several genera that are not presently recognised (Pons et al. 2005).

Recognising that strongly supported groups are also the ones that are most likely to be stable (i.e. robust to additional data), we recommend a taxonomic arrangement that is intermediate between the two extremes proposed by Chu (1998) and Pons et al. (2005). This

**Taxonomic sequence of shanks *Tringa***

A recent molecular study of the shanks (Pereira & Baker 2005) offers a well-resolved phylogeny of the shanks (*Tringa, Actitis, Heteroscelus, Catoptrophorus*) based on mitochondrial and nuclear DNA sequences. The results of Pereira & Baker (2005) indicate that it is not necessary to include Common and Spotted Sandpiper (e.g. Johnsgard 1981) and Terek Sandpiper (e.g. Sibley & Monroe 1990) in *Tringa*. Their results also show that the tattlers *Heteroscelus* and Willet *Catoptrophorus semipalmatus* are part of the *Tringa* clade and that a revision is warranted. The current sequence of the Dutch species of shanks (sensu Voous 1977) does not accurately reflect their phylogenetic relationships and is to be revised as follows:

- Terek Sandpiper *Xenus cinereus*
- Common Sandpiper *Actitis hypoleucos*
- Spotted Sandpiper *Actitis macularius*
- Green Sandpiper *Tringa ochropus*
- Solitary Sandpiper *Tringa solitaria*
- Spotted Sandpiper *Tringa erythropus*
- Greater Yellowlegs *Tringa melanoleuca*
- Common Greenshank *Tringa nebularia*
- Lesser Yellowlegs *Tringa flavipes*
- Marsh Sandpiper *Tringa stagnatilis*
- Wood Sandpiper *Tringa glareola*
- Common Redshank *Tringa totanus*
arrangement recognises the genera Creagrus, Rissa, Xema, Pagophila, Chroicocephalus, Rhodostethia, Hydrocoloeus and Larus. Recognition of each of these groups is consistent with the results of Chu (1998) and Pons et al. (2005) and is supported by high bootstrap values in Pons et al. (2005). Little Gull and Ross’s Gull are sister taxa but are placed in separate genera in view of their long branch lengths in Pons et al. (2005).

The arrangement proposed by Pons et al. (2005), which includes two additional genera ‘Leucophaeus’ (for some New World gulls including Franklin’s Gull L. pipixcan and Laughing Gull L. atricilla) and ‘Ichthyaetus’ (for southern Palearctic gulls, including Mediterranean Gull L. melanocephalus, Audouin’s Gull L. audouinii and Pallas’s Gull L. ichthyaetus), is not warranted due to low bootstrap support for the restricted ‘Larus’. The phylogenetic position of Saunders’s Gull L. saundersi is too poorly resolved and does not support the recognition of a monotypic genus ‘Saundersilarus’ (Pons et al. 2005). It is tentatively placed in Chroicocephalus, consistent with its traditional place near the ‘masked gulls’ and the results of Chu (1998).

We recommend to re-arrange the species on the Dutch List as follows. The sequence of the large white-headed gulls (L. fuscus through L. marinus) is left unchanged (cf. Voous 1977), pending more detailed information on their relationships.

- Ivory Gull Pagophila eburnea
- Sabine’s Gull Xema sabini
- Black-legged Kittiwake Rissa tridactyla
- Slender-billed Gull Chroicocephalus genei
- Bonaparte’s Gull Chroicocephalus philadelphia
- Black-headed Gull Chroicocephalus ridibundus
- Little Gull Hydrocoloeus minutus
- Ross’s Gull Rhodostethia rosea
- Laughing Gull Larus atricilla
- Franklin’s Gull Larus pipixcan
- Mediterranean Gull Larus melanocephalus
- Audouin’s Gull Larus audouinii
- Pallas’s Gull Larus ichthyaetus
- Common Gull Larus canus
- Ring-billed Gull Larus delawarensis
- Lesser Black-backed Gull Larus fuscus
- Herring Gull Larus argentatus
- Yellow-legged Gull Larus michahellis
- Caspian Gull Larus cachinnans
- Iceland Gull Larus glaucaoides
- Glaucous Gull Larus hyperboreus
- Great Black-backed Gull Larus marinus

**Onychoprion anaethetus** Bridled Tern
**Brilstern**
**Sternula albifrons** Little Tern
**Dwergstern**
**Hydroprogne caspia** Caspian Tern
**Reuzenstern**

A molecular study based on mitochondrial DNA sequences has provided a well-resolved phylogeny of the terns (Bridge et al. 2005). The study strongly supports the monophyly of several species groups, including the brown-winged terns (Onychoprion), little terns (Sternula), marsh terns (Chlidonias) and crested terns (Thalasseus). Monophyly of the typical black-capped terns was poorly supported due to the uncertain position of Forster’s Tern S. forsteri and Trudeau’s Tern S. trudeaui. The crested terns and typical black-capped terns (Sternula) were identified as sister-groups, with the marsh terns, Inca Tern Larosterna inca, Caspian and Gull-billed Terns and Large-billed Tern Phaetusa simplex as their successive outgroups. The little terns and brown-winged terns were placed outside this group, which means that ‘Sternula’, as currently recognised (Voous 1977), is a paraphyletic group. Bridge et al. (2005) proposed a revision of the terns in which 12 genera are recognised. We have adopted this arrangement with the exception of Thalasseus, recognition of which is contra-indicated by the low bootstrap support (cf. Sangster et al. 2005). With this exception, we follow the taxonomy proposed by Bridge et al. (2005). As a result, the taxa on the Dutch List are to be listed as follows:

- Bridled Tern Onychoprion anaethetus
- Little Tern Sternula albifrons
- Gull-billed Tern Gelochelidon nilotica
- Caspian Tern Hydroprogne caspia
- Whiskered Tern Chlidonias hybrida
- Black Tern Chlidonias niger
- White-winged Tern Chlidonias leucopterus
- Sandwich Tern Sterna sandvicensis
- Forster’s Tern Sterna forsteri
- Common Tern Sterna hirundo
- Roseate Tern Sterna dougallii
- Arctic Tern Sterna paradisaea

**Megaceryle alcyon** Belted Kingfisher
**Bandijsvogel**

A recently published phylogenetic analysis of the kingfishers indicates that Pied Kingfisher Ceryle rudis is the sister taxon of the ‘green’ kingfishers Chloroceryle and is not closely related to Ceryle alcyon (Moyle 2006). This implies that the current treatment of Megaceryle as a subgenus of Ceryle does not accurately reflect their phy-
logenetic relationships. In view of their distinctive morphology and to avoid paraphyly of Ceryle, three genera of ceryline kingfishers are recognised, i.e. Megaceryle, Ceryle and Chloroceryle. Both Miller (1912, 1920) and Fry (1980) emphasised anatomic differences among the three groups in support for treatment as three genera (see also Pascotto et al. 2006). These data indicate that Belted Kingfisher should be reclassified in the genus Megaceryle. Belted Kingfisher (currently Ceryle alcyon) therefore becomes Megaceryle alcyon (cf. AOU 1998).

**Cecropis daurica Red-rumped Swallow**

Roodstuitzwaluw
Red-rumped Swallow is traditionally included in Hirundo. Previous studies suggest that ‘Hirundo’ (sensu Voous 1977) does not represent a monophyletic group of species and indicate that the red-rumped swallows Cecropis are not part of the clade of typical mud-nesting martins (Sheldon & Winkler 1993, Sheldon et al. 1999). A recent study, which included nearly all recognised swallow species, provided strong support for the position of Red-rumped Swallow in Cecropis (Sheldon et al. 2005). The scientific name of Red-rumped Swallow (currently Hirundo daurica) thus becomes Cecropis daurica (cf. Dickinson 2003, Sangster et al. 2005).

The current sequence of the Dutch species of swallows (sensu Voous 1977) does not accurately reflect their phylogenetic relationships and is to be revised as follows:
- Sand Martin Riparia riparia
- Eurasian Crag Martin Ptyonoprogne rupestris
- Barn Swallow Hirundo rustica
- Common House Martin Delichon urbicum
- Red-rumped Swallow Cecropis daurica

**Tarsiger cyanurus Red-flanked Bluetail**

Blauwstaart
Red-flanked Bluetail and Himalayan Bluetail T. rufilatus differ in song, calls, adult plumage and biometrics (Cramp 1988, Martens & Eck 1995, Roselaar & Shirihai, in prep.). Red-flanked and Himalayan Bluetail are therefore best treated as two species. As a result, Red-flanked Bluetail becomes a monotypic species (cf. Knox et al. 2008).

**Oenanthe pleschanka Pied Wheatear**

Bonte Tapuit

**Geokichla sibirica Siberian Thrush**

Siberische Lijster
Recent phylogenetic studies have shown that the genus Zoothera – as recognised by Voous (1977) – comprises two clades that are not closely related (Klicka et al. 2005, Voelker & Klicka 2008). One clade (the Zoothera clade) includes Zoothera dauma and several Indomalayan and Australasian species. The other clade (the Geokichla clade) includes several African and Indomalayan species. Siberian Thrush is not part of the Zoothera clade but part of the Geokichla clade (Klicka et al. 2005, Voelker & Outlaw 2008; see also Voelker & Klicka 2008). We follow Voelker & Outlaw (2008) and place Siberian Thrush in Geokichla. Consequently, the scientific name of Siberian Thrush (currently Zoothera sibirica) becomes Geokichla sibirica.

**Turdus eunomus Dusky Thrush**

Bruine Lijster
Naumann’s Thrush T. naumanni and Dusky Thrush show differences in the pattern and/or coloration of head, upperparts, breast, tail, bill and legs (e.g. Cramp 1988, Clement 1999) and in habitat (Roselaar & Shirihai, in prep.). Naumann’s and Dusky Thrushes are therefore best treated as two distinct species (cf. Stepanyan 1990, Helbig 2005, Knox et al. 2008). Until recently, Naumann’s Thrush T. naumanni and Dusky Thrush were combined in a single species based on the existence of intermediate specimens. However, no detailed studies of the interactions of Naumann’s and Dusky Thrushes in the zone of contact are available and there is no evidence to suggest that these taxa are merging into a single population. A recent study concluded that the breeding ranges of Naumann’s and Dusky Thrushes do not overlap and that hybridisation is relatively rare (Roselaar & Shirihai, in prep.).

**Turdus atrogularis Black-throated Thrush**

Zwartkeellijster

Red-throated and Black-throated Thrushes co-exist in a zone that spans several 100 km. Both taxa are
found together near Razdolinsk, Russia (Gibet et al. 1967), in the Kuraj plateau, eastern Altay mountains, Russia (Ernst 1992, 1996), in the Zapadny Sayan (= West Sayan) mountains (Yanushevich & Yurlov 1950, Prokofyev 1988, Rogacheva 1992), in the Tuva region (Berman & Zabelin 1963) and in the Manskoye Belogorye mountains (Kim & Pakulov 1959) and other parts of the Vostochny Sayan (= East Sayan) mountains (Yudin 1952). In some areas, Red-throated and Black-throated Thrushes occur syntopically. Both taxa are found in all forests in the Bolshiye Ury river basin, Zapadny Sayan mountains (Prokofyev 1988) and in both the dark-coniferous taiga and subalpine belt of the Manskoye Belogorye mountains, Vostochny Sayan mountains (Kim & Pakulov 1959). Nests of Red-throated and Black-throated Thrushes have been found within 30–40 m of each other in the Tuva region, Russia (Berman & Zabelin 1963). In other parts of the overlap zone, Red-throated and Black-throated Thrushes occupy different habitats (Folitarek & Dementiev 1938, Yudin 1952, Stakeev 1979, Ernst 1992, 1996, Rochacheva 1992).

Field observations suggest that interbreeding between Red-throated and Black-throated Thrushes is very limited in Mongolia (Mauersberger 1980) and absent in the eastern Altay, Russia (Ernst 1992, 1996). Mixed pairs of Red-throated and Black-throated Thrushes have never been observed (Ernst 1996). In the Sayan mountains, young Black-throated Thrushes have been found two to three weeks earlier than young Red-throated Thrushes (Ernst 1992). It has been suggested that a difference in the timing of breeding may prevent hybridisation of Red-throated and Black-throated Thrushes (Ernst 1996) and may contribute to reproductive isolation.

Previous reports of extensive intergradation may have been based on misidentification of ‘pure’ specimens. Occurrence of black malar stripes or throat streaks in ruficollis-like birds is not an indication of hybridisation but fall within the normal range of variation of Red-throated Thrushes (Roselaar & Shirihai, in prep.).

A preliminary study of vocalisations, based on a small sample of Red-throated Thrushes and one Black-throated Thrush, indicated that their songs might be very different (Arkhipov et al. 2003).

**Sylvia cantillans** Subalpine Warbler
Baardgrasmus

**Sylvia subalpina** Moltoni’s Warbler
Moltoni’s Baardgrasmus

Moltoni’s Warbler (currently ‘S. c. moltonii’) differs from other Subalpine Warbler taxa in plumage, moult, timing of breeding, habitat and contact calls (Gargallo 1994, Shirihai et al. 2001, Brambilla et al. 2007). Recent studies have shown that the breeding ranges of Moltoni’s Warbler and nominate Subalpine Warbler *S. c. cantillans* overlap at several localities in mainland Italy without evidence for interbreeding (Brambilla et al. 2006, 2008a,c). Playback tests conducted within and outside the area of overlap in Italy have demonstrated that the two groups do not respond to each other’s songs (Brambilla et al. 2008a). A molecular phylogenetic study indicated that Moltoni’s Warbler and Subalpine Warbler form separate clades and failed to find evidence for gene flow, even in areas where the two forms have overlapping breeding ranges (Brambilla et al. 2008b). The level of sequence divergence between Moltoni’s Warbler and other Subalpine Warbler taxa is consistent with those typically observed in species taxa, including several pairs of *Sylvia* warblers (Brambilla et al. 2008b). Therefore, Moltoni’s Warbler and Subalpine Warbler are best treated as separate species (cf. Brambilla et al. 2008a,b,c). The correct scientific name for Moltoni’s Warbler is *Sylvia subalpina* Temminck, 1820, rather than *Sylvia moltonii* Orlando, 1937 (Baccetti et al. 2007). Pending further research, Subalpine Warbler includes the forms cantillans, albistriata and inornata (cf. Brambilla et al. 2008b).

**Generic limits of tits**

Molecular phylogenetic analysis of the tits (Paridae) based on mitochondrial DNA sequences (Gill et al. 2005) suggests the existence of six major clades among species traditionally included in *Parus*: blue tits (‘Cyanistes’), great tits (‘Parus’), North American crested tits (‘Baeolophus’), Eurasian crested tits (‘Lophophanes’), coal tits (‘Periparus’) and chickadees (‘Poecile’). The data indicate that the blue tits (*P. caeruleus, P. cyanus*) are sister to all other species of tits (Paridae). However, their phylogenetic position relative to Yellow-browed Tit *Sylviparus modestus* and Sultan Tit *Melanochlora sultanea* differed between analyses. Hume’s Ground-Jay *Pseudopodoces humilis*, previously misclassified in Corvidae, was sister to the great tits in one analysis but sister to all tits except ‘Cyanistes’, *Sylviparus* and *Melanochlora* in another. The position of *Pseudopodoces humilis* among tits was previously suggested by James et al. (2003) based on morphological and preliminary mitochondrial DNA data. Gill et al. (2005) proposed to recognise nine genera of tits. They argued that, in addition to *Pseudopodoces, Sylviparus* and *Melanochlora*, the six groups of *Parus* should each be elevated to generic
level. We have adopted the arrangement proposed by Gill et al. (2005) based on the following considerations: (i) *Parus* would not be monophyletic if the status quo is maintained, (ii) inclusion of *Pseudpodoces*, *Sylviparus* and *Melanochlora* in *Parus* would result in an even more diverse taxon, (iii) *Parus* is one of the largest genera of birds; its subdivision into several genera would add phylogenetic information, (iv) the major groups of tits are characterised by high genetic distances in all molecular data sets, i.e. proteins (Gill et al. 1989), DNA–DNA hybridisation (Sheldon et al. 1992, Slikas et al. 1996) and mitochondrial DNA sequences (Gill et al. 2005), and (v) there is growing international support for the break-up of *Parus* into several genera (e.g. AOU 1997, Gill et al. 2005, Sangster et al. 2005, Clements 2007). The gender of the name *Poecile* is controversial; we follow David & Gosselin (2008) and treat *Poecile* as masculine. The tits on the Dutch List should be listed as follows: 

- Blue Tit *Cyanistes caeruleus*
- Great Tit *Parus major*
- Crested Tit *Lophophanes cristatus*
- Coal Tit *Periparus ater*
- Willow Tit *Poecile montanus*
- Marsh Tit *Poecile palustris*

**Generic limits and sequence of starlings**

Phylogenetic analyses of mitochondrial and nuclear DNA sequences (Lovette & Rubenstein 2007, Lovette et al. 2008, Zuccon et al. 2008) have clarified the evolutionary relationships among the starlings. These studies indicate that Rosy Starling and Daurian Starling are more closely related to the mynas than to Common and Spotless Starlings. We adopt the generic revision proposed by Lovette et al. (2008) and Zuccon et al. (2008). Rosy Starling (currently *Sturnus roseus*) becomes *Pastor roseus*, and Daurian Starling (currently *Sturnus sturninus*) becomes *Agropsar sturninus*. The starlings on the Dutch list should be listed in the following sequence:

- Common Starling *Sturnus vulgaris*
- Rosy Starling *Pastor roseus*
- Daurian Starling *Agropsar sturninus*

**Melospiza melodia Song Sparrow**

Zangors

Although the name *Melospiza melodia* has been used for Song Sparrow for a long time (e.g. AOU 1983), the species was placed in *Zonotrichia* by Voous (1977). Phylogenetic studies based on allozymes (Zink 1982), mitochondrial DNA sequences (Zink & Blackwell 1996, Carson & Spicer 2003), and morphological, behav-


**SAMENVATTING**

In dit derde overzicht sinds de publicatie van Voous (1977) worden de beslissingen besproken die de Commissie Systematiek Nederlandse Avifauna (CSNA) in de periode van januari 2004 tot december 2008 heeft genomen over taxonomische wijzigingen van vogelsoorten die op de Nederlandse lijst staan. De wijzigingen kunnen worden onderverdeeld in vijf groepen: (1) de volgorde van sommige soorten en groepen is aangepast, zodat deze overeenkomt met de huidige inzichten over hun fylogenetische verwantschap (flamingo’s en futen, aren, ruiters, meeuwen, sterns, zwaluwen en mezen); (2) 20 wetenschappelijke namen zijn gewijzigd als resultaat van revisies op het genussniveau (Aquila pennata, A. fasciata, Chroicocephalus genei, C. philadelphia, C. ridibundus, Hydrocoloeus minutus, Onychoprion anaethetus, Sterna albifrons, Hydroprogne caspia, Megaceryle alcyon, Cercops dauricus, Geokichla sibirica, Cyanistes caeruleus, Lophophanes cristatus, Periparus ater, Poecile montanus, P. palustris, Pastoral roseus, Agropsar sturninus, Melospiza melodya); (3) de namen van twee soorten worden gewijzigd, omdat de taxa waartoe deze voorheen werden gerekend nu als aparte soorten worden beschouwd (Turdus eunomus, T. atrogularis); (4) één soort wordt toegevoegd aan de Nederlandse Lijst, omdat dit taxon nu als aparte soort wordt beschouwd (Sylvia subalpina); (5) twee soorten worden monotypisch, omdat ondersoorten die niet in Nederland zijn vastgesteld, nu als aparte soorten worden beschouwd (Tarsiger cyanurus, Oenanthe pleschanka).