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Penguins reduced olfactory receptor genes common to other waterbirds

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The sense of smell, or olfaction, is fundamental in the life of animals. However, penguins (*Aves: Sphenisciformes*) possess relatively small olfactory bulbs compared with most other waterbirds such as *Procellariiformes* and *Gaviiformes*. To test whether penguins have a reduced reliance on olfaction, we analyzed the draft genome sequences of the two penguins, which diverged at the origin of the order *Sphenisciformes*; we also examined six closely related species with available genomes, and identified 29 one-to-one orthologous olfactory receptor genes (i.e. *ORs*) that are putatively functionally conserved and important across the eight birds. To survey the 29 one-to-one orthologous *ORs* in penguins and their relatives, we newly generated 34 sequences that are missing from the draft genomes. Through the analysis of totaling 378 *OR* sequences, we found that, of these functionally important *ORs* common to other waterbirds, penguins have a significantly greater percentage of *OR* pseudogenes than other waterbirds, suggesting a reduction of olfactory capability. The penguin-specific reduction of olfactory capability arose in the common ancestor of penguins between 23 and 60 Ma, which may have resulted from the aquatic specializations for underwater vision. Our study provides genetic evidence for a possible reduction of reliance on olfaction in penguins.

Traditionally, animals are believed to have five basic senses: sight, hearing, taste, touch, and smell¹. All the five sensory modalities are able to perceive stimuli from the external environment and are thus of fundamental importance for animals' survival. However, one or more of the five senses could be absent in some species of animals^{2,3}. Even when animals possess same sensory modalities, their reliance on each sense may vary significantly among species. For example, mice have an increased reliance on olfaction compared to humans⁴, while vampire bats showed decreased dependence on taste relative to other bats^{5,6}.

Of the five basic senses, the sense of smell, or olfaction, is fundamentally important in the life of animals, underpinning many essential behaviors such as food location, mate recognition, and predator avoidance⁷. Most mammals and reptiles typically possess two distinct olfactory systems: the main olfactory system (MOS) and the vomeronasal system (VNS), which were generally assumed to perceive environmental odorants and intraspecific pheromones, respectively⁸. The MOS was observed to primarily express olfactory receptors (*ORs*), which are encoded by olfactory receptor genes (*ORs*). The binding of odorants to *ORs* triggers the transduction of olfactory signals to the olfactory bulb in the brain, which results in olfactory perception⁹. The *ORs* make up one of the largest gene families in most vertebrate genomes, but the total number of *ORs* in each species varies dramatically, ranging from 125 in the pufferfish to 2129 in the cow¹⁰. The striking variation in the number of *ORs* may result from ecological adaptation. For instance, the loss of *ORs* occurred independently in the multiple lineages of aquatic mammals such as cetaceans and sirenians, which coincided with their habitat transition from land to water^{11,12}. Furthermore, differences in the number of *ORs* may also reflect a tradeoff between olfaction and other senses. For instance, the reduction of *ORs* coincided with the independent acquisition of trichromatic color vision in multiple lineages of primates¹³. As such, investigating the evolutionary changes of *ORs* would provide a valuable route to understanding how genomes have been shaped by habitat transitions, sensory tradeoffs and other ecological adaptations.

Birds are the most species-rich group among tetrapod vertebrates, with diverse and distinct olfactory abilities. In general, they are assumed to have a poor olfactory system, as they seem to rely more on vision and vocalizations¹⁴. Indeed, birds were observed to have a much smaller *OR* gene repertoire than their closely related cousin,

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the reptiles^{15,16}, which suggested a reduced reliance on olfaction. By contrast, numerous studies have argued that birds definitely use olfactory cues in many crucial behaviors, such as foraging, navigation and individual recognition^{17–20}, which was also evidenced by recent genetic data²¹. The contrasting arguments with respect to avian olfaction call for further investigations.

As the only extant group of birds that occupy a secondarily aquatic niche with flightless wing-propelled diving, penguins (order Sphenisciformes) have undergone remarkable adaptations, such as streamlined bodies, flipper-like wings, dense bones and scale-like feathers^{22–24}. In terms of sensory ecology, penguins are considered visual specialists, with a flat cornea and a spherical lens for underwater adaptation^{25,26}. Consistent with the morphological adaptations, genetic studies have observed positive selection on phototransduction genes and accelerated evolution of visual opsin genes in penguins, which were also linked to the aquatic lifestyle^{27,28}. By contrast, penguins have long been believed to lack a sense of smell, as they primarily rely on vision for underwater foraging²². In fact, multiple lines of evidence have demonstrated that penguins possess a functional sense of smell. For example, they smell the dimethyl sulphide (DMS) for prey location^{29–31} and perceive odors for kin recognition³². At the molecular level, penguins, along with other waterbirds (or aquatic birds), were identified to carry a significantly greater number of olfactory receptor genes, as compared with vocal-learning birds in a recent genomic analysis¹⁵, which also suggested that penguins rely heavily on olfaction. The recent genomic analysis classified the 48 birds into four categories: birds of prey, waterbirds, land birds and vocal learners and attempted to link the differences in *OR* gene numbers to ecological variations in the four categories¹⁵. However, the differences in *OR* gene numbers within one of the four categories were not examined¹⁵. Specifically, differences in olfaction between penguins and other waterbirds remain largely unknown. Compared with most other waterbirds, such as Procellariiformes, Ciconiiformes and Gaviiformes, penguins possess relatively small olfactory bulbs³³, which are commonly used as a proxy for olfactory capability³⁴. As such, we hypothesize that penguins may have a reduced number of *OR* genes as compared to other waterbirds. To test this hypothesis, we analyzed the draft genome sequences from the two penguins, which diverged at the origin of the order Sphenisciformes and represented the two major clades of the penguin species tree³⁵; we also examined six closely related outgroup species with available genomes (Fig. 1), and identified 29 one-to-one orthologous olfactory receptor genes that are putatively functionally conserved and important across the eight birds. With additional sequencing of these orthologous genes, we found that penguins have a significantly higher percentage of pseudogenes than other waterbirds, although they still retain many intact and putatively functional genes.

Results

Survey of *OR* genes in the genomes of penguins and other waterbirds. Our genomic dataset of birds represented four avian orders, including two species of Sphenisciformes (Emperor penguin, *Aptenodytes forsteri*, 60× coverage; Adélie penguin, *Pygoscelis adeliae*, 60×), one species of Procellariiformes (Northern fulmar, *Fulmarus glacialis*, 33×), four species of Pelecaniformes (Crested ibis, *Nipponia nippon*, 105×; Little egret, *Egretta garzetta*, 74×; Great cormorant, *Phalacrocorax carbo*, 24×; Dalmatian pelican, *Pelecanus crispus*, 34×), and one species of Gaviiformes (Red-throated loon, *Gavia stellata*, 33×) (Fig. 1; Supplementary Table S1)^{36,37}. The four orders of birds are closely related, and were referred to as the core waterbirds³⁶. Specifically, the penguin order (Sphenisciformes) is the most closely related to the order Procellariiformes; the two orders form a monophyletic group, which is clustered with the order Pelecaniformes; and the fourth order Gaviiformes falls outside of the other three orders (Fig. 1)³⁶. In addition, the two penguins (i.e. the emperor penguin and the Adélie penguin) with genome sequences diverged at the origin of the order Sphenisciformes and represented the two major clades of the penguin species tree³⁵.

A total of 344 full-length and intact *ORs* (see the identification procedure in Materials and Methods) were identified from the draft genome sequences of the emperor penguin (gene number: 32), Adélie penguin (26), northern fulmar (33), great cormorant (36), crested ibis (47), little egret (106), Dalmatian pelican (20), and red-throated loon (44) (Supplementary Table S1). The numbers of identified intact *ORs* in the present study are similar to those from a recent study with minor differences (Supplementary Table S1), which may result from slightly different bioinformatics approaches between the current work and a previous study¹⁵. Relative to most mammals, the low number of intact *ORs* in birds suggests a reduced reliance on olfaction, which is consistent with the common view that most birds are primarily visual animals³⁸, because the reduction of *ORs* was coincident with the occurrence of better color vision in primates¹³. Notably, the little egret has an extraordinarily large number of *ORs*, indicating an extraordinary expansion as compared to other waterbirds¹⁵.

Phylogenetic analysis was performed using all intact *ORs* from the eight avian genomes. The resulting phylogenetic tree revealed a major clade comprising mostly the little egret genes, although the clade was not well supported by both phylogenetic methods (Supplementary Fig. S1). This clade consisted of 94 genes in which 75 genes are from the little egret, whereas the remaining clades contain only 31 little egret genes, suggesting an apparent gene expansion in the little egret (Supplementary Fig. S1), which was also observed in a recent analysis¹⁵. Of note, the monophyly of the major clade remains to be resolved in future. While the basal clades of the phylogenetic trees did not receive high supporting values, well-supported clades were found at the tips of many groupings (Supplementary Fig. S1). We identified 29 potentially one-to-one orthologous genes with the following criteria. First, we selected well-supported clades with a bootstrap value greater than 85%; Second, there is only one single-copy gene from each species; Third, the single-copy gene was detected from at least four avian species in a well-supported clade. The nomenclature of the 29 genes followed the HORDE database (Supplementary Fig. S1)³⁹. For convenience, we also named each of the 29 genes numerically in the order of appearance on the phylogenetic tree (Supplementary Fig. S1). These one-to-one orthologous genes are assumed to be functionally conserved in the eight birds, because the same olfactory receptors tend to detect similar odorants⁴⁰. As such, the 29 orthologous genes are expected to be present in most of the eight avian species, and some genes are absent possibly because of incomplete genome sequencing or poor genome assembly.

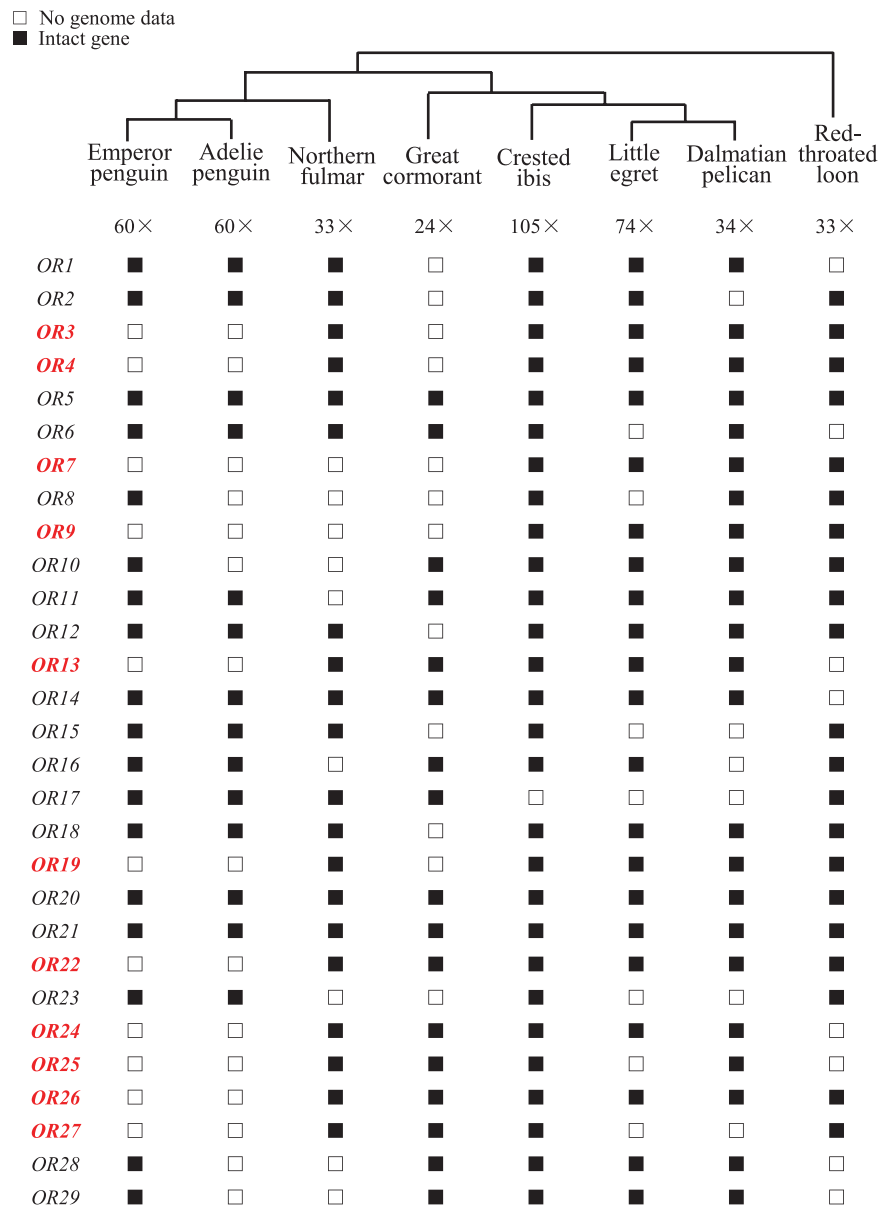


Figure 1. Genomic survey of olfactory receptor genes in the two penguins and six other waterbirds. The eight birds represent four avian orders, their phylogeny follows a recent study³⁶. The sequencing coverage of each genome was shown under each common name of birds. A filled square indicates a gene with a full-length coding sequence and an intact open reading frame, whereas an open square refers to either a partial gene or an absence of genomic data. Genes that are potentially lost in penguins were highlighted in red.

To test whether penguins have specifically lost some of the 29 orthologous genes, we mapped these genes onto the species phylogeny of the two penguins and six related waterbirds³⁶. Although 163 ORs were detected, a total of 69 ORs were not identified with a full-length and intact ORF (open reading frame) from the draft genomes of the emperor penguin (number of unidentifiable genes: 11), Adelie penguin (15), northern fulmar (9), great cormorant (12), crested ibis (1), little egret (7), Dalmatian pelican (6), and red-throated loon (8) (Fig. 1). It is understandable that the crested ibis has just 1 of the 29 OR genes that cannot be identified from its genome, because its genome coverage is the highest (105×). Similarly, the large number (12) of unidentifiable genes in the great cormorant could be attributed to its having the lowest genome coverage (24×) (Fig. 1). However, there are 11 and 15 unidentifiable genes in the emperor penguin and Adelie penguin with high-coverage genomes, respectively, and the numbers of unidentifiable genes in both penguins are even greater than those in three other waterbirds (the northern fulmar, red-throated loon, and Dalmatian pelican) with low-coverage genomes (Fig. 1). This finding suggests that penguins may have lost more functionally conserved ORs than other waterbirds. In particular, 11 ORs (OR3-4, OR7, OR9, OR13, OR19, OR22, OR24-27) were not identified in both penguins (Fig. 1), indicating penguin-specific losses.

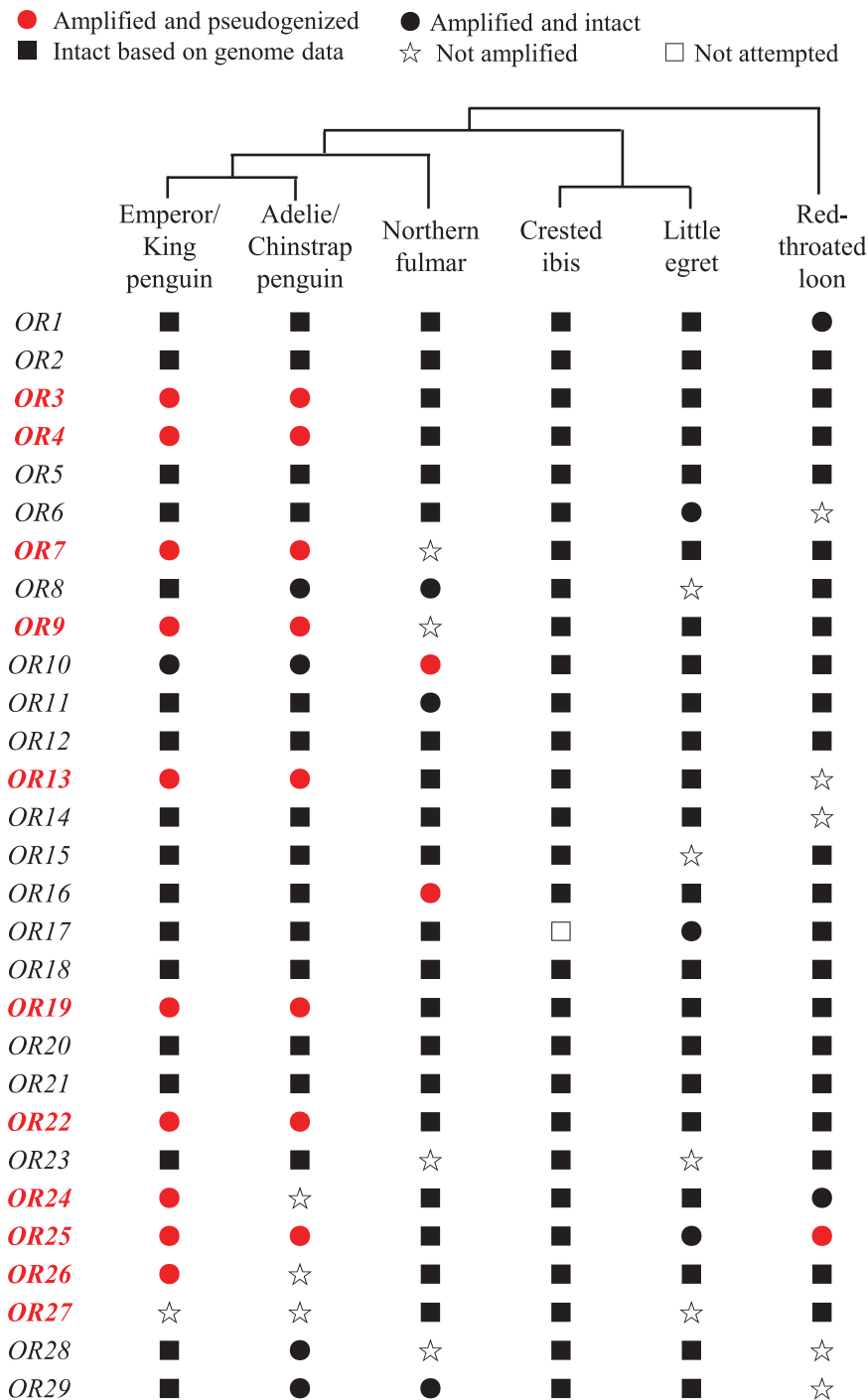


Figure 2. Survey of avian olfactory receptor genes by additional sequencing. In case that *OR* gene sequences are missing from the two penguin genomes, genomic DNAs of their congeneric species (King penguin and Chinstrap penguin) were used to perform amplification and sequencing. The great cormorant and Dalmatian pelican were not included because of the lack of genetic material, but the examined species still represent the four avian orders. Genes that are potentially lost in penguins were highlighted in red.

Pseudogenization of *OR* genes in penguins. To examine whether some orthologous *OR*s were specifically lost in penguin lineages, we attempted to sequence all missing data (Fig. 1). In case of missing data from the two penguin genomes, we performed gene sequencing using the genomic DNAs of their respective congeners (King penguin and Chinstrap penguin); the northern fulmar, red-throated loon, and little egret were examined with PCRs; the crested ibis was also included for comparison without additional sequencing, because this bird only missed one *OR* gene from its genome, which appeared to be intact in penguins (Fig. 2). We did not examine the great cormorant and Dalmatian pelican due to the absence of genetic material, although this dataset of six birds still represents the four avian orders³⁶. Of note, we did not sequence the two species of penguins with

OR3	Northern fulmar (201)	GCTGGCCATT GCTGACCTGA TACTGTGCAC CACAACCTCTG CCCAAGATGC TGGCTCTGTT CTGGTTCAAC GCCGGGGAGA TTTCTTTTGG TGCCTGCCTG
	King penguin	GCTGGCAGTG TG GACCTGC GTTTGTCTAC TGCCACCCTG CCCAAAACTC TCAGTGTCTC CTGGTCTCTG TCCACCCAAA TC1CTTTTCAG TG6GTCCTG
	Chinstrap penguin	GCTGGCAGTG TGCGACCTGC GTTTGTCCAC TGCCACCCTG CCCAAAACTC CCAGCTCTCT CTGA CTCTG TCCACCCAAA TC1CTTTTCAG TG6GTCCTG
OR4	Northern fulmar (31)	CCTCCCTATT TCCTACTCAT TGGCATCCCT GGGGTGGAGA AGGAGCAGTT CTGGATTGCC TTCCCTTCTC GCATCATGTA TGTCAATTGCT GTGCTGGGA
	King penguin	CCTCCCTATT TCCTACTCAT TGGCATCCCT GGGGTGGAGA AGGAG CTAG TT CTGGATTGCC TTCCCTTCTC GTGTCATGTA TGCCATTGCT GTGCTGGGG
	Chinstrap penguin	CCTCCCTATT TCCTACTCGT TGGCATCCCT GGACTGGAGA AGGAA CTAG TT CTGGATTGCC TTCCCTTCTC GTGTCATGTA TGCCATTGCT GTGCTGGGG
OR7	Crested ibis (761)	ACATAGGTGG CCTACTCTCC ATGTACCTGC AGATGTTCTC TTTTGGCTTG GCTCCTCATG TCCAAGTCTC AGTGGCTGAT TTCTATTTGA CAGTCCCTCC
	King penguin	ACATAGGTGG CCTTCTCTCC ATGTACCTGC AGATGTTCTC TTTTCAAGATTG GCACCTCA --- GA TGGCTGAT TTCTATT TGA CGGTCCCTCC
	Chinstrap penguin	ACATAGGTGG CCTTCTCTCC ATGTACCTGC AGATGTTCTC TTTTCAAGATTG GCACCTCA --- GA TGGCTGAT TTCTATT TGA CGGTCCCTCC
OR9	Crested ibis (901)	AAGCAGATTC GTGATGGAGT ACGCAGGGCG ATCTCCGGGA GGAGACCCCTG GGCAGGACGG ATTGGGCATG GCCTT --- GGG CACAGGGCTG GGAATCATGA
	King penguin	AAGCAGATTC ATGATGGAGT ACGCAGGGCG ATCTCC CTAG A GGAGACCCAT GGCAGGACGG ATTGGGCCTG GCCTT --- GGG CACAGAGCTG GGAATCATGA
	Chinstrap penguin	AAGCAGATTC GTGATGGAGT ACGCAGGGCG ATCTCCAGGA GGAGACCCAT GGCAGGACGG ATTGGGCCTG GCCTT --- GGG CACAGGGCTG GGAATCATGA
OR13	Northern fulmar (101)	TGTTCTACGT GATCACTCTG CTGGGGAATC TGGGGGTGCT CGTGTAAATC AGGCTGGATG CCCAGCTTCA CACCCCATG TACTTCTTCC TGAGCAGCCT
	King penguin	TGATCTACGT GATCACTCTG CTGGGGAATC TGGGGATGCT CATGTAAATC AGGCTGGATG CCCAGCTTCA CACCCCATG --- ACTTCTTCC TGA GAGCAGCT
	Chinstrap penguin	TGATCTATGT GATCCCTCTG CTGGGGAATC TGGGGATGCT CGTGTAAATC AGGCTGGATG CCCAGCTTCA CACCCCATG --- ACTTCTTCC TGA GAGCAGCCT
OR19	Northern fulmar (71)	AGGTCAATTCT TTTTGTGCTG TTTCTTCTGA TCTGTGTAC CTCGTTGGTG GGGAAATCTCA GCATGATTGC ATTAATCAGG CTTGACTCTC GACTCCACAC
	King penguin	AGGT --- GT CTTTGTGCTG TTTCTTCTGA TCTGTGTAC CTCGTTGGTG GGGAAATCTCG GCATGATTGC ATTAATCAGG CTTGACTCTC GACTCCACAC
	Chinstrap penguin	AGGT --- GT CTTTGTGCTG TTTCTTCTGA TCTGTGTAC CTCGTTGGTG GGGAAATCTCA GCATGATTGC ATTAATCAGG --- CT GA CTCTT GACTCCACAC
OR19	Northern fulmar (371)	TGGCCATCTG TAACCTCTG CTCTACATGG TCACCATGTC TCAAAAAGTTT TGTGTCCAAC TGGCTGTGGG ATCTACATA ATAGCTGCTG TGAGTCAAAC
	King penguin	TGGCCATCTG TTAC --- CTG CTCTGTGGGG CCACCATGTC TCAAAAAGGCT TGTGTCCAAC TGGCTGTGGG ATCTACATA ATAG CTACTG TGA TGAAAT
	Chinstrap penguin	TGGCCATCTG TAACCTCTG CTCTACATGG CCACCATGTC TCAAAAAGGCT TGTGTCCAAC TGGCTGTGGG ATCTACATA ATAGCTACTG TGA TGAAAT
OR19	Northern fulmar (591)	TGTGCTTTT ACCATTGCTA CTCTATTGC ATTCAGCACT TTAGCGTTCA TTGTGTGCTC TTATAGTTAT ATCCTTACCA CTGTCTGAG GATGCTCTCC
	King penguin	TGTGCTTTT ACC --- ATTGC ATTCAGCACT TTAGTATTCA TTGTGTGCTC TTATGGTTAT ATCTTACCA CTGTCCCGAG GACCCACTCC
	Chinstrap penguin	TGTGCTTTT ACC --- ATTGC ATTCAGCACT TTAGTATTCA TTGTGTGCTC TTATGGTTAT ATCTTACCA CTGTCCCGAG GACCCACTCC
OR22	Northern fulmar (71)	CTCCAGAAGT --- CCGTTTTCT TCTCTTTGG CTGTTTTTGA TCATTTATTT GACCACCATG CGAGGCAACA TCACAATCCT TGTGTCCATT GGCACAGACA
	King penguin	CTCCGGAAGT --- CTGTTTTCT TCTCTTTGG CTGTTTTTGA TCATTTATTT GGCTACCATG GCTGGCAACA TGACAATCCC TGTGCCATTT AG ACAGACA
	Chinstrap penguin	CTCCGGAAGT --- CTGTTTTCT TCT --- TTGG CTGTTTTTGA TCATTTATTT GGCTACCATG GCTGGCAACG TGACAATCCT TGTGCCATTT AG ACAGACA
OR24	Northern fulmar (131)	CCCTCGTGC CTGGATCCC CATCTCCACA GCCCATGTGA CTCTTCTCTC AGTCACTGTG CTTGCCTGGA CATTGTCTAT TCATCAGTGA CCGTGCCCAA
	King penguin	CCCTCGTGC CTGGATCCC --- ACCTCCACA GCCCATGTGA CTCTTCTCTC AGTCACTGTG CTTGCCTGGA CATTGTCTAT TCATCAGTGA --- CGTGCCCAA
	Chinstrap penguin	CCCTCGTGC CTGGATCCC --- ACCTCCACA GCCCATGTGA CTCTTCTCTC AGTCACTGTG CTTGCCTGGA CATTGTCTAT TCATCAGTGA --- CGTGCCCAA
OR25	Northern fulmar (101)	TGTGCTTCTC GCTCATTAT CTGGTGACGG --- TGTGGGGA ACCTGCTCAT CGTGACCCTC GTCTGGCTGG ATGCCACCTC GCACTCCCCC ATGATTTTCT
	King penguin	TGTGCTTCTC ATTCATTATC CTGGTGACGG --- TAAATGGGGA ACCTGCTCAT CGTGACCCTC ATCTGGCTGG ATGCCACCTC GCACTCCCCC ATGATTTTCT
	Chinstrap penguin	TGTGCTTCTC --- AC CTGGTGATGG --- GCTGGGGA ACCTGCTCAT CGTGACCCTT GTCTGGCTGG ATGCCACCTC GCACTCCCCC ATGATTTTCT
OR25	Northern fulmar (201)	TCCTGGGCA CCTCTCTTC CTGGACATCT GCTACTCTCT TGTCACCCTC CTAAGATCC TGGAGACTC CTCTCACCA CAGAAGACCA TCTCTTTTGT
	King penguin	TCCTGGGCA CCTACCTTC CTGGACATCT GCTGCTCTCT TGTCACCCTC CTAA GATCC ATGGAGACTC CTCTCACCC CAGAAGACCA TCTATTTTGT
	Chinstrap penguin	TCCTGGGCA CCTACCTTT CTGGACATCT GCTGCTCTCT TGTCACCCTC CTAA GATCC GTGGAGACTC CTCTCACCT CAGAAGACCG TCTACTTTGT
OR26	Northern fulmar (294)	AGAGAGAAAG GTGATTTCCC TGCCCTGGTT TTTCTTCCAG ATGCTGCTTT TCTTTTACCT GGGTACTGAC ACATTTTCCC ATGTGGCAAC AATGCTCTTT GA T
	King penguin	AE GGAGAG ACGATTTCCC TGCCCTGGTT TTACCTCCAG ATGCTGCTTT TCTTTTACT GGGTACTGAC ACATTTCTCC ATGTGGCAAC AATATTCTT GA T
	Chinstrap penguin	AE GGAGAG ACGATTTCCC TGCCCTGGTT TTACCTCCAG ATGCTGCTTT TCTTTTACT GGGTACTGAC ACATTTCTCC ATGTGGCAAC AATATTCTT GA T

Figure 3. Nucleotide alignments of avian olfactory receptor genes. The first ORF-disrupting mutations and the followed common mutations were boxed. Dashes indicate alignment gaps and numbers in parentheses represent nucleotide positions following the reference sequences from either Northern fulmar or Crested ibis.

available genomes due to the lack of genomic DNAs, but their congeneric species are still appropriate to infer pseudogenization events in the common ancestor of all penguins by identifying shared frameshifts or interrupting stop codons.

We sequenced 34 *OR* gene segments from the five birds as mentioned earlier (Fig. 2), which ranged from 612 to 964 base pair (bp), with an average of 805 bp (National Center for Biotechnology Information accession numbers: KX171590-KX171621 and KX189196-KX189197). Phylogenetic analysis was used to confirm the orthology of each gene. The newly acquired 34 sequences were aligned with 121 *ORs* identified from draft genomes, which resulted in a total of 155 *OR* sequences for subsequent analysis. We found 134 out of 155 *ORs* to have intact open reading frames (ORFs) (Fig. 2). Among the four non-penguin birds (the northern fulmar, crested ibis, little egret, and red-throated loon), 99 out of 102 *ORs* (99/102 = 97.1%) were identified with intact ORFs (Fig. 2), supporting our assumption that these genes are functionally important across non-penguin waterbirds. By contrast, 36 out of 54 *ORs* (36/54 = 66.7%) were found to be intact in penguins (Fig. 2). Among those pseudogenized *ORs* containing ORF-disrupting mutations such as nonsense mutations and frame-shifting insertions or deletions, 18 were found in penguins; the remaining 3 genes are from non-penguin birds (Fig. 2). In 17 out of the 21 pseudogenized *ORs*, the first nonsense mutations resulted from ORF-disrupting mutations are located near 5' end of each gene (Fig. 3), which would lead to the loss of multiple transmembrane domains of each protein. The 3 pseudogenes (*OR7* of the king penguin, *OR7* of the chinstrap penguin, and *OR9* of the king penguin) contained the first nonsense mutations located near the 3' end of each gene (Fig. 3 and Supplementary Fig. S2), which could also result in the loss of the final transmembrane domain of an olfactory receptor⁴¹. We did not observe a nonsense mutation in the pseudogenized *OR9* of the chinstrap penguin, but we observed a 2-bp deletion shared by both penguins (Fig. 3). This finding suggested that none of the 21 pseudogenes could encode a functional olfactory receptor. Therefore, after examining these functionally important *ORs* common to non-penguin waterbirds, we found that the percentage of nonfunctional *ORs* is significantly greater in penguins (18/54 = 33.3%) than in their closely related non-penguin waterbirds (3/102 = 2.9%) ($p < 0.0001$, Fisher's exact test), which suggested a penguin-specific reduction of olfactory capability.

Among the 29 orthologous *ORs*, 8 were sequenced from both penguins (the king penguin and chinstrap penguin) (Figs 2 and 3). With an exception of *OR19*, at least one common ORF-disrupting mutation was identified between the two penguins for each orthologous *OR* gene. For example, *OR3* contained one 2-bp deletion and one 2-bp insertion that are shared between the two penguins; *OR4* included one shared nonsense mutation; *OR7* has one shared 10-bp deletion and two common nonsense mutations (Fig. 3 and Supplementary Fig. S2).

We did not observe any shared ORF-disrupting mutations in *OR19*, but we identified a relatively large deletion (12-bp) that are common in the two penguins; coupled with multiple nonsense mutations ahead of the 12-bp deletion, this finding suggested that *OR19* was pseudogenized prior to the divergence of the two penguins (Fig. 3). Given that the king penguin and the chinstrap penguin diverged at the origin of the order Sphenisciformes, our genetic evidence strongly suggests that at least 8 functionally important ORs in other waterbirds were lost in all penguins, and the relaxation of functional constraints on these olfactory receptor genes occurred predating the divergence of penguins. Because penguins diverged 23 million years ago (Ma) and penguins diverged from their closest relatives (order Procellariiformes) approximately 60 Ma^{28,36}, the penguin-specific reduction of olfactory capability took place in the common ancestor of penguins between 23 and 60 Ma. In addition, we observed three independent pseudogenizations in non-penguin waterbirds (*OR10* and *OR16* in the northern fulmar, *OR25* in the red-throated loon) (Supplementary Fig. S2).

To understand why penguins could afford to lose some important ORs that are common in other waterbirds, we assigned each pseudogenized OR into a specific OR gene family following a recent study⁴². Among the 29 putative one-to-one orthologous ORs (*OR1-OR29*), 8 genes (*OR3*, *OR4*, *OR7*, *OR9*, *OR13*, *OR19*, *OR22*, and *OR25*) were found to have common disruptive mutations between the two penguins, suggesting an ancestral pseudogenization in the common ancestor of penguins; 2 genes (*OR24* and *OR26*) were sequenced in one of the two penguins because of the failure of PCRs; 1 gene (*OR27*) was not able to be amplified in both penguins even after trying several primer pairs (Figs 2 and 3). The failure of amplification suggests either severe degeneration or loss of these genes, we thus infer that 11 out of 29 ORs were pseudogenized in penguins. After using the OR family Assigner⁴², four genes (*OR3*, *OR4*, *OR7*, and *OR9*), three genes (*OR13*, *OR19*, and *OR22*), two genes (*OR24* and *OR25*), and the remaining two genes (*OR26* and *OR27*) were assigned into the OR gene family 52, family 5, family 10 and family 6, respectively. According to the traditional classification based on sequence similarity, ORs are divided into 18 families. Class I families (i.e. OR gene family 51–56) are assumed to detect water-borne molecules, whereas Class II families (i.e. OR gene family 1–14) are believed to recognize air-borne compounds^{42–44}. Consequently, penguins have pseudogenized 4 ORs that could function underwater and 7 ORs that could smell in the air. In addition, an earlier study suggested that OR gene family 5 was associated with the foraging behavior of predatory birds, and that OR gene families 6 and 10 were prominent in vocal-learning birds¹⁵. Therefore, penguins have lost several ORs that are important in vocal learner and birds of prey.

Discussion

Through examination of 8 draft genomes of 2 penguins and 6 non-penguin waterbirds that are closely related to penguins, we identified 29 ORs that are putative one-to-one orthologs among all 8 waterbirds by phylogenetic analysis. We next attempted to survey the functionality of the 29 ORs by sequence analysis in penguins and their relatives. With the aid of additional sequencing, we found that, of these functionally important ORs common to other waterbirds, penguins were found to have a significantly greater percentage of pseudogenized ORs than other waterbirds, suggesting a major reduction of olfactory capability in penguins relative to other waterbirds. However, the small number of olfactory receptor genes does not necessarily represent a reduced importance of olfaction in penguins, because olfactory receptors could evolve to recognize more odorants and develop novel receptors, as reported in taste receptors^{45,46}. Despite this, our genetic evidence suggests that penguins appear to have a less developed sense of smell than most other waterbirds, as a higher number of chemosensory receptor genes allows the evolution of more specialized receptors⁴⁵. Since genetic evidence is indirect, our study awaits a behavioral test to verify the possible reduction of olfaction in penguins.

In support of our genetic evidence, anatomical reduction of the olfactory bulb in penguins was observed as compared to most other waterbirds, which suggested that penguins generally have a reduction of olfactory acuity relative to other waterbirds^{33,34,47}. Fossil evidence revealed that ancient penguins had much larger olfactory bulbs than extant penguins, suggesting that the reduction of olfactory acuity started shortly before the divergence of penguins⁴⁸. However, the reduced olfaction does not suggest that penguins do not use the sense of smell. Behavioral studies have convincingly demonstrated that penguins can use olfaction to locate prey and recognize kins^{29,30,32}. Indeed, our genetic analysis also revealed that penguins still retain many intact ORs, suggesting a functional role of olfaction in these birds. In fact, penguins were found to possess even more ORs than vocal-learning birds, suggesting that they have a better sense of smell than some other birds¹⁵.

Why could penguins afford to reduce the reliance on olfaction compared to other waterbirds? Penguins are the only surviving birds that inhabit a secondarily aquatic environment with flightless wing-propelled diving behavior; their reduced reliance on olfaction parallels the reduction in marine mammals that independently occupy a secondarily aquatic niche^{11,12,48}. Indeed, we found penguins to have lost several OR genes that encode olfactory receptors detecting air-borne molecules, suggesting that penguins do not need to smell some air-borne molecules in the aquatic environment. Within mammals, sensory tradeoffs were proposed^{49,50}; the reduction of OR genes in trichromatic rather than dichromatic primates has been explained by a trade-off between vision and olfaction¹³. However, this explanation cannot be the case in penguins, because penguins are trichromatic while most other birds are tetrachromatic^{27,28}. On the other hand, positive selection on phototransduction genes and accelerated evolution of visual opsin genes were detected in penguins, which were associated with aquatic adaptation²⁸. Furthermore, the photic adaptation in penguins has also been detected by morphological specializations such as flat corneas and spherical lens^{25,26}. In addition, unlike other diving waterbirds, penguins spend the entire search, chase and capture underwater, some species of penguins are even able to dive 200 meters in depth and 30 minutes in duration⁵¹. Therefore, the aquatic specializations for underwater vision in penguins may have rendered their olfaction less important. Other ecological traits may also account for the reduction of olfactory acuity in penguins. For example, since penguins originated in the coldest niche on Earth, the extremely cold temperature of the Antarctic may have influenced the evolution of olfactory perception⁵², a hypothesis awaiting future empirical investigation. Taken together, we found genetic evidence for a possible reduction of reliance on olfaction in

penguins, and highlighted the power and necessity of in-depth genetic analysis based on draft genome sequences. Although the loss of three primary tastes in penguins has already been revealed⁵³, future studies of other sensory systems in penguins and other waterbirds would provide a better understanding of how penguins could sense and survive in their unique ecological niche.

Materials and Methods

Genome data and gene identification. The draft genome sequences of the eight species of waterbirds were retrieved from the Avian Phylogenomics Project (<http://avian.genomics.cn/en/>, last accessed March 25, 2015). Vertebrate ORs are single-exon genes that encode seven-helix transmembrane proteins⁴⁰. To identify full-length and intact ORs from the eight waterbird genomes, we followed a standard protocol as described previously⁵⁴. Briefly, we used full-length OR protein sequences^{55,56} as queries to conduct TBLASTN searches⁵⁷ with an e-value cutoff of 1e-5. The best hits were determined with the criteria of the lowest e-value and the longest alignment, and the putative start and stop codons were identified by extending in both 5' and 3' directions. All these potential OR genes were then compared (BLASTX) back to the NCBI non-redundant database, and those with the best blast hit of a non-OR gene were discarded. Sequences that are longer than 250 amino acids and have no interrupting stop codons or frameshifts were aligned to known OR genes, and those with a gap of five or more amino acids within transmembrane domains or other conserved regions were excluded. The remaining sequences were considered to be the full-length and intact OR genes, which are used for further analysis.

Phylogenetic reconstruction and OR gene family assignment. Phylogenetic reconstruction was conducted to identify putative one-to-one orthologous genes across the eight birds with draft genomes. A total of 344 complete and intact ORs identified from the eight avian genomes were analyzed with a zebrafish OR gene (GenBank: NM_001083869) as the outgroup. The 345 full-length ORs were translated into protein sequences in MEGA version 6⁵⁸ and were next aligned by MUSCLE⁵⁹ with manual adjustments. The protein sequence alignment was subsequently translated back to nucleotide sequence alignment, which was used to reconstruct phylogenetic trees. Phylogenetic analyses were performed with both Maximum Likelihood (ML) and Bayesian Inference (BI) approaches. The jModelTest2 program⁶⁰ was used to infer the best-fitting substitution model, and the model GTR + I + G was selected. The RAxML version 7.2.6⁶¹ was used to reconstruct ML trees with bootstrap replicates of 1000. The Bayesian tree was constructed by MrBayes version 3.2⁶² with six Markov chains and six million generations.

Genes identified from the whole genomes were assigned into OR gene families using the OR family Assigner, ORA version 1.9⁴². Specifically, we undertook the domain-based hmmscan searches against the HMM (hidden Markov models) database using the program HMMER version 3.1b1⁶³. We assigned a given OR gene into an OR gene family with the lowest e-value produced from the hmmscan searches. The nomenclature of each OR gene (Supplementary data set S1) followed the best hit after conducting BLASTN searches against the HORDE database³⁹. For convenience, we also named each gene with the order in which they were identified (Supplementary data set S1).

Taxon sampling and DNA sequencing. Due to the incomplete genome sequencing or poor genome assembly, some putative one-to-one orthologous genes were not identified with a complete and intact ORF (open reading frame) from the draft genomes (Fig. 1). To obtain the missing data, we designed new primers (Supplementary Table S2) to resequence all missing sequences based on the nucleotide sequence alignments of each gene. The two penguins (i.e. the emperor penguin and the Adelie penguin) with genome sequences are from the two major clades of penguin species tree³⁵, the ancestor of both penguins thus represents the common ancestor of all extant penguins. In case that OR gene sequences are missing from the penguin genomes, we attempted to amplify from the genomic DNAs of their congeneric species (King penguin, *Aptenodytes patagonicus*; Chinstrap penguin, *Pygoscelis antarctica*) (Fig. 2), which were left from a previous project⁵³. The genomic DNAs of the northern fulmar and red-throated loon were from the same project in which we loaned all avian samples from the University of Michigan Museum of Zoology⁵³. The muscle tissue of the little egret (Sample ID: IOZ-9748) was obtained from the Institute of Zoology, Chinese Academy of Sciences. We also included the crest ibis in our resequencing dataset but did not conduct the sequencing, because this bird only missed one OR gene from its genome, which appeared to be intact in penguins (Fig. 2). As a result, our dataset of resequencing contained six avian species: the king penguin, chinstrap penguin, northern fulmar, red-throated loon, little egret, and crested ibis (Fig. 2), which can still represent the four orders (Sphenisciformes, Procellariiformes, Pelecaniformes, and Gaviiformes)³⁶.

Genomic DNA of the little egret was isolated with Qiagen DNeasy kit. Polymerase chain reactions (PCRs) and DNA sequencing were conducted according to procedures previously described^{3,5,6}. Newly generated sequences by PCRs were aligned with their respective orthologous OR genes identified from the whole genomes. The phylogenetic tree of each gene was inferred to confirm the orthology relationship using a Bayesian approach as implemented in MrBayes version 3.2⁶². Pseudogenes were identified when nonsense and/or frame-shifting mutations were observed in an OR sequence. All new sequences have been submitted to GenBank under accession numbers KX171590-KX171621 and KX189196-KX189197.

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Author Contributions

Q.L. carried out the molecular lab work, participated in data analysis and the design of the study; K.W. helped with data analysis; F.L. helped with sample collection and commented the manuscript; D.Y. commented the manuscript; H.Z. conceived of the study, designed the study, coordinated the study and wrote the manuscript. All authors gave final approval for publication.

Additional Information

Accession Codes: DNA sequences: Genbank accessions KX171590-KX171621 and KX189196-KX189197.

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