



HAL
open science

A gull species recognizes mhc-ii diversity and dissimilarity using odor cues

Maxime Pineaux, Pierrick Blanchard, Léa Ribeiro, Scott A Hatch, Sarah Leclaire

► **To cite this version:**

Maxime Pineaux, Pierrick Blanchard, Léa Ribeiro, Scott A Hatch, Sarah Leclaire. A gull species recognizes mhc-ii diversity and dissimilarity using odor cues. Benoist Schaal; Diane Rekow; Matthieu Keller; Fabrice Damon. *Chemical Signals in Vertebrates 15*, Springer International Publishing, pp.139-152, 2023, 978-3-031-35159-4. 10.1007/978-3-031-35159-4_7. hal-03918940v4

HAL Id: hal-03918940

<https://hal.science/hal-03918940v4>

Submitted on 10 Nov 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

27 1. Introduction

28 Most birds do not display any apparent olfactory behavior, such as sniffing or scent-marking. Therefore, it was
29 long thought that birds had little or no sense of smell and relied primarily on visual or acoustic cues. However,
30 there is now abundant evidence that birds have a functional olfactory system (Bang and Cobb 1968; Steiger et
31 al. 2008) and use olfaction in various non-social contexts, including foraging, navigation or nest sanitation
32 (e.g., Caro and Balthazart 2010; Abankwah et al. 2020; Potier 2020; Bonadonna and Gagliardo 2021). In
33 contrast, the role of olfactory cues in avian social life is still poorly known (Caro et al. 2015), albeit being a
34 rapidly growing research area (Whittaker and Hagelin 2021).

35 As in other vertebrates, recent research suggests that the major histocompatibility complex (MHC)
36 may be an important force involved in mate choice in birds (Zelano and Edwards 2002; Løvlie et al. 2013).
37 The MHC is a polymorphic group of genes that plays a critical role in immunity. In general, higher MHC
38 diversity is considered to provide resistance to a wider range of parasites and to increase fitness (Milinski
39 2006). Accordingly, species from diverse taxa have developed MHC-based mate choice, such as mate choice
40 for MHC-dissimilar partners (i.e., MHC-compatible partners), thereby avoiding the production of offspring
41 with low MHC diversity (Strandh et al. 2012; Kamiya et al. 2014; Hoover et al. 2018), or mate choice for
42 MHC-diverse partners, which may provide both genetic and non-genetic benefits (Richardson et al. 2005;
43 Griggio et al. 2011). However, high MHC diversity may also be associated with costs, such as an increased
44 risk of autoimmune disorders or a reduction in the potential for inducing an immune reaction due to negative
45 selection of T-cells (Nowak et al. 1992; Simmonds and Gough 2007; Woelfing et al. 2009; Migalska et al.
46 2019). There is therefore increasing support for an intermediate optimum of MHC-diversity (Madsen and
47 Ujvari 2006; Kalbe et al. 2009; Rekdal et al. 2019).

48
49 Whatever the optimum in MHC-diversity, MHC characteristics needs to be encoded in phenotypic
50 cues for animals to assess the MHC characteristics of potential partners during mate choice. However, while
51 several mammals, lizards or fish have been shown to assess MHC characteristics using odor cues (reviewed in
52 Schubert et al. 2021), this ability in birds has been poorly explored. To the best of our knowledge, only the
53 blue petrel (*Halobaena caerulea*), a Procellariiform seabird, and the song sparrow (*Melospiza melodia*) and
54 the house sparrow (*Passer domesticus*), two Passeriform birds, have been tested. While blue petrels and song
55 sparrows were shown to discriminate MHC-II characteristics using odor cues (Leclaire et al. 2017; Grieves et
56 al. 2019), house sparrows did not discriminate MHC-I characteristics using olfaction (Amo et al. 2022). To
57 estimate the taxonomic range of olfactory assessment of MHC in birds, more avian taxa need to be studied.

58 The black-legged kittiwake (*Rissa tridactyla*) is a genetically monogamous Charadriiform seabird with
59 a functional sense of smell (Leclaire et al. 2009). In this species, preen gland secretions encode information
60 about MHC dissimilarity (Leclaire et al. 2014) and offspring sex-ratio varies with the MHC dissimilarity
61 between parents (Pineaux et al. 2022), suggesting that kittiwakes might be able to recognize the MHC
62 characteristics of conspecifics. Here, we used behavioral tests to investigate whether female kittiwakes can use

63 odor cues to distinguish the MHC characteristics of males. We used a protocol inspired by Leclaire et al.
64 (2009), which showed differential pecking response of incubating females to different odor samples (skunk,
65 banana, fish or control odor) put in their nest. Here, we put a single odor sample of a male to the nest of an
66 incubating female and assessed her behavioral response. Although differential response of females cannot be
67 interpreted as female preference, we consider that the fact that different females react on average differently
68 along a continuum of males' MHC characteristics indicate discrimination. Because the MHC-based mating
69 pattern of kittiwake is unknown, we tested recognition of both MHC diversity and MHC dissimilarity, and
70 always included both the linear and the quadratic term of MHC diversity.

71

72 **2. Materials and methods**

73 *2.1 Study site*

74 The study was conducted during the 2018 incubating period (May-June) in a population of black-legged
75 kittiwakes nesting on an abandoned US Air Force radar tower on Middleton Island, Alaska (59°26'N,
76 146°20'W). Nests on artificial ledges were visible from inside the building through sliding one-way glass
77 windows (Gill and Hatch 2002). This experiment was conducted under the approval of the USGS Alaska
78 Science Centre Animal Care and Use Committee, in accordance with US law and under permits from the US
79 Fish and Wildlife Service and the State of Alaska.

80

81 *2.2 Behavioral tests*

82 We assessed female's response to male odor samples placed on the edge of the nest bowl. Odor samples were
83 a mixture of cloacal samples (potentially related to fecal odor) and nest materials (potentially related to skin,
84 plumage and preen gland odor passively deposited on the nest when birds are sitting). We collected odor
85 samples from 43 incubating males. We collected cloacal samples as in Leclaire et al. (2023). Briefly, after
86 capture, we injected 1 mL of sterile phosphate-buffered saline solution into male's cloaca with a sterile
87 needleless syringe and drew the solution out. A piece of nest material was used as the method of odor delivery
88 to reduce perturbation of the incubating female. At the time of capture, a piece of nest material (i.e., a blend of
89 mosses and grasses of ca. 4 cm diameter) was collected from the center of the nest bowl of the captured male,
90 using clean nitrile gloves. The piece of nest material was immediately mixed with the cloacal sample and
91 stored in plastic bags at -20°C until the test. Odor samples were stored on average for 17 ± 1 days (range: 8-
92 24 days). The time the odor sample was kept in the freezer did not affect the behavioral response of the females
93 (Spearman's correlation test between the time the sample was kept in the freezer and the time the female took
94 to peck at the odor sample during the test: $S = 13678$, $P = 0.077$, $r = -0.28$).

95 Fifty-two incubating females were each tested once. They were never tested with the odor of their
96 partner. All odor samples ($n = 43$) were used at least once. Just before the test, a small piece (ca. 2 cm diameter)
97 of an odor sample was defrosted for 15 minutes. The remaining odor sample was kept frozen. Nine of these
98 remaining odor samples were used in tests later on. The odor sample was placed on the edge of the nest bowl,

99 just under the beak of an incubating female (Figure 1). Because we had to open the sliding window of the
100 nesting site to put the odor sample on the nest, all females, except one, took off. Behaviors were recorded by
101 an observer as soon as the female landed back on her nest. Females returned to their nest on average \pm se: 14
102 \pm 5 sec after the odor sample was placed on the nest (range: 0-462 sec). For each test, we recorded the time
103 taken by the female to peck at the odor sample for the first time. 93 % of the females who pecked at the odor
104 sample took the sample with their bill and moved it along the nest bowl, as they often do with nest material
105 when maintaining the nest structure. We therefore also recorded the time taken by the female to move the odor
106 sample for the first time. Observation lasted until the female pecked at the odor sample or for 15 min when she
107 did not peck at the odor sample. Tests were carried out by 3 observers who were blind to MHC-characteristics
108 of the males concerned.



109

110 **Figure 1:** Picture of a kittiwake's nest in which an odor sample (encircled in red) was put on the edge of the
111 nest. This picture was taken during a preliminary test on a non-incubating bird. However, in all tests considered
112 in this study, the female was incubating.

113

114 2.3 MHC analyses

115 Details about MHC analyses are given in Pineaux et al. (2020). Briefly, DNA was extracted from blood
116 samples, and 258 bp fragments of exon 2 of MHC class-IIB were amplified using PCR and sequenced in 4
117 runs with an Illumina MiSeq platform. Amplicon sequences were analyzed with AmpliSAS (substitution
118 errors: 1%, indel errors: 0.001%, minimum frequency with respect to dominant: 33%, minimum amplicon
119 sequence frequency: 2.5%) (Sebastian et al. 2016). Considering the larger set of samples analysed in the 4
120 Illumina MiSeq runs, we detected a maximum of 6 alleles per individual, suggesting the presence of a
121 minimum of 3 MHC class-IIB loci. We focused on the amino acid sequences of the peptide binding region
122 (Leclaire et al. 2014). MHC-IIB diversity and MHC-IIB dissimilarity were each estimated using two indices.
123 First, MHC-IIB diversity was estimated using the number of MHC-IIB alleles, while MHC-IIB dissimilarity
124 between the female and the sampled male was estimated on a pure shared/non-shared allele basis. The percent

125 difference in MHC-IIB allele sharing was calculated as $100 * \text{TOT}_{\text{FM}} / (\text{N}_{\text{F}} + \text{N}_{\text{M}})$, where TOT_{FM} = total number
126 of different alleles present in the male and the female (shared allele count as 1) and N = number of alleles
127 within an individual (Strandh et al. 2012). Second, we estimated MHC-IIB diversity as the degree of functional
128 diversity (or divergence) of alleles across all loci, and MHC-IIB dissimilarity as the functional distance
129 between two individuals. We described the chemical binding properties of each amino acid in the PBR with
130 Sandberg's five physicochemical descriptors (z-descriptors; Sandberg et al. 1998). This Sandberg's matrix was
131 used to construct a UPGMA dendrogram of alleles (function `hclust` in R), which represents clusters of
132 functionally similar MHC-IIB sequences. The dendrogram was used as a reference to calculate the functional
133 MHC-IIB diversity of an individual as the minimum total length of all the branches required to span its MHC-
134 IIB alleles (function `treedive` in package *vegan*) (Petchey and Gaston 2006). MHC-IIB functional dissimilarity
135 between the male odor donor and the female was estimated using the tree distance (function `treedist` in package
136 *vegan*), which is found by combining species in a common dendrogram and seeing how much of the
137 dendrogram height is shared and how much is unique. Because five females were not genotyped at the MHC-
138 IIB, we could not calculate the MHC-IIB dissimilarity between the female and the sampled male for five tests.
139 The number of alleles was correlated with the functional diversity (Spearman's rank correlation test: $S = 1110$,
140 $P < 0.0001$, $r = 0.92$, $n = 43$ males), and the percent difference in allele sharing was correlated with the
141 functional dissimilarity (Spearman's rank correlation test: $S = 2619$, $P < 0.0001$, $r = 0.85$, $n = 47$ male-female
142 pairs).

143

144 2.4 Statistics

145 To test for difference in females' behavioral response according to the MHC-II diversity of the male odor donor
146 and to the MHC-II dissimilarity between the female and the male odor donor, first we used a generalized linear
147 mixed model (GLMM) with the probability to peck at the odor sample (0 when the female did not peck at the
148 sample or 1 when the female pecked at the sample) as the binomial response variable. Fixed effects included
149 MHC-II dissimilarity, male MHC-II diversity and the quadratic term of male MHC-II diversity. Although the
150 MHC-II diversity of the male odor donor was negatively related to the MHC-II dissimilarity to the female
151 (Spearman rank test between the number of alleles and the percent difference in allele sharing: $S = 22305$, $r =$
152 -0.29 , $P = 0.048$ and between the functional diversity and the functional dissimilarity: $S = 24936$, $r = -0.44$, P
153 $= 0.002$; $n = 47$ tests for which we have both MHC-II diversity and dissimilarity), we included the two variables
154 together in the models as the variance inflation factors were < 1.5 (Zuur et al. 2010). Fixed effects also included
155 the difference between the date of the test and the laying date, as female reaction to male MHC-II
156 characteristics might potentially change across the breeding season (Manning et al. 1992; Leclaire et al. 2017).
157 The identity of the male odor donor was included as a random effect, while the observer was not included as
158 a random effect because its variance estimate was 0. Second, for females who pecked at the samples, we used
159 a linear mixed model (LMM) with the time taken to peck at the odor sample as the response variable (log-
160 transformed to meet normality of residuals), and the same fixed effects as above. Both the observer and the

161 identity of the male odor donors were included as random effects. Third, for females who moved the odor
162 sample, we used a binomial GLMM model to test whether the probability to delay the move of the odor sample
163 after the first pecking (0 when the female immediately moved the sample after the first pecking or 1 when the
164 female delayed the move of the sample) varied with MHC-II characteristics. Fixed and random effects were
165 similar as above.

166 We performed all statistical analyses using the R statistical software (R Core Team 2019). In GLMMs,
167 we used Wald's tests to assess the significance of variables. In LMMs, significance of each predictor variable
168 was calculated using the Satterthwaite approximation as implemented in the package *lmerTest* (Kuznetsova et
169 al. 2017). Normality and homogeneity of variance were checked visually (Zuur et al. 2010). Data can be found
170 at doi.org/10.17605/OSF.IO/H2KFN.

171

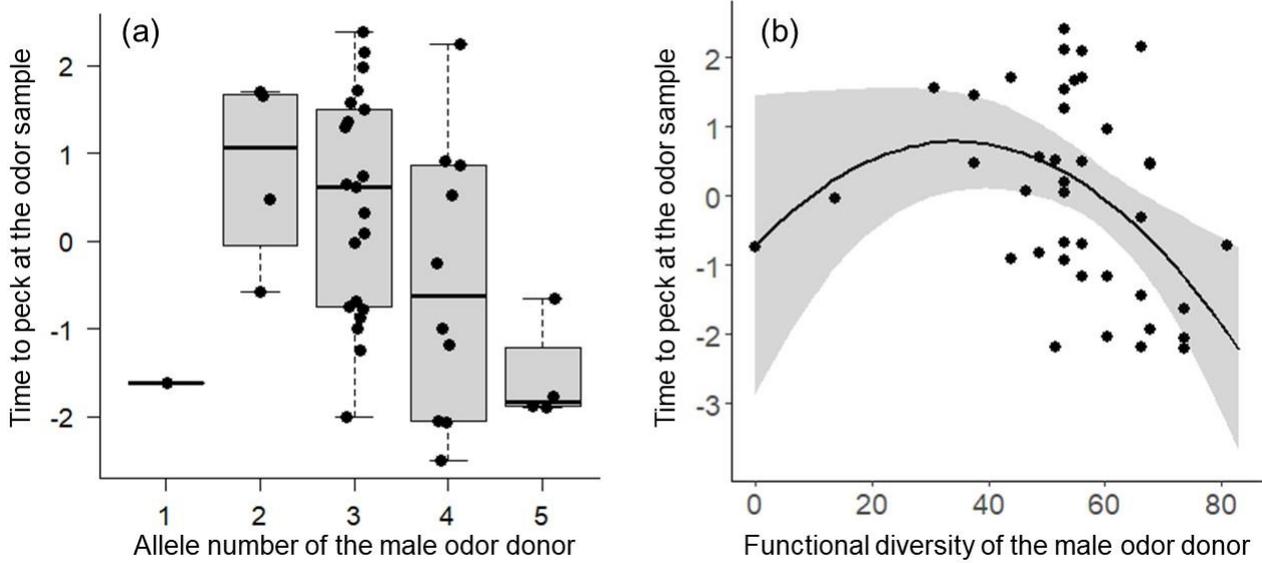
172

173 3. Results

174 When considering the tests for which we had both the MHC-II diversity of the male odor donor and the MHC-
175 II dissimilarity between the male odor donor and the female (n = 47 tests), seven females (15 %) did not peck
176 at the odor sample. The probability of pecking at the sample did not vary with male MHC-II diversity (allele
177 number: quadratic term: $\chi^2_1 = 0.01$, P = 0.94 and linear term: $\chi^2_1 = 0.17$, P = 0.68; functional diversity: quadratic
178 term: $\chi^2_1 = 0.01$, P = 0.93 and linear term: $\chi^2_1 = 0.12$, P = 0.73) or MHC-II dissimilarity (percent difference in
179 allele sharing: $\chi^2_1 = 0.06$, P = 0.80 and functional dissimilarity: $\chi^2_1 = 0.01$, P = 0.94).

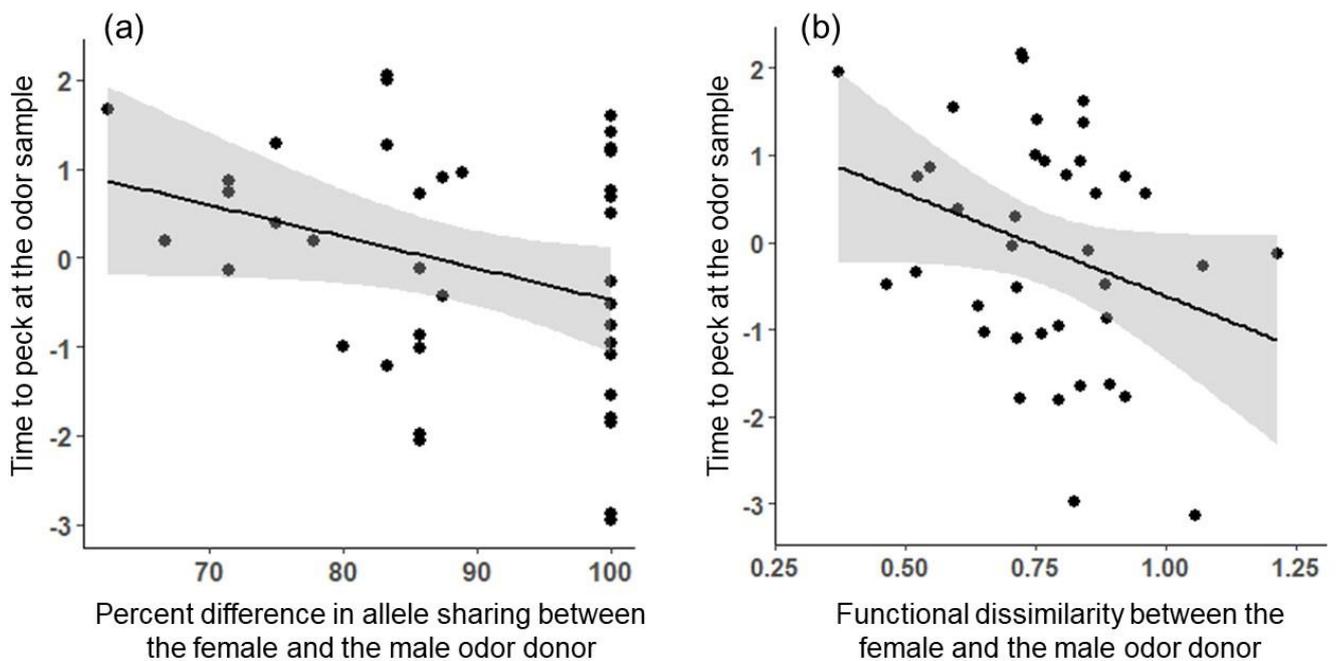
180 Among the females who pecked at the sample (n = 40 tests for which we had both the male MHC-II
181 diversity and the MHC-II dissimilarity between male and female), females took more time to peck at the odor
182 sample when the male had an intermediate MHC-II diversity (allele number: quadratic term: $\chi^2_1 = 5.49$, P =
183 0.025 and linear term: $\chi^2_1 = 6.60$, P = 0.015, Figure 2a; functional diversity: quadratic term: $\chi^2_1 = 5.97$, P =
184 0.020 and linear term: $\chi^2_1 = 3.91$, P = 0.056; Figure 2b). When excluding the test where the single male odor
185 donor had only one MHC-II allele (Fig. 2a), females took less time to peck at the odor sample when the male
186 had higher MHC-II diversity (allele number: linear term: $\chi^2_1 = 13.73$, P < 0.001 and quadratic term: $\chi^2_1 = 0.36$,
187 P = 0.55; functional diversity: linear term: $\chi^2_1 = 6.98$, P = 0.012 and quadratic term: $\chi^2_1 = 2.43$, P = 0.13; Figure
188 2). This result suggests that this male carrying a single MHC-II allele drives the quadratic relationship between
189 the time taken to peck at the sample and the MHC-II diversity. Females who pecked at the sample took also
190 less time to peck at the odor sample when they were more MHC-II dissimilar to the male odor donor (percent
191 difference in allele sharing: $\chi^2_1 = 6.08$, P = 0.019 and functional dissimilarity: $\chi^2_1 = 6.89$, P = 0.013; Figure 3).

192



193

194 **Figure 2:** Time taken by females to peck at the odor sample according to (a) the number of MHC-II alleles
 195 and (b) the functional MHC-II diversity of the male odor donor. The time to peck at the sample was represented
 196 by the residuals of a linear mixed model in which the time to peck at the sample was explained by all variables
 197 except the MHC-II diversity of the male. The black line and the grey shadow in (b) represent prediction line
 198 and 95% confidence interval.

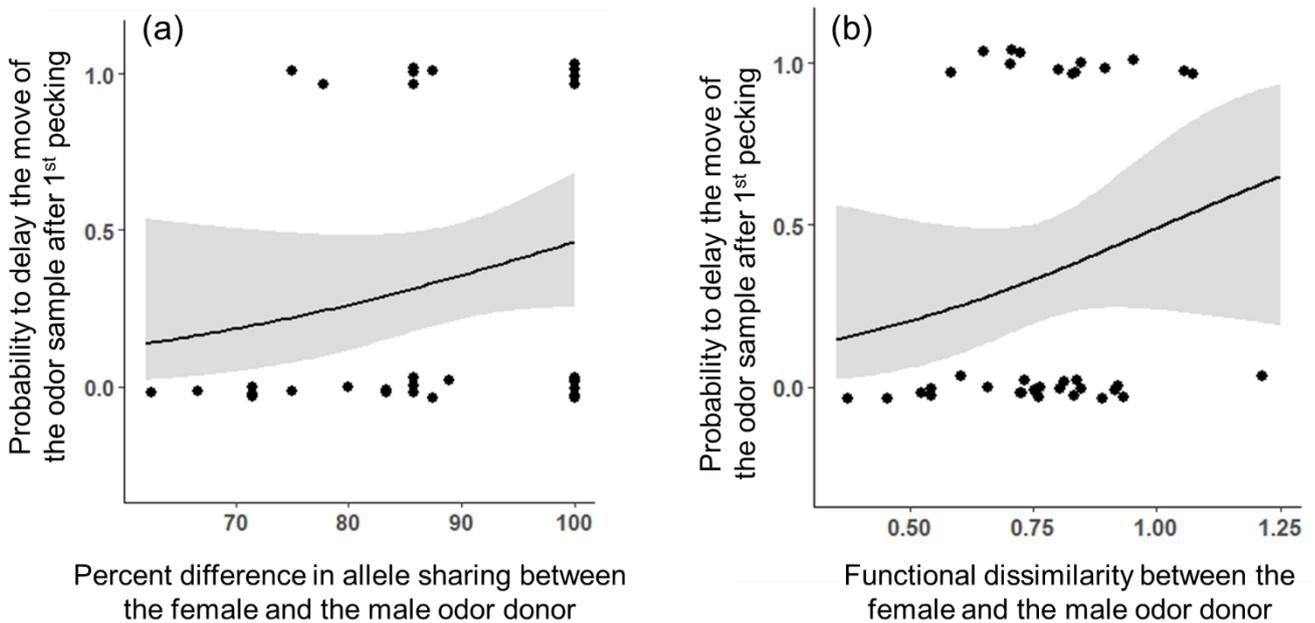


199

200 **Figure 3:** Time taken by females to peck at the odor sample according to (a) the percent difference in MHC-
 201 II allele sharing and (b) the functional MHC-II dissimilarity to the male odor donor. The time to peck at the
 202 sample was represented by the residuals of a linear mixed model in which the time to peck at the sample was
 203 explained by all variables except the MHC-II dissimilarity. The black lines and grey shadows represent
 204 prediction line and 95% confidence interval.

205

206 93 % of the females who pecked at the odor sample took the sample with their bill and moved it along
 207 the nesting bowl (n = 37 tests for which we have both the MHC-II diversity and MHC_II dissimilarity). 65%
 208 of those females (n = 24 females) moved the sample just after the first pecking, while the others (n = 13
 209 females) delayed the move of the odor sample. The probability to delay the move of the odor sample after the
 210 first pecking increased with the dissimilarity to the male odor donor (percent difference in allele sharing: $\chi^2_1 =$
 211 5.39, P = 0.020 and functional dissimilarity: $\chi^2_1 = 8.35$, P = 0.004; Figure 4). The probability to delay the move
 212 of the odor sample did not vary with the MHC-II diversity of the male odor donor (all P values > 0.10).



213

214 **Figure 4:** Probability for the females to delay the move of the odor sample after the first pecking (0: the female
 215 moved the sample just after the first pecking and 1: the female delayed the move of the sample after the first
 216 pecking) according to (a) the percent difference in MHC-II allele sharing and (b) the functional MHC-II
 217 dissimilarity to the male odor donor. The black lines and grey shadows represent prediction line and 95%
 218 confidence interval of a GLMM between the probability to delay the move of the sample after the first pecking
 219 and the MHC-II dissimilarity to the male odor donor.

220

221 5. Discussion

222 Using behavioral tests, we investigated whether, in black-legged kittiwakes, females discriminated the MHC-
223 II characteristics of males. First, we found that females took more time to peck at the odor sample when it
224 came from a male with intermediate MHC-II diversity. However, the quadratic relationship between MHC-II
225 diversity and the time taken to peck at the sample was only due to the single male who had only one MHC-II
226 allele (Fig. 1). When excluding this male, the relationship between male MHC-II diversity and female behavior
227 became linear. Clearly, more tests including male odor donors carrying a single MHC-II allele would have
228 been needed to ascertain the quadratic nature of the relationship between male MHC-II diversity and the
229 female's reaction to the odor sample. However, in this kittiwake population, very few individuals carry a single
230 MHC-II allele (< 1 % of the individuals; unpublished data), suggesting that carrying a single MHC-II allele is
231 counter-selected. Recently, several studies in fish, snakes and birds have tested the "golden mean hypothesis"
232 and have shown that individuals with intermediate MHC-diversity have higher reproductive success (Kalbe et
233 al. 2009), better immunity (Rekdal et al. 2021) and lower parasite load (Wegner et al. 2004; Madsen and Ujvari
234 2006). In kittiwakes, the optimum in MHC-II diversity has been tested in chicks only, and was found to be at
235 maximum diversity in female chicks (Pineaux et al. 2020). However, the optima in MHC diversity can vary
236 according to individual traits that affect the trade-off between the benefits and costs associated with high MHC
237 diversity (Roved et al. 2018; Pineaux et al. 2020). Therefore, the optimum in MHC-II diversity may differ
238 between adults and chicks, because of age-differences in exposure to parasites, acquired immunity and
239 predisposition to infection (Benskin et al. 2009). Further studies are needed to determine whether, in
240 kittiwakes, intermediate or maximum MHC-II diversity is optimum in adult males.

241 We also found that females took less time to peck at an odor sample coming from a male with higher
242 MHC-II dissimilarity. Almost all females who pecked at the odor sample moved it along the nesting bowl, as
243 they commonly do with nest material during nest maintenance. However, while some females moved the odor
244 sample just after the first pecking, other delayed the move of the sample. We found that the probability to delay
245 the move of the odor sample was higher when the odor sample came from a male with higher MHC-II
246 dissimilarity. Female pecking response and sample moving response cannot be interpreted as preference or
247 aversion for certain odors. However, our results show that female kittiwakes may use odor cues to discriminate
248 MHC-II diversity and MHC-II dissimilarity. Further studies are needed to determine the contexts in which
249 females may use this ability (e.g., mate choice, adjustment of parental investment, offspring sex-ratio
250 distortion). Although the role of olfaction in the recognition of MHC dissimilarity has been shown in several
251 vertebrate species (reviewed in Schubert et al. 2021), its role in the recognition of MHC diversity has been less
252 studied, probably because MHC diversity, by influencing health, can be reflected in any condition-dependent
253 traits (Lie et al. 2008; Dunn et al. 2013; Slade et al. 2017). However, three-spined sticklebacks (*Gasterosteus*
254 *aculeatus*), ring-tailed lemurs (*Lemur catta*) and song sparrows (*Melospiza melodia*) can discriminate MHC
255 diversity using odor cues (Milinski et al. 2005; Grieves et al. 2019; Grogan et al. 2019).

256 In birds, preen gland secretions are often suggested to be the main source of body odors and have been
257 shown to be used in social communication in a few species (Hirao et al. 2009, Zhang et al. 2010). However,
258 in most birds, the sources of body odors are unknown (Hagelin and Jones 2007). Here, we tested whether

259 females could discriminate male MHC-II characteristics using a mixture of odor sources (i.e., cloacal samples
260 mixed with nest material), thereby preventing us to identify precisely the sources of MHC-related odors. In
261 kittiwakes, preen secretions encode information about MHC-II dissimilarity (Leclaire et al. 2014), but studies
262 are required to determine the role of other sources such as feces, skin or plumage microbiota (Leclaire et al.
263 2019; Schubert et al. 2021). For instance, in kittiwakes, the outside edge of the nest is usually full of feces
264 suggesting that fecal odor might play a role in communication. In addition, while our results are consistent
265 with odor-based discrimination of MHC-II characteristics, our methods do not allow us to determine whether
266 discrimination is based on broader genome-wide genetic variation or on other polymorphic genes whose
267 variations covary with those in the MHC, such as the major urinary protein (MUP) genes in natural populations
268 of mice (Sherborne et al. 2007). Finally, the development of inventive odor discrimination tests based on more
269 relevant behavioral responses is key to better appreciate the contexts in which social odor discrimination
270 abilities can be used in kittiwakes, but also more generally in non-burrowing large wild birds.

271 Altogether, our results, by adding evidence for olfactory discrimination of MHC characteristics in
272 birds, suggest that this capacity may be widespread in this taxon. However, whether birds use it in mate choice
273 or more generally to maximize fitness has still to be demonstrated.

274

275 **Acknowledgments**

276 We are grateful to T. Rinaud, and C. Maillotte for their help in the field. This study is part of the Laboratoire
277 d'Excellence (LABEX) entitled TULIP (ANR-10- LABX-41). This work was supported by grants from the
278 French Polar Institute (IPEV; Program 1162 to SL) and the Fondation Fyssen (to SL).

279

280

281 **References**

282 Abankwah, V., Deeming, D.C., Pike, T.W. (2020). Avian Olfaction: A Review of the Recent Literature.
283 *Comparative Cognition & Behavior Reviews*, 15.

284 Amo, L., Amo de Paz, G., Kabbert, J., Machordom, A. (2022). House sparrows do not exhibit a preference
285 for the scent of potential partners with different MHC-I diversity and genetic distances. *Plos one*, 17,
286 e0278892. doi: 10.1371/journal.pone.0278892

287 Bang, B.G., Cobb, S. (1968). The Size of the Olfactory Bulb in 108 Species of Birds. *The Auk*, 85, 55–61.

288 Benskin, C.M.W.H., Wilson, K., Jones, K., Hartley, I.R. (2009). Bacterial pathogens in wild birds: a review
289 of the frequency and effects of infection. *Biological Reviews*, 84, 349–373. doi:10.1111/j.1469-
290 185X.2008.00076.x.

- 291 Bonadonna F, Gagliardo A. 2021. Not only pigeons: avian olfactory navigation studied by satellite telemetry.
292 *Ethology, Ecology & Evolution*, 33(3), 273–289.
- 293 Caro SP, Balthazart J. 2010. Pheromones in birds: myth or reality ? *Journal of Comparative Physiology A*,
294 196(10), 751-766. doi: 10.1007/s00359-010-0534-4
- 295 Caro SP, Balthazart J, Bonadonna F. 2015. The perfume of reproduction in birds: Chemosignaling in avian
296 social life. *Hormones and Behavior*, 68(0), 25–42. doi:10.1016/j.yhbeh.2014.06.001.
- 297 Dunn PO, Bollmer JL, Freeman-Gallant CR, Whittingham LA. 2013. MHC variation is related to a sexually
298 selected ornament, survival, and parasite resistance in common yellowthroats. *Evolution: International*
299 *Journal of Organic Evolution*, 67(3), 679–687.
- 300 Gill VA, Hatch SA. 2002. Components of productivity in black-legged kittiwakes *Rissa tridactyla*: response
301 to supplemental feeding. *Journal of Avian Biology*, 33(2), 113–126.
- 302 Grieves LA, Gloor GB, Bernards MA, MacDougall-Shackleton EA. 2019. Songbirds show odour-based
303 discrimination of similarity and diversity at the major histocompatibility complex. *Animal Behaviour*, 158,
304 131–138.
- 305 Griggio M, Biard C, Penn DJ, Hoi H. 2011. Female house sparrows "count on" male genes: experimental
306 evidence for MHC-dependent mate preference in birds. *BMC Evolutionary Biology*, 11(44), 1-7.
307 doi:10.1186/1471-2148-11-44.
- 308 Grogan KE, Harris RL, Boulet M, Drea CM. 2019. Genetic variation at MHC class II loci influences both
309 olfactory signals and scent discrimination in ring-tailed lemurs. *BMC Evolutionary Biology*, 19(1), 1–16.
- 310 Hagelin J, Jones IL. 2007. Bird odors and other chemical substances: A defense mechanism or overlooked
311 mode of intraspecific communication? *The Auk*, 124(3), 741-761.
- 312 Hirao A, Aoyama M, Sugita S. 2009. The role of uropygial gland on sexual behavior in domestic chicken
313 *Gallus gallus domesticus*. *Behavioural Processes*, 80(2), 115-120.
- 314 Hoover B, Alcaide M, Jennings S, Sin SYW, Edwards SV, Nevitt GA. 2018. Ecology can inform genetics:
315 Disassortative mating contributes to MHC polymorphism in Leach's storm-petrels (*Oceanodroma*
316 *leucorhoa*). *Molecular Ecology*, 27(16), 3371–3385.
- 317 Kalbe M, Eizaguirre C, Dankert I, Reusch TBH, Sommerfeld RD, Wegner KM, Milinski M. 2009. Lifetime
318 reproductive success is maximized with optimal major histocompatibility complex diversity. *Proceedings of*
319 *the Royal Society B*, 276(1658), 925–934. doi:10.1098/rspb.2008.1466.
- 320 Kamiya T, O'Dwyer K, Westerdahl H, Senior A, Nakagawa S. 2014. A quantitative review of MHC-based
321 mating preference: the role of diversity and dissimilarity. *Molecular Ecology*, 23(21), 5151–5163.

322 Kuznetsova A, Brockhoff PB, Christensen RHB. 2017. lmerTest Package: Tests in linear mixed effects
323 models. *Journal of Statistical Software*, 82(1), 1–26. <https://doi.org/10.18637/jss.v082.i13>

324 Leclaire S, van Dongen WF, Voccia S, Merklings T, Ducamp C, Hatch SA, Blanchard P, Danchin É, Wagner
325 RH. 2014. Preen secretions encode information on MHC similarity in certain sex-dyads in a monogamous
326 seabird. *Scientific Reports*, 4, 6920.

327 Leclaire S, Mulard H, Wagner RH, Hatch SA, Danchin E. 2009. Can Kittiwakes smell? Experimental
328 evidence in a Larid species. *Ibis*, 151(3), 584–587.

329 Leclaire S, Pineaux M, Blanchard P, White J, Hatch SA. 2023. Microbiota composition and diversity of
330 multiple body sites vary according to reproductive performance in a seabird. *Molecular Ecology*. Published
331 online. doi:10.1111/mec.16398

332 Leclaire S, Strandh M, Dell’Ariccia G, Gabirot M, Westerdahl H, Bonadonna F. 2019. Plumage microbiota
333 covaries with the major histocompatibility complex in blue petrels. *Molecular Ecology*, 28(4), 833–846.

334 Leclaire S, Strandh M, Mardon J, Westerdahl H, Bonadonna F. 2017. Odour-based discrimination of
335 similarity at the major histocompatibility complex in birds. *Proceedings of the Royal Society B*, 284(1846),
336 20162466.

337 Lie HC, Rhodes G, Simmons LW. 2008. Genetic diversity revealed in human faces. *Evolution*, 62(10),
338 2473–2486. doi:10.1111/j.1558-5646.2008.00478.x.

339 Løvlie H, Gillingham MA, Worley K, Pizzari T, Richardson DS. 2013. Cryptic female choice favours sperm
340 from major histocompatibility complex-dissimilar males. *Proceedings of the Royal Society London B*,
341 280(1769), 20131296.

342 Madsen T, Ujvari B. 2006. MHC class I variation associates with parasite resistance and longevity in tropical
343 pythons. *Journal of Evolutionary Biology*, 19(6), 1973–1978. doi:10.1111/j.1420-9101.2006.01158.x.

344 Manning C, Wakeland E, Potts W. 1992. Communal nesting patterns in mice implicate MHC genes in kin
345 recognition. *Nature*, 360, 581–583. doi: 10.1038/360581a0

346 Migalska M, Sebastian A, Radwan J. 2019. Major histocompatibility complex class I diversity limits the
347 repertoire of T cell receptors. *Proceedings of the National Academy of Sciences*, 116(11), 5021–5026.

348 Milinski M. 2006. The major histocompatibility complex, sexual selection, and mate choice. *Annual Review*
349 *of Ecology Evolution and Systematics*, 37, 159–186.

350 Milinski M, Griffiths S, Wegner KM, Reusch TBH, Haas-Assenbaum A, Boehm T. 2005. Mate choice
351 decisions of stickleback females predictably modified by MHC peptide ligands. *Proceedings of the National*
352 *Academy of Sciences USA*, 102(12), 4414–4418. doi:10.1073/pnas.0408264102.

353 Nowak MA, Tarczy-Hornoch K, Austyn JM. 1992. The optimal number of major histocompatibility complex
354 molecules in an individual. *Proceedings of the National Academy of Sciences USA*, 89(22), 10896–10899.
355 doi:10.1073/pnas.89.22.10896.

356 Petchey OL, Gaston KJ. 2006. Functional diversity: back to basics and looking forward. *Ecology Letters*, 9,
357 741–758.

358 Pineaux M, Merklung T, Danchin E, Hatch S, Duneau D, Blanchard P, Leclaire S. 2020. Sex and hatching
359 order modulate the association between MHC-II diversity and fitness in early-life stages of a wild seabird.
360 *Molecular Ecology*, 29(17), 3316–3329.

361 Pineaux M, Merklung T, Danchin E, Hatch SA, Leclaire S, Blanchard P. 2022. MHC-II distance between
362 parents predicts sex allocation decisions in a genetically monogamous bird. *Behavioral Ecology*, 33(1), 245–
363 251.

364 Potier S. 2020. Olfaction in raptors. *Zoological Journal of the Linnean Society*, 189(3), 713–721.
365 doi:10.1093/zoolinnean/zlz121.

366 R Core Team. 2019. R: A language and environment for statistical computing.

367 Rekdal SL, Anmarkrud JA, Lifjeld JT, Johnsen A. 2019. Extra-pair mating in a passerine bird with highly
368 duplicated major histocompatibility complex class II: Preference for the golden mean. *Molecular Ecology*,
369 28(23), 5133–5144.

370 Rekdal SL, Anmarkrud JA, Lifjeld JT, Johnsen A. 2021. Elevated phytohaemagglutinin-induced skin-
371 swelling response at an intermediate number of MHC class II alleles in bluethroat nestlings. *Journal of Avian*
372 *Biology*, 52(5). doi:10.1111/jav.02734.

373 Richardson DS, Komdeur J, Burke T, von Schantz T. 2005. MHC-based patterns of social and extra-pair
374 mate choice in the Seychelles warbler. *Proceedings of the Royal Society B*, 272, 759–767. doi:
375 10.1098/rspb.2004.3028

376 Roved J, Hansson B, Tarka M, Hasselquist D, Westerdahl H. 2018. Evidence for sexual conflict over major
377 histocompatibility complex diversity in a wild songbird. *Proceedings of the Royal Society B*, 285(1884),
378 20180841.

379 Sandberg M, Eriksson L, Jonsson J, Sjöström M, Wold S. 1998. New chemical descriptors relevant for the
380 design of biologically active peptides. A multivariate characterization of 87 amino acids. *Journal of*
381 *medicinal chemistry*, 41(14), 2481–2491.

382 Schubert N, Nichols HJ, Winternitz JC. 2021. How can the MHC mediate social odor via the microbiota
383 community? A deep dive into mechanisms. *Behavioral Ecology*, 32(3), 359–373.

384 Sebastian A, Herdegen M, Migalska M, Radwan J. 2016. amplisas: A web server for multilocus genotyping
385 using next-generation amplicon sequencing data. *Molecular Ecology Resources*, 16(2), 498–510.

386 Sherborne AL, Thom MD, Paterson S, Jury F, Ollier WE, Stockley P, Beynon RJ, Hurst JL. 2007. The
387 genetic basis of inbreeding avoidance in house mice. *Current biology*, 17(23), 2061-2066.

388 Simmonds MJ, Gough SCL. 2007. The HLA Region and Autoimmune Disease: Associations and
389 Mechanisms of Action. *Current Genomics*, 8(7), 453–465. doi:10.2174/138920207783591690.

390 Slade JWG, Watson MJ, MacDougall-Shackleton EA. 2017. Birdsong signals individual diversity at the
391 major histocompatibility complex. *Biology Letters*, 13(11), 20170430. doi:10.1098/rsbl.2017.0430.

392 Steiger SS, Fidler AE, Valcu M, Kempenaers B. 2008. Avian olfactory receptor gene repertoires: evidence
393 for a well-developed sense of smell in birds? *Proceedings of the Royal Society B*, 275(1649), 2309–2317.

394 Strandh M, Westerdahl H, Pontarp M, Canback B, Dubois M-P, Miquel C, Taberlet P, Bonadonna F. 2012.
395 Major histocompatibility complex class II compatibility, but not class I, predicts mate choice in a bird with
396 highly developed olfaction. *Proceedings of the Royal Society B*, 279(1746), 4457–4463.
397 doi:10.1098/rspb.2012.1562.

398 Wegner KM, Kalbe M, Schaschl H, Reusch TBH. 2004. Parasites and individual major histocompatibility
399 complex diversity—an optimal choice? *Microbes and Infection*, 6(12), 1110–1116.
400 doi:10.1016/j.micinf.2004.05.025.

401 Whittaker DJ, Hagelin JC. 2021. Female-Based Patterns and Social Function in Avian Chemical
402 Communication. *Journal of Chemical Ecology*, 47(1), 43–62. doi:10.1007/s10886-020-01230-1.

403 Woelfing B, Traulsen A, Milinski M, Boehm T. 2009. Does intra-individual major histocompatibility
404 complex diversity keep a golden mean? *Philosophical Transactions of the Royal Society B*, 364(1513), 117–
405 128. doi:10.1098/rstb.2008.0174.

406 Zhang JX, Wei W, Zhang JH, Yang WH. 2010. Uropygial gland-secreted alkanols contribute to olfactory sex
407 signals in budgerigars. *Chemical Senses*, 35(5), 375-382.

408 Zelano B, Edwards SV. 2002. An MHC component to kin recognition and mate choice in birds: predictions,
409 progress, and prospects. *American Naturalist*, 160(S6), S225-S237.

410 Zuur AF, Ieno EN, Elphick CS. 2010. A protocol for data exploration to avoid common statistical problems.
411 *Methods in Ecology and Evolution*, 1(1), 3-14. doi: 10.1111/j.2041-210X.2009.00001.x