

Strong breeding colony fidelity in northern gannets following high pathogenicity avian influenza virus (HPAIV) outbreak

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 Influenza Virus (HPAIV) outbreak

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David Grémillet^{1,2}, Aurore Ponchon^{3,4}, Pascal Provost⁵, Amandine Gamble^{6,7}, Mouna AbedZahar⁸, Alice Bernard¹, Nicolas Courbin¹, Grégoire Delavaud⁵, Armel Deniau⁵, Jérôme Fort⁹,
Keith C. Hamer¹⁰, Ruth Jeavons¹⁰, Jude V. Lane¹¹, Liam Langley¹², Jason Matthiopoulos⁶,
Timothée Poupart¹³, Aurélien Prudor¹, Nia Stephens¹⁴, Alice Trevail¹², Sarah Wanless¹⁵,
Stephen C. Votier¹⁶ and Jana W.E. Jeglinski⁶

- 9
- 10 ¹ CEFE, Univ Montpellier, CNRS, EPHE, IRD, Montpellier, France
- ² FitzPatrick Institute, DST/NRF Excellence Centre at the University of Cape Town, Rondebosch 7701, South Africa
- 12 ³ School of Biological Sciences, University of Aberdeen, Scotland, UK
- 13 ⁴ IMBE, Aix Marseille Univ., Avignon Univ., CNRS, IRD, Marseille, France
- ⁵ Ligue pour la Protection des Oiseaux, Réserve Naturelle Nationale des Sept-Iles, Pleumeur Bodou, France
- ⁶ School of Biodiversity, One Health and Veterinary Medicine, University of Glasgow, Scotland, UK
- 16 ⁷ Department of Public and Ecosystem Health, Cornell University, New York, United States
- 17 ⁸ LABOCEA, 2 rue du sabot, 22440 Ploufragan, France
- ⁹ Littoral, Environnement et Sociétés, LIENSs, UMR 7266 CNRS-La Rochelle University; La Rochelle, France
- ¹⁰ School of Biology, University of Leeds, UK
- 20 ¹¹ RSPB Centre for Conservation Science, Cambridge, UK
- 21 ¹² Centre for Ecology and Conservation, University of Exeter, Penryn, Cornwall, UK
- 22 ¹³ PatriNat, OFB-CNRS-MNHN, Muséum national d'Histoire naturelle, Paris, France
- 23 ¹⁴ RSPB Ramsey Island, St Davids, Pembrokeshire UK
- 24 ¹⁵ UK Centre for Ecology & Hydrology, Bush Estate, Penicuik, Scotland, UK
- 25 ¹⁶ Lyell Centre, Institute for Life and Earth Sciences, Heriot-Watt University, Edinburgh, UK
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- 27
- 28

29 Abstract:

30 High pathogenicity avian influenza virus (HPAIV) caused the worst seabird mass-mortalities in Europe across 2021-2022. The northern gannet (Morus bassanus) was one of the worst 31 affected species, with tens of thousands of casualties in the northeast Atlantic between April-32 33 September 2022. Disease outbreaks can modify the movement ecology of animals by diminishing spatial consistency, thereby increasing the potential for disease transmission. To 34 detect potential changes in movement behaviour, we GPS-tracked breeding adults following 35 36 the initial HPAIV outbreak, at three of the largest northern gannet breeding colonies where major mortality of adults and chicks occurred (Bass Rock, Scotland, UK; Grassholm, Wales, 37 UK; Rouzic, Brittany, France). We also gathered background epidemiological information and 38 northern gannet colony dynamics during the outbreak. Our data indicate that HPAIV killed at 39 40 least 50% of northern gannets, and suggest the presence of HPAIV H5N1 antibodies in juveniles. GPS-tracked adult northern gannets remained faithful to their breeding sites 41 42 despite the HPAIV outbreak and did not prospect other breeding colonies. They performed regular foraging trips at sea, similar to their behaviour before the outbreak. Comparison with 43 GPS-tracking data gathered in 2019, i.e. before the HPAIV outbreak, suggested lower foraging 44 effort in birds which survived HPAIV in 2022, potentially as a consequence of reduced intra-45 and interspecific food competition. Breeding colony fidelity of surviving adult northern 46 47 gannets following HPAIV mass-mortalities indicates limited capacity for viral spread during 48 our study. This may contrast with the behaviour of adults during the initial disease outbreak, and with that of younger individuals. 49

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Keywords: Avian pathogens, Behavioural latency, Human/wildlife interaction, Movement
ecology, Seabird conservation, Viral transmission

54 Introduction

55 Avian influenza was first reported in farmed poultry in 1878 in Northern Italy (Perroncito, 1878). Outbreaks of the virus occurred worldwide in domestic fowl across the 20th century 56 (Swayne and Suarez, 2000). During this period, wild birds were also regularly affected 57 58 (Gauthier-Clerc et al., 2007). In 1996, a form of highly pathogenic avian influenza virus (HPAIV; 59 H5Nx clade 2.3.4.4) evolved in farmed poultry in Southern China. It subsequently spilled over to wild birds, and occasionally to humans (Alexander and Brown, 2009). HPAIV has since 60 61 occurred in 61 countries and is endemic in poultry farms around the world. In 2021/2022, the worst-ever HPAIV outbreak was recorded in poultry farms, especially in Europe (Wille and 62 Barr, 2022), resulting in the culling of an estimated 47.7 million birds (Authority et al., 2022). 63 These events deeply challenge intensive bird farming, as high-density housing conditions and 64 65 long-distance poultry transport lead to the spread of HPAIV (Kuiken and Cromie, 2022). Rapid evolution in high-density, confined poultry farms also enhances the likelihood of mutations 66 leading to the emergence of HPAIV as the next human pandemic (Roberts Jr and Krilov, 2022). 67 Finally, HPAIV is now causing substantial mortalities to wild birds, including in species already 68 challenged by other human activities (Gamarra-Toledo et al., 2023). 69

70 This is the case for seabirds, which are currently the most endangered bird group apart from parrots (Phillips et al., 2023). Half of the worldwide abundance of seabirds has been lost since 71 72 1970 (Grémillet et al., 2018), mainly because of breeding habitat loss, mortality caused by 73 fishing gear, invasive species (e.g. cats and rats), food competition with fisheries, direct and 74 indirect consequences of climate change, and pollution (Young and VanderWerf, 2023). 75 Pathogens can also have significant impacts on seabird populations, as demonstrated by the 76 effects of avian cholera (Pasteurella multocida) on Cape cormorants (Phalacrocorax capensis) in South Africa (Crawford et al., 1992), and on common eiders (Somateria mollissima) in North 77 78 America (Iverson et al., 2016). While seabirds are common hosts of low pathogenicity avian influenza viruses (LPAIV) (Lang et al., 2016), HPAIV had rarely been detected before the 2021-79 2022 outbreak, except in Southern Africa where recurrent HPAIV outbreaks have affected 80 81 seabirds since 2016 (Molini et al., 2020). Now, for the first time, HPAIV is significantly affecting European seabird populations, with the virus spreading to 12 species in the UK (Falchieri et 82 al., 2022). Tens of thousands of seabirds are thought to have been affected in the Northeast 83 84 Atlantic in 2022, with northern gannets (Morus bassanus; hereafter gannets) among the most severely impacted species (Lane et al., 2023), together with great skuas (*Stercorarius skua*)
(Banyard et al., 2022) and sandwich terns (*Thalasseus sandvicensis*) (Rijks et al., 2022).
Gannets are an iconic species that attract conservation and media interest, in their own right,
but also as umbrella species for the marine environment. Despite living in some of the most
anthropogenically modified marine regions of the planet (e.g. the North Sea), gannet
populations consistently increased across their distribution zone in the northeast Atlantic
during the second half of the 20th century (Grandgeorge et al., 2008).

92 The present HPAIV panzootic highlights the urgent need for a better understanding of the 93 impact of such disease outbreaks on the movement ecology of affected species, both during and following HPAIV outbreaks, and the associated consequences for disease transmission. 94 Seabirds such as gannets are organised as metapopulations where colonies are connected 95 96 through dispersal movements of pre-breeding birds (Jeglinski et al., 2022). In contrast, 97 breeding seabirds generally show very high fidelity to their colony and to their breeding site (Hamer et al., 2001). As central place foragers, they travel large distances away from their 98 99 breeding colony to their foraging sites at sea, but many species show a marked degree of 100 repeatability in their individual movement and space use patterns (Guiry et al., 2022). 101 Gannets in particular have also been shown to forage in colony-specific non-overlapping areas 102 (Wakefield et al., 2013) suggesting a limited capacity for close contact (and thus potential transmission routes) between breeders from different colonies. 103

104 However, dense seabird colonies also function as information centres (Evans et al., 2016) 105 where birds acquire public information from their conspecifics, such as the location of 106 potential food resources at sea (Courbin et al., 2020), or the quality of local breeding habitats 107 (Danchin et al., 1998). During the 2022 HPAIV outbreak, when many chicks and adult gannets 108 died at breeding colonies, surviving adult gannets were exposed to public information 109 signalling that they were breeding in a highly hazardous habitat. As an effect of such 110 disturbance, we might expect to see drastic changes in movement and space use patterns. 111 Indeed, recent work has shown that surviving adults gannets that had lost their chick and 112 partner drastically modified their movement patterns in May/June 2022, during the initial phase and peak of the HPAIV outbreak on the Bass Rock (Jeglinski et al., 2023): Birds thereby 113 switched from exclusively commuting between their nest and foraging areas at sea, to visiting 114 115 other breeding colonies. Such changes in movement patterns increase the potential for

disease transmission, by increasing the likelihood of contact, be it on land or at sea, between
birds from different colonies (Boulinier, 2023; Boulinier et al., 2016).

118 However, it is unclear if the behavioural responses to the initial HPAI outbreak found by 119 Jeglinski and colleagues (2023) translate to longer term and more permanent modifications 120 in movement ecology and space use of surviving gannets. For example, seabird massmortalities are likely to reduce food competition for surviving individuals and may therefore 121 lead to modified foraging patterns and changes in at-sea distribution of gannets which are 122 123 relevant for the conservation management of the species. Short-term effects on movement, 124 such as the increase in adult prospecting frequency described above, could become a more permanent feature. This would lead to increased connectivity between usually segregated 125 126 breeding colonies and thus have the potential to maintain enhanced disease transmission, 127 within gannet metapopulations and at the scale of multispecies seabird communities 128 (Boulinier et al., 2016). Finally, survivors could abandon their breeding colony permanently, 129 as shown in Cape cormorants or Double-crested cormorants (Phalacrocorax auritus) which desert breeding colonies when exposed to avian cholera or Newcastle disease virus (Crawford 130 131 et al., 1992; Leighton et al., 2021). It is uncertain whether gannets display such longer-term behavioural shifts, because they are known for their high fidelity to nesting (Nelson, 1966), 132 and foraging sites (Votier et al., 2017; Wakefield et al., 2015). Also, studies on closely-related 133 134 Cape gannets (Morus capensis) showed that, even when confronted with strongly degraded 135 environmental conditions, adult breeders kept the same breeding and foraging locations (Grémillet et al., 2016; Pichegru et al., 2010). 136

137 Previous investigations showed that, in Indian yellow-nosed albatrosses (Thalassarche carteri) exposed to avian cholera, failed breeders showed higher flexibility in habitat use 138 (Ponchon et al., 2021). Yet, to the best of our knowledge, no study has investigated seabird 139 140 movements following an HPAIV outbreak, and very few have done so in other birds (Gaidet 141 et al., 2010), generally because of the unpredictability of outbreaks and restrictions regarding 142 colony access in an HPAIV context. We used the rare opportunity to fill this critical knowledge 143 gap by collecting data in three of the largest gannet breeding colonies in the Northeast Atlantic which all experienced very high levels of HPAIV-related chick and adult mortality in 144 2022; the Bass Rock in Scotland (UK), Grassholm in Wales (UK), and Rouzic in Brittany (France). 145 146 Bass Rock was, before the HPAIV outbreak, the largest northern gannet colony in the world,

with an estimated 75,259 breeding pairs (Murray et al., 2014). Taken together, the three
studied colonies totalled ca. 26% of the northern gannet world population (134,259 out of
525,694 pairs (Murray et al., 2015)).

Our primary objective was to better understand the effect of the HPAIV outbreak on breeding gannet space use, since potential persistent behavioural shifts may maintain a high degree of transmission potential in the metapopulation (Boulinier, 2023). Specifically, we tested the hypothesis that gannets which survived the initial HPAIV outbreak modified their movement patterns relative to their behaviour prior to the outbreak. We predicted (1) that surviving birds would prospect for alternative breeding sites and (2) they also modified their foraging patterns in response to the reduction of food competitors.

Our second objective was to provide background epidemiological information, and data on gannet colony dynamics in our three study colonies during the outbreak. The HPAI outbreak disrupted ecological data collection in seabird colonies in 2022. Consequently, there are very limited ecological and epidemiological insights based on field data available, making it paramount to share contextual information with the scientific community.

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163 Methods

164 Gannets were primarily studied in May-October 2022 on Bass Rock, Scotland (56°04'N, 2°29'E), Grassholm, Wales (51°43'N, 05°28'W), and Rouzic, Brittany (48°54'N, 3°26'W). 165 Gannet spatial ecology was also compared between 2022 and 2019 (i.e. before the HPAIV 166 167 outbreak). Gannets breed between February and October, with peak hatching during the first half of June. Time of hatching is influenced by latitude, with median hatching occurring on 168 average two weeks later on Bass Rock than on Grassholm and Rouzic (Wanless et al., 2008). 169 The chick-rearing phase lasts 11 to 12 weeks, with chicks fledging from late August to early 170 October. All personnel involved in field operations were equipped with full-body suits and 171 172 disposable gloves, face masks, goggles and caps. Biocides (Virkon[®] or SafeFour[®]) were used 173 between each manipulated bird to clean clothing, shoes and equipment.

174

175 Characterization of the HPAIV outbreak:

176 - Bass Rock:

On 4th June 2022, unusual numbers of dead and dying gannets were observed on Bass Rock
(Scottish Seabird Centre, pers. comm., see also Suppl. 1). Due to permit issues, gannets
equipped with GPS-GSM tags (see below) were not screened for HPAIV.

180 - Grassholm:

Following an unusually high number of dead gannets at the colony, HPAIV was confirmed from Grassholm on 3rd August with no further access to site permitted for the rest of the breeding season.

184 - Rouzic:

Mortality affecting adult gannets was first recorded on 1st July 2022 on the live camera 185 monitoring the Rouzic colony. Samples were subsequently collected from 31 live or dead 186 gannets in, and around the Rouzic colony between July and September 2022, for HPAIV 187 screening and characterization. We performed opportunistic necropsies on four adult birds 188 found dead on the colony, from which we collected tracheal and cloacal swabs and/or lung 189 190 and trachea samples. We also collected cloacal swabs, tracheal swabs and/or external wipes 191 impregnated with sterile distilled water (applied to the feathers and featherless areas of the birds) from live individuals showing no HPAIV symptoms, including 15 adult birds equipped 192 with GPS-GSM loggers (see below), and 12 recently fledged juvenile birds captured at sea or 193 194 in the colony. We also collected plasma samples from seven of these juvenile birds. All samples were stored at -20°C until laboratory analyses. 195

Samples were analysed using the protocols recommended by the French Ministry of 196 Agriculture and based on the recommendations provided by the OIE/FAO international 197 reference laboratory for avian influenza. Tissue and swab samples were screened for HPAIV 198 genetic material by real-time reverse transcription polymerase chain reaction (rRT-PCR) 199 targeting the M gene. To identify the subtype of the circulating virus, positive samples were 200 then typed using an rRT-PCR targeting either the H5 or H7 type of the haemagglutinin gene. 201 202 One sample testing positive for H5 was analysed for further characterization of the virus with an RT-PCR discriminating HP H5 of the 2.3.4.4b clade, and an RT-PCR targeting the N1 type of 203 204 the neuraminidase gene. Samples testing negative for host genetic material were classified as potential false negative (Zhang et al., 2020), likely due to the degradation of the samples, and 205

were excluded from the study. Plasma samples were screened for antibodies specifically
targeting H5N1, H5N3, H5N5 or H5N8 by haemagglutination inhibition (HI). Collected samples
and associated laboratory results are summarized in Table S2 (Suppl. 2).

209

210 GPS tracking:

211 Gannets were tracked (1) \sim 2 months following the first signs of an HPAIV outbreak in each respective colony in 2022. This period, spanning mid-August to early October 2022, 212 213 corresponded to the late chick-rearing phase. This information was compared with (2) GPS tracking data collected in 2019, a normal year prior to the occurrence of HPAIV in gannets. 214 For logistical reasons, this second data set was collected during June-July 2019, a period 215 corresponding to early chick-rearing. Since gannet foraging effort may differ between early 216 217 and late chick-rearing this comparison requires some caution. Notably, because chick energy 218 requirements double between early and late chick-rearing (Montevecchi et al., 1984), and 219 because food resources may become depleted around seabird colonies at the end of the breeding season (Weber et al., 2021), adult gannet foraging effort should increase between 220 221 early and late chick-rearing.

(1) To study gannet movement ecology following the initial HPAIV outbreak, we deployed 222 GPS-GSM tags on breeding adults which showed no HPAIV symptoms on the Bass Rock (10 223 birds between 11th - 13th August 2022) and on Rouzic (15 birds between 23rd - 26th August 224 2022). GPS-GSM tags were pre-programmed to send data to a server using the 2G mobile-225 226 phone network so that data can be transmitted from anywhere within 2G coverage and 227 accessed by the user in near-real-time. At Grassholm, 11 birds had been fitted with remotelydownloadable tags that send data via a UHF link to a base station deployed at the breeding 228 colony, in May 2022, prior to the HPAIV outbreak. Some of these tags were still functional 229 230 across August-September 2022.

For all GPS deployments, adults rearing chicks (2 to 8 weeks old) were caught at the nest and handled so as to minimize stress: the procedure lasted < 10 min and birds were kept in the shade. Tags were attached with Tesa[®] tape to the three central tail feathers. For Bass Rock gannets, we used nanofix tags (Pathtrack Ltd., solar powered, mass 18 g, 0.7% of bird body mass, dimensions 56x28x15mm plus ~40 mm external whip antenna). For Grassholm gannets, 236 we used axy-trek remote tags (Technosmart solar powered, mass 15 g, < 0.5% of bird body mass, dimensions 52x25x15 mm). For Rouzic gannets, we used OrniTrack-9 tags (Ornitela, 237 solar powered, mass 9 g, 0.3% of bird body mass, dimensions 37×19×12 mm, plus ~10 cm 238 239 external whip antenna). All tags recorded a GPS position every 15 to 60 min, depending on 240 battery voltage. We planned for tags to fall off once birds were starting to moult their tail 241 feathers - previous deployments lasted up to 3 - 5 months (J. Jeglinski, D. Grémillet, unpublished data). At all three colonies we weighed gannets to the nearest 10 g. All birds 242 were ringed with a metal ring and plastic ring with a unique alphanumeric combination. Once 243 244 released, most birds returned immediately to their nests. We monitored chicks until the 245 captured parent had returned, generally immediately, at the latest within 1 h after capture.

246 (2) We studied the movements of breeding adult gannet before the HPAIV outbreak, during 247 early chick-rearing in June-July 2019. We used the same methodology as above, yet slightly different GPS recorders. On Bass Rock, 22 gannets were fitted with i-gotU GT600 tags (Mobile 248 Action Technology, mass 30g, 1% of body mass, dimensions 47 × 30 × 20 mm, set to record 249 GPS position every 1 min). On Grassholm 7 gannets were fitted with i-gotU GT120 tags 250 251 (Mobile Action Technology, mass 18g, 0.7% of body mass, dimensions $47 \times 30 \times 20$ mm, set to record GPS position every 1 min). On Rouzic, 14 gannets were fitted with CatTraQ[™] tags 252 (Catnip Technologies, mass 20g, 0.8% of bird body mass, dimensions 47 × 30 × 13 mm, set to 253 254 record GPS position every 1 min).

255 GPS Data processing:

Data were analyzed using R version 4.1.2. Data from Rouzic, which are stored in the Movebank
database, were imported with the *move* R package (Kranstauber et al., 2022) while data from
Bass Rock and Grassholm were imported from csv files.

For all tracking data recorded in 2022 and 2019 (Tab. 1), at-sea trips were discriminated from periods in the colony when the birds were > 1 km away from the colony for > 1 h. GPS recordings which were interrupted for > 10 hours were excluded. At-sea locations were linearly interpolated with a 15 min time resolution using the *pastecs* package (Grosjean et al., 2018). Trip data were checked for prospecting visits to other gannet colonies, which we defined as two or more consecutive locations in any other gannet known colony. We calculated trip characteristics for the 2019 and 2022 data sets (maximal distance to the colony, total trip duration and total distance travelled), as well as the time spent in the colony between at-sea trips, and presented these averaged for each individual and then averaged by colony in Table 1. Further, we fitted linear mixed models on each colony separately to test whether log-transformed trips characteristics and colony attendance changed significantly between 2022 and 2019.

To test our hypotheses, we were specifically interested in temporal dynamics of foraging patterns following the HPAIV outbreak. Hence, for the 2022 data set, we fitted linear mixed models separately for each colony using the respective trip characteristics for each bird as response variables to test whether log-transformed trip characteristics and time spent in the colony between at-sea trips changed significantly over time (converted as day since 10th August 2022, first day of the study period). Bird ID was included as a random effect.

277 Inferring at-sea behavioural states:

278 To test for temporal dynamics in behavioural patterns across the 2022 data set, we also fitted 279 a 3-state hidden Markov model (HMM) to the at-sea interpolated location data from all three colonies combined, using the moveHMM package (Michelot et al., 2016). The states can be 280 interpreted to reflect three different activities at sea: (1) resting, characterised by a small step 281 282 length and low turning angle, (2) travelling, characterised by a long step length and low turning angle and (3) foraging, characterised by an intermediate step length and a large 283 284 turning angle. A set of different initial parameter values was used to ensure that the global 285 maximum log-likelihood had been reached. The Viterbi algorithm was used to classify the most likely behaviour at each location and proportions of each activity occurring during one 286 at-sea trip were calculated, averaged by individual and then, by colony. We then fitted logistic 287 regressions to the proportions of each activity during a trip for each bird as response variables 288 using the *glmmTMB* package (Brooks et al., 2017), accounting for zero-inflated data, to test 289 whether activity proportions changed over time (converted as day since 10th August 2022, 290 291 first day of the study period). Bird ID was included as a random effect.

292

293 Results:

294 Gannet colony dynamics:

295 The impact of HPAIV on the Bass Rock was extremely high, with thousands of dead gannets recorded in the colony and washed up on the surrounding beaches. A drone survey on 30th 296 297 June 2022 counted 21,277 gannets (Lane et al., 2023), whereas a previous census counted 298 75,259 apparently occupied sites (AOS) in 2014 (Murray et al., 2015). Although the two counts 299 use different count units, they indicate a substantial decline in numbers of around 70% during 300 the 2022 HPAIV outbreak (Lane et al., 2023). Direct observations on Bass Rock also indicated 301 that at least 75% of active nests disappeared during the 2022 breeding season (Lane et al., 2023). On Grassholm, adult and chick mortality were extremely high with many thousands of 302 303 birds dead on the colony and in the surrounding waters. On Rouzic, aerial pictures of the 304 colony revealed that AOS numbers declined from 18,839 on 17/05/2022, to 8,625 on 305 28/08/2022 (54% decline during the breeding season). Observations via the live camera installed on the breeding colony estimated that >90% of chicks died during the same period 306 307 (Suppl. 1). More detailed, weekly counts performed between 11/07/2022 and 30/09/2022 on five sections of the colony containing 40-102 AOS, suggested that between 58-87% of 308 breeding adults, and between 67-94% of the chicks died (see Suppl. 4). 309

310

311 Characterization of the HPAIV outbreak

312 - Bass Rock:

Samples collected on the 4th June 2022 from dead gannets and analysed by the Animal and
Plant Health Agency (APHA), UK, confirmed an outbreak of HPAIV H5N1 (Scottish Seabird
Centre, pers. comm.).

316 - Grassholm:

Following unusual gannet mortality in late July, four birds found dead on 21st July 2022 were confirmed as positive for HPAIV H5N1 by APHA.

319 - Rouzic:

The first necropsy samples collected from a dead adult found on the colony on 11th July 2022 tested positive for HPAIV. Laboratory analyses conducted on samples collected from a bird

found dead on the colony on 30th September 2022 confirmed the circulation of HPAIV H5N1 322 clade 2.3.4.4b in the colony. HPAIV H5 was also detected in live birds: 1/9 cloacal swabs from 323 adults subsequently equipped with GPS, and 2/7 external wipes from juveniles (recently 324 325 fledged and captured on land/at sea) tested positive for HPAIV H5. All the cloacal and tracheal swabs collected from these juveniles, as well as from 5 other juveniles were classified as 326 327 negative or inconclusive, suggesting varying detection probabilities across sample types (see Suppl. 2). Antibodies against H5N1 were detected in 4/7 juveniles (including the 2 with RT-328 PCR-positive external swipes). These individuals also tested positive for antibodies against 329 330 H5N5 and H5N8, and to a lesser degree, for antibodies against H5N3, although higher titers 331 were systematically observed for H5N1 (Suppl. 2), suggesting cross-reactions with other 332 serotypes. None of the samples tested positive for HPAIV H7.

333

334 Movement ecology:

All 10 GPS tags deployed on Bass Rock gannets in 2022 sent GPS positions. On Grassholm, 5 335 out of the 11 tags which had been deployed in May 2022 provided data during the study 336 period (see Table 1 for details). Of the 15 tags deployed on Rouzic, 14 provided data; 13 of 337 the 15 remained in the English Channel. One gannet, sampled at tag deployment, tested 338 339 positive to HPAIV and never provided GPS positions, and another (tested negative at tag deployment) initiated migration after being equipped, moving toward West Africa without 340 touching land until the tag stopped sending data on 16th November 2022 (Table 1). Average 341 gannet body mass was 3230±298g (Bass Rock), 3004±325g (Grassholm), and 2920±240g 342 (Rouzic), values which were similar to those in previous years (Le Bot et al., 2019). 343

While alive, none of the gannets tagged in 2022 came ashore anywhere outside of their 344 respective breeding colonies during the GPS data transmission period. Overall, gannets from 345 Bass Rock, Grassholm and Rouzic did not change their space use across the 4-8 week 2022 346 study period, and foraged consistently in the same areas (Fig. 1 & 2). Birds from Rouzic did 347 not change their at-sea trip characteristics during the 2022 study period (similar duration, 348 349 maximal distance to the colony and total distance travelled; Table 2; Fig. S3a-c), but they 350 slightly decreased the time spent at the colony between at-sea trips (Table 2; Fig. S3d). Among them, one individual was found dead on a beach on the island of Guernsey (82 km Northeast 351

of Rouzic), 14 days after being equipped. This individual was not tested for HPAIV when found 352 dead, and its behaviour for the time period during which we received GPS data did not differ 353 354 from that of other Rouzic birds we tracked. During the 2022 study period, birds nesting on 355 Bass Rock spent the same amount of time attending their colony but increased the duration of their at-sea trips marginally, travelling slightly further and being absent from the colony for 356 slightly longer (Table 2; Fig. S3). During the same period, birds from Grassholm did not change 357 any trip characteristics nor their nest attendance patterns. Considering their activity budgets 358 during trips, birds maintained the same proportions of time spent foraging, flying and resting 359 360 on the water, regardless of their colony (Table 2; Fig. 3). For the 3 colonies, compared to early 361 chick-rearing in 2019, at-sea trips in 2022 were 47-58% shorter in maximal distance and total 362 distance travelled and 10-53% shorter in duration (Table 1; S3). Overall, foraging effort as 363 conveyed through foraging trip indicators was significantly lower in 2022 compared to 2019, 364 except for foraging trip duration in Rouzic gannets (Fig. 4; Table S3).

Table 1. Details of the GPS tracking data set for gannets nesting on Rouzic, Grassholm and

367 Bass Rock in 2022 and 2019. Results are shown as mean ± SE

	Bass Rock	Grassholm	Rouzic	Bass Rock	Grassholm	Rouzic			
		202	22	2019					
Total nb	10	12	15	22	7	14			
of									
equipped									
individuals									
Nb of	10	5	13	22	7	14			
individuals									
retained									
Total nb	310	53	257	66	11	27			
of									
foraging									
trips									
Average	31 ± 4	10 ± 5	20 ± 3	3.0 ± 0.3	1.5 ± 0.3	1.9 ± 0.3			
nb of									
foraging									
trips per									
individual									
Total Nb	49	31	36	6	0	7			
of periods									
on the									
colony									
Average	30 ± 4	12 ± 5	18 ± 2	1.8 ± 0.3	-	2.9 ± 0.3			
nb of									
periods on									
the colony									

per						
individual						
Tracking	11/08/2022	10/08/2022	24/08/2022 –	23/06/2019	15/07/2019	21/06/2019 -
period	-	_	28/09/2022	- 30/07/019	_	28/06/2019
	12/10/2022	18/09/2022			17/07/2019	
Average	44.2 ± 5.1	13.8 ± 5.8	22.0 ± 2.4	4.8 ± 0.5	1.6 ± 0.4	4.2 ± 0.5
tracking						
duration						
per						
individual						
(days)						
Maximal	98 ± 8	65 ± 8	62 ± 4	186 ± 25	147 ± 18	127 ± 12
distance						
to the						
colony						
(km)						
Total	254 ± 21	191 ± 28	171 ± 11	450 ± 60	450 ± 78	328 ± 35
distance						
travelled						
per trip						
(km)						
Trip	19 ± 2	16 ± 4	18 ± 1	27 ± 3	34 ± 8	20 ± 2
duration						
(h)						
Time	21.7 ± 10	23.4 ± 3.2	42.4 ± 1.5	-	-	-
spent						
resting						
during a						
trip (%)						
Time	54.4 ± 1.2	55.7 ± 2.9	36.9 ± 1.2	-	-	-
spent						

foraging						
during a						
trip (%)						
Time	23.9 ± 0.8	20.9 ± 2.2	20.7 ± 0.9	-	-	-
spent						
flying						
during a						
trip (%)						
Time at	16 ± 1	18 ± 2	11 ± 1	26 ± 2	-	22 ± 2
the colony						
between						
at-sea						
trips (h)						

- **Table 2**. Results from the models testing the effects of time for the 2022 data set, on gannet trip characteristics and nest attendance (linear
- 371 mixed models) and proportion of time spent in the 3 inferred behavioural states (logistic regressions). Individual identity is included as a
- 372 random effect. Significant results (p < 0.05) are in bold.

Linear mixed models		Bass Rock Grassholm Rouzic					zic					
	Estimate	df	t-value	p-	Estimate ±	df	t-value	p-	Estimate ±	df	t-value	p-value
	± SE			value	SE			value	SE			
Maximal distance	0.009 ±	299	2.03	0.043	-0.012 ±	44	-0.85	0.40	-0.003 ±	243	-0.53	0.60
	0.005				0.014				0.006			
Total distance	0.011 ±	299	2.34	0.02	-0.017 ±	44	-1.07	0.29	1.8e10 ⁻⁵ ±	243	0.003	0.99
travelled	0.005				0.016				6.0e10 ⁻³			
Trip duration	0.013 ±	299	3.29	0.001	-0.014 ±	44	-0.74	0.46	0.011 ±	243	1.73	0.09
	0.004				0.019				0.006			
Time at the colony	-0.003 ±	288	-0.77	0.45	-0.011 ±	56	-1.13	0.26	-0.015 ±	220	-2.09	0.038
between at-sea trips	0.003				0.0010				0.007			
Logistic regressions	Bass Rock		Grassholm			Rouzic						
	Estimate	df	z-value	p-	Estimate ±	df	z-value	p-	Estimate ±	df	z-value	p-value
	± SE			value	SE			value	SE			
Proportion of a trip	0.0053 ±	307	0.63	0.53	-0.05 ± 0.05	47	-1.18	0.24	0.018 ±	253	1.24	0.21
spent resting	0.0086								0.014			384
Proportion of a trip	-0.0017 ±	307	-0.24	0.81	0.037 ±	47	1.05	0.29	-0.014 ±	254	-0.91	0.36
spent foraging	0.007				0.034				0.015			
Proportion of a trip	-0.0028 ±	307	-0.33	0.74	-0.0021 ±	47	-0.05	0.96	-0.008 ±	254	-0.43	0.67 387
spent flying	0.008				0.040				0.018			
L												388



391 Figure 1. Tracks of gannets nesting in 2022 (left) and 2019 (right) on (a) Bass Rock, Scotland,

392 (b) Grassholm, Wales and (c) Rouzic, Brittany, (yellow diamonds). Orange circles represent

- neighbouring gannet colonies to the respective study colonies. Gradual changes in colour
- 394 represent time in days since start of GPS tracking.



Figure 2. Rose diagrams illustrating the bearings in 30 degree bins of at-sea locations relative

to the nesting colony of gannets nesting in 2022 (left) and 2019 (right) on (a) Bass Rock,

398 Scotland, (b) Grassholm, Wales and (c) Rouzic, Brittany. The centre of each rose diagram

399 represents the colony location, the length of each wedge represents the number of locations

400 recorded in that direction over time, in coloured weekly bins.



401

Figure 3. Proportion of inferred behavioural states [(a) resting, (b) foraging, (c) flying] during
at-sea trips of gannets nesting on Bass Rock (orange), Grassholm (yellow) and Rouzic (cyan),
according to dates from August to October 2022. The dots represent raw data and the line
and shadow, predicted average slope ± 95% confidence interval.





408 Figure 4. Predicted means ± 95% confidence interval of trip characteristics and nest

- 409 attendance of gannets nesting on Bass Rock, Grassholm and Rouzic in 2022 (black) and 2019
- 410 (orange). Note that nest attendance values were unavailable for Grassholm in 2019.
- 411

413 Discussion

414 - Epidemiology

415 Our analyses confirmed that gannets contracted HPAIV, and other investigations also pointed to HPAIV as the cause of 2022 seabird mass mortalities in western Europe (Falchieri et al., 416 417 2022; Lane et al., 2023). More specifically, we identified H5N1 (clade 2.3.4.4b) in Rouzic birds. This contrasts with recent HPAIV outbreaks in southern African seabirds (Molini et al., 2020), 418 which were caused by H5N8 (clade 2.3.4.4b). Our study adds to the evidence that HPAIV has 419 become established in seabirds, and will probably recurrently re-emerge, as observed in 420 421 southern Africa (Molini et al., 2020). We also found that some juvenile gannets had H5N1 422 antibodies, but no live virus (Suppl. 2). This is in line with recent investigations (Caliendo et al., 2022) suggesting that birds that survived HPAIV develop an immune response, which could 423 protect against future infections. Further longitudinal monitoring will nonetheless be 424 necessary to fully test this hypothesis. Those studies will also clarify the factors leading to intra 425 and interspecific heterogeneity in avian responses to HPAIV (Keawcharoen et al., 2008), which 426 427 are key to our understanding of the potential role of different species as HPAIV maintenance 428 host or spreaders (Huang et al., 2019).

429 Only one of the 15 birds equipped with GPS on Rouzic tested HPAIV positive using swab 430 samples (Suppl. 2), and gannets fitted with GPS on Bass Rock and Grassholm could not be 431 tested. Thus, the epidemiological status of most tracked gannets was not known. Ideally, swab 432 and plasma samples should have been collected in all birds. Yet, even in the presence of both sample types, some uncertainty would remain. Notably, a positive plasma sample could reflect 433 a former, rather than an ongoing infection, and such samples are not adequate to infer 434 whether a bird is a HPAIV carrier and potential spreader at the time of the blood sample 435 (Gilbert et al., 2013). Indeed, experimentally infected birds stop excreting the virus after a 436 437 week or less (van den Brand et al., 2018). Swab samples are therefore theoretically adequate 438 during this brief excretion period, but half of those for gannets equipped with GPS on Rouzic were inconclusive. External wipes were useful indicators of virus circulation in the colony, but 439 cannot be used with confidence for individual infection status considering the risk of 440 environmental contamination. Overall, we may therefore conclude that HPAIV was extremely 441 widespread and circulating at all three gannet colonies given observational data on the degree 442 of mortality, and that an unknown proportion of GPS-tracked birds could have been 443

444 symptomatic or asymptomatic carrier of the virus. This knowledge gap clearly calls for further445 epidemiological studies during future seabird breeding seasons.

446 - Movement ecology

Contrary to our first prediction, we did not detect any change in breeding colony fidelity in the 447 context of HPAIV outbreaks that started approximately two months previous to data 448 collection. In contrast to the study performed by Jeglinski and colleagues (2023) during the 449 450 initial HPAIV outbreak, none of the gannets we tracked came ashore outside of their respective breeding colonies while alive. We also found that GPS-tracked gannets did not 451 452 significantly modify their foraging patterns across the study period (Table 2; Fig. 1-4). Since 453 our visits to gannet breeding colonies were extremely limited due to the restrictions in place, 454 we could not monitor the survival of the chicks of the GPS-tracked gannets. Some birds may have lost their chicks during the study period. Yet, all tracked birds continued to regularly 455 456 commute between at-sea feeding sites and their respective colonies, and none of them rested on the mainland or on other islands in-between trips. 457

Further, gannet foraging effort seemed lower than during the 2019 breeding season (hence before HPAIV) at our three study sites (Grémillet et al., 2006; Hamer et al., 2007; Patrick et al., 2014) (Fig. 1, 2 and 4, Table S3). Therefore, in accordance with our second prediction, gannets surviving HPAIV may have benefited from reduced food competition following the death of adults and chicks. Nevertheless, these results have to be taken with caution since, as mentioned in the methods section, the 2022 GPS tracking sessions occurred during late chickrearing, whereas the 2019 tracking data were collected during early chick-rearing.

Our results are coherent with high breeding and foraging site fidelity in colonial seabirds 465 (Danckwerts et al., 2021), and contrary to the idea that gannets that have witnessed and 466 survived mass mortality at their breeding colony modify their movement patterns as a 467 468 consequence of the disease outbreak and maintain these changes several months after the event. Thus, it appears that longer-term enhanced HPAIV transmission throughout the 469 470 metapopulation and potentially throughout the co-existing seabird populations is unlikely for 471 adult breeding gannets. This is an essential piece of information that contributes to a better 472 understanding of HPAIV transmission dynamics, since wild birds carrying HPAIV are

473 recurrently presented as virus spreaders to farm poultry (Global Consortium for H5N8 and474 Related Influenza Viruses, 2016).

475 However, the data we presented here are collected following the initial disease outbreak to 476 study long-term behavioural responses, and they are only representative of the adult breeding 477 age class. Other age classes may differ in their propensity to act as a vector for HPAIV. Notably, 478 immature gannets have been shown to perform visits to other breeding colonies throughout 479 the breeding season (Votier et al., 2011) and thus likely regularly move between colonies. 480 These prospecting movements would appear to require limited time/energy investment: For 481 gannets from Bass Rock, the closest alternative colony is Troup Head on the Scottish mainland 482 (ca. 210 km), for Grassholm it is Great Saltee in Ireland (ca. 90 km), and for Rouzic it is Ortac in the British Channel Islands (ca. 130 km) (Fig.1). Reaching these neighbouring colonies would 483 take 3.2 hrs (Bass Rock), 1.4 hrs (Grassholm), or 2 hrs (Rouzic), assuming a 65 km.h⁻¹ travelling 484 485 speed (Grémillet et al., 2004). Forthcoming studies will clarify the respective potential of juvenile and immature gannets to act as vectors in HPAIV transmission. Also, even if rated as 486 rare (Boulinier et al., 2016), at-sea HPAIV transmission may occur within, and between seabird 487 488 species. This might be facilitated by aggregations at natural foraging sites or whilst feeding on 489 fishery wastes behind trawlers, or through kleptoparasitism and scavenging (Wille et al., 2016). Studying interspecific fine scale space-use overlap at sea is therefore a high priority for 490 491 future monitoring and evaluation of disease transmission scenarios (Boulinier, 2023).

492

493 - Outlook

It remains unclear how gannets contracted HPAIV, since they were either at sea, or at their 494 breeding colony during the outbreak. Larids (Larus sp.) or great skuas that klepto-parasitise 495 gannets might be potential vectors since they use similar terrestrial and marine habitats 496 497 (Falchieri et al., 2022), but further analyses will be necessary to test these hypotheses. HPAIV first affected gannets in Iceland, Québec and Scotland (from early April 2022), and 498 499 subsequently arrived in Brittany (from early July 2022)(Lane et al., 2023). Hence, it is possible 500 that immature gannets moving between these colonies may have spread the virus, but this 501 pathway is still hypothetical. Equally unknown are HPAIV dynamics during gannet migration, 502 which started in September-October 2022. These inter-breeding movements took gannets from the British Isles and Brittany to the Mediterranean or West Africa (Fort et al., 2012). Off Africa, gannets met with some of their North American conspecifics, as well as with a vast community of North Atlantic seabirds spending the winter in tropical waters (Grecian et al., 2016). In February 2023, surviving gannets returned from migration and started breeding again. Further investigations are now required, notably to clarify HPAIV impacts on gannet movement ecology and population dynamics across age classes, and multiple years.

509 Our study is a key example of the common fate of wildlife and humanity facing global changes (Díaz et al., 2019). Gannets are affected by the direct and indirect consequences of climate 510 511 change (heat waves and storms, changes in the distribution and abundance of marine 512 resources), by pollution (e.g. mercury in fish affecting seabird and human health), and by 513 uncontrolled fishing operations which threaten food security for seabird and human populations alike (Grémillet et al., 2020). In addition, the current HPAIV outbreak 514 515 demonstrates that the anthropogenic environmental crisis enhances the potential for emerging infectious disease, contaminating wild animals and humans (Carlson et al., 2022; 516 Kuiken and Cromie, 2022). Indeed, current industrial farming practices are responsible for the 517 518 emergence and the spread of HPAIV in poultry and subsequently in wild birds, potentially also 519 in humans (Yamaji et al., 2020).

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availability: 551 Data Data available the following archives: are on 552 https://www.movebank.org/cms/webapp?gwt_fragment=page=studies,path=study2296851236 553 https://datadryad.org/stash/share/MmNkFWcQV79wnYDMQ8VTav-jRmHBUomyRohKVoAsNvE and https://www.movebank.org/cms/webapp?gwt_fragment=page=studies,path=study2658117564. All 554 555 statistical analyses found on the GitHub repository can be (https://github.com/auponchon/NorthernGannets2022). 556

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