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2 Risk assessment of Avian Influenza and Newcastle disease viruses exposure from

3 peridomestic wild birds in a conservation breeding site in the United Arab Emirates

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6 Risk assessment of avian viruses exposure from wild peridomestics birds

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19

20 Summary

21 Worldwide, wild birds are frequently suspected to be involved in the occurrence of outbreaks

22 of different diseases in captive-bred birds although proofs are lacking and most of the

dedicated studies are insufficiently conclusive to confirm or characterize the roles of wild birds in such outbreaks. The aim of this study was to assess and compare, for the most prevalent peridomestic wild birds, the different exposure routes for Avian Influenza and Newcastle disease viruses in conservation breeding sites of Houbara bustards in the United Arab Emirates.

To do so, we considered all of the potential pathways by which captive bustards could be exposed to Avian Influenza and Newcastle disease viruses by wild birds, and ran a comparative study of the likelihood of exposure via each of the pathways considered. We merged data from an ecological study dedicated to local wild bird communities with an analysis of the contacts between wild birds and captive bustards and with a prevalence survey of AIV and NDV in wild bird populations. We also extracted data from an extensive review of the scientific literature and by the elicitation of expert opinion.

Overall, this analysis highlighted that captive bustards had a high risk of being exposed to pathogens by wild birds. This risk was higher for Newcastle disease virus than Avian influenza virus, and House sparrows represented the riskiest species for the transmission of both viruses through indirect exposure from consumption of water contaminated from the faeces of an infectious bird that got inside the aviary.

Thus, this analysis reveals that wild peridomestic birds may play a role in the transmission of avian pathogens to captive bred birds. These results also reaffirm the need to implement sanitary measures to limit contacts between wild and captive birds and highlight priority targets for a thoughtful and efficient sanitary management strategy.

47

Main text

Introduction

Within the field of One Health, there is deep interest in the role of wildlife – livestock interfaces in disease ecology (Hassell, Begon, Ward, & Fèvre, 2017; Okello, Gibbs, Vandersmissen, & Welburn, 2011). The interface between wild birds and domestic poultry is studied in particular (Wiethoelter, Beltrán-Alcrudo, Kock, & Mor, 2015) as wild birds frequently are suspected to be involved in the occurrence of outbreaks of different diseases in captive-bred birds. While many studies are insufficiently conclusive to confirm or characterize the roles of wild birds in such outbreaks (Caron, Cappelle, & Gaidet, 2017; Gaidet & Caron, 2016), limiting contact between wild and captive-bred birds is usually advocated in poultry breeding biosecurity guidelines.

The sanitary and economic consequences of epizootic events may explain these precautionary measures. Avian influenza (AIV) and Newcastle disease viruses (NDV), two of the most important avian pathogens worldwide (D J Alexander, 2008; Dennis J. Alexander, 2007; Capua & Alexander, 2004), have been responsible for mass mortalities and severe economic losses over recent decades (McElwain & Thumbi, 2017; Ramos, MacLachlan, & Melton, 2017; Thompson, Trejo-Pech, & Pendell, 2019). In most of the associated epizootic events, the question of the epidemiological role of wild birds has been raised (Bodewes & Kuiken, 2018; V. R. Brown & Bevins, 2017; Chatziprodromidou et al., 2018).

In particular, populations of waterfowl and shorebirds are known to be natural reservoirs of AIV and NDV (Gavier-Widén, Duff, & Meredith, 2012; Munster & Fouchier, 2009; Olsen et al., 2006), and their role in the global spread of these viruses has been proven (Lisovski et al., 2018; Marks et al., 2014; Mase & Kanehira, 2015; Mine et al., 2019; The Global Consortium

71 for H5N8 and Related Influenza Viruses, 2016). However, these populations are mainly

72 restricted to wetlands, their natural habitats, and thus are not usually in close contact with

73 captive-bred birds. Given the ubiquity of these two viruses and the extent of their host range,

74 the absence of classical maintenance populations in some environmental contexts suggests

75 that other bird species may play a role in the epidemiological framework (Caron et al., 2017).

76 In the Middle East, despite the arid environment, unfavourable weather conditions and

77 limited populations of wild waterfowl, AIV and NDV are regularly detected in poultry

78 (Aamir, Wernery, Ilyushina, & Webster, 2007; Al Shekaili, Clough, Ganapathy, & Baylis,

79 2015; Al-Azemi et al., 2008; Alkhalaf, 2010; A. A. Alsahami, Ideris, Omar, Ramanoon, &

80 Sadiq, 2018; A. Alsahami, Ideris, Omar, Ramanoon, & Sadiq, 2018; Haroun, Mohran,

81 Hassan, & Abdulla, 2015; Hirschinger et al., 2019; Kent et al., 2006; Khan et al., 2009;

82 Mohran, Haroun, & Hassan, 2011; Nagy, Mettenleiter, & Abdelwhab, 2017; Naldo &

83 Samour, 2004; Obon et al., 2009; Wernery et al., 2013). In the United Arab Emirates (UAE),

84 the poultry industry is an important sector, especially broiler and layer chickens (Seifarth &

85 Tarraf, 2018). Numerous wildlife conservation initiatives also are regularly implemented in

86 the country. A prime example involves the endangered Asian Houbara Bustard (*Chlamydotis*

87 *maqueenii*) ("Vulnerable" IUCN Red List of Threatened Species, 39), a semi-desertic avian

88 species inhabiting the Middle East and central Asia. In the UAE, this bird is captive-bred in

89 dedicated breeding stations to maintain a self-sustaining captive population and to produce

90 individuals for reinforcement programmes (around 20,000 birds are released into the wild

91 every year).

92 On these breeding stations, captive bustards are housed in outdoor aviaries to prepare them to

93 be released in the wild and maximize their chances of survival. Such facilities create an oasis

94 in the middle of the desert, and are a godsend for wild birds, offering vital resources (water,

95 food, shelter) that allow them to establish flourishing communities (Bock, Jones, & Bock,

96   2008). Due to the combined effect of these two factors (outdoor housing, oasis), captive

97   bustards are highly exposed to wild birds and whatever pathogens may accompany them.

98   Due to the conservation status of Houbara bustards, conventional poultry sanitary control

99   strategies, especially "stamping out", cannot be considered, and all efforts are focused on

100   preventing the introduction and spread of pathogens. This is achieved through the

101   implementation of risk-based biosecurity measures, which are based primarily on an

102   assessment of the probability of pathogens exposure from wild birds.

103   The aim of this study was to assess and compare, for the most prevalent peridomestic wild

104   birds, the different exposure routes of Houbara bustards for AIV and NDV in order to

105   recommend preventive measures. To do so, we considered all of the potential pathways by

106   which captive bustards could be exposed to AIV and NDV by wild birds, and ran a

107   comparative study of the likelihood of exposure via each of the pathways considered. We

108   merged data from an ecological study dedicated to local wild bird communities with an

109   analysis of the contacts between wild birds and captive bustards and with a prevalence survey

110   of AIV and NDV in wild bird populations (Hirschinger, 2020). We also extracted data from

111   an extensive review of the scientific literature and by the elicitation of expert opinion.

112   Finally, we identified the most significant wild bird species and pathways of exposure,

113   representing priority targets for a thoughtful and efficient sanitary management strategy.

114

115 ## Materials and Methods

116 This study, which is part of a research project dedicated to the evaluation of the sanitary risks

117 associated with the exposure of poultry farms to wild birds, was conducted at the National

118 Avian Research Center (NARC, N24.39600 E55.43630), a Houbara bustard conservation

119 breeding project in the UAE (Figure 1).

120

121 Figure 1.

122

123 ## Scenario tree and pathways of exposure

124 Following the methodological framework of the World Organisation of Animal Health (OIE)

125 for risk analysis (Office international des épizooties, 2005a, 2005b), we investigated the

126 likelihood of exposure of captive Houbara bustards to AIV and NDV from the four

127 peridomestic species identified as dominant in this ecosystem and involved in the majority of

128 contacts with captive bustards (Hirschinger, 2020): the House sparrow (*Passer domesticus,*

129 PASDOM), the White-eared bulbul (*Pycnonotus leucotis,* PYCTIS), the Laughing dove

130 (*Spilopelia senegalensis*, STRSEN) and the Collared dove (*Streptopelia decaocto,* STRDEC).

131 As previously described (Hernández-Jover, Schemann, East, & Toribio, 2015; Scott et al.,

132 2018), we used scenario trees to consider all of the potential exposure pathways by which

133 bustards housed in outdoor aviaries can be in contact with AIV and NDV by target species in

134 order to estimate exposure probabilities.

135 The exposure pathways considered in this study were divided into two groups due to the

136 nature of the contacts between wild birds and captive bustards. The first group considered all

137 pathways of exposure resulting from the presence of wild birds perched on an aviary,

138   including exposure through the falling of contaminated faeces or contaminated feathers

139   (Figure 2). The second group considered all pathways resulting from the presence of wild

140   birds inside an aviary, including exposure through contaminated faeces, contaminated

141   feathers, contaminated aerosols and contaminated carcasses (Figure 3).

142

143   Figure 2.

144   Figure 3.

145

146   Exposure probabilities

147   All of the probabilities and their definitions are summarised in Table 1.

148   The overall probability of exposure P_i that we aimed to estimate was the daily probability of

149   exposure to the virus (AIV or NDV) of at least one captive bustard by at least one wild bird

150   of species i (i = PASDOM, PYCTIS, STRSEN, STRDEC), accounting for all exposure

151   pathways. It was calculated as follows:

152    $P_i = 1 - (1 - p_i)^{n_i}$

153   with n_i being the number of wild birds of species i present in aviaries areas and p_i being the

154   daily probability of exposure to the virus of at least one captive bustard by one wild bird of

155   species i present in aviaries areas.

156   Assuming the exposure pathways are mutually exclusive, p_i was calculated as the sum of the

157   probability of each exposure pathway (*feces.perch*, *feathers.perch*, *feathers.in*, *carcass*,

158   *aerosols* and *feces.in*) for species i. More specifically, p_i was given by:

159    $p_i = p.infect_i * ¿$

160   with $p.infect_i$, $p.perch_i$ and $p.int_i$ being the daily probabilities of a bird of species i to be

161   infectious, to be perched on an aviary, and to get inside an aviary, respectively, and p_a and p_b

162   defined as the probability of exposure of at least one captive bustard by at least one wild bird

163   perched on an aviary, and as the probability of exposure of at least one captive bustard by at

164   least one wild bird inside an aviary, respectively, and given by:

165    $p_a = 1 - ¿$

166   and

167    $p_b = 1 - ¿$

168   with probabilities $p.fecal.perch$, $p.feather.perch$, $p.fecal.int$, $p.feather.int$, $p.respi$ and $p.organ$

169   defined in Table 1 and calculated as detailed in the Supplementary Materials.

170

171   Table 1

172

173   Model calibration

174   To calibrate the model, we used field observations, a literature review and an elicitation of

175   expert opinion. Table S1 summarises all of the parameters, their estimation method and the

176   estimated range of values for both AIV and NDV in the four target species.

177   Briefly, the average daily number of wild birds of species i present in aviaries areas (n_i) was

178   estimated by on-site experts using data from bird censuses in aviaries areas and population

179   size estimates.

180   Probabilities of excretion in the faeces, the feathers, the organs and the aerosols, which

181   contribute to the computation of the above-mentioned probabilities (Supplementary

Materials), were estimated from published experimental infections with AIV and NDV on House sparrows and related species (Ayala et al., 2019; Boon et al., 2007; Bosco‑Lauth, Marlenee, Hartwig, Bowen, & Root, 2019; J. D. Brown, Stallknecht, Berghaus, & Swayne, 2009; Forrest, Kim, & Webster, 2010; Fujimoto, Usui, Ito, Ono, & Ito, 2015; Gutiérrez, Sorn, Nicholls, & Buchy, 2011; Han et al., 2012; Hiono et al., 2016; Iqbal, Yaqub, Mukhtar, Shabbir, & McCauley, 2013; Jones et al., 2014; Q. Liu et al., 2010; Nemeth et al., 2013; Nemeth, Thomas, Orahood, Anderson, & Oesterle, 2010; Perkins & Swayne, 2003; Poetranto et al., 2016; Umar et al., 2016; Yamamoto, Nakamura, Yamada, & Mase, 2013) and on Feral rock pigeons (*Columba livia)* and related species (Abolnik, Stutchbury, & Hartman, 2018; Achenbach & Bowen, 2011; Aziz-ul-Rahman et al., 2019; Barbezange & Jestin, 2003; Boon et al., 2007; Bosco‑Lauth et al., 2019; J. D. Brown et al., 2009; Carrasco, Seki, Benevenute, Ikeda, & Pinto, 2016; Carrasco, Seki, de Freitas Raso, Paulillo, & Pinto, 2008; Carrasco, Seki, de Sousa, Raso, & Pinto, 2009; Dortmans, Koch, Rottier, & Peeters, 2011; Ellakany et al., 2019; Guo et al., 2014; Hayashi et al., 2011; Jia et al., 2008; Kang et al., 2016; Kapczynski, Wise, & King, 2006; Klopfleisch, Werner, Mundt, Harder, & Teifke, 2006; Kwon et al., 2017; Leigh Perkins & Swayne, 2002; Y. Liu et al., 2007; Mansour, ElBakrey, Ali, Knudsen, & Eid, 2014; Perkins & Swayne, 2003; Shriner et al., 2016; Śmietanka et al., 2011; Śmietanka, Olszewska, Domańska-Blicharz, Bocian, & Minta, 2014; Uchida, Kanehira, Takemae, Hikono, & Saito, 2017; Wakamatsu, King, Kapczynski, Seal, & Brown, 2006; Werner et al., 2007; Xiang et al., 2017, 2019; Yamamoto, Nakamura, Yamada, & Mase, 2012). Due to the lack of available data, data on viral excretion in White-eared bulbuls were extrapolated from House sparrows, and in Laughing and Collared doves from Feral rock pigeons.

205 Probabilities *p.waterfeces.perch*, *p.foodfeces.perch* and *p.fecesground.perch* were estimated

206 from the ratio between the surface area of the aviaries and the surface area occupied by water

207 and food dishes.

208 Finally, we elicited expert opinion to estimate the remaining 17 probabilities (Table S1). The

209 experts consulted (n=10) were selected based on their expertise in one or several of the

210 following fields: avian virology, epidemiology of animal diseases, avian medicine or poultry

211 biosecurity. They were asked by email to answer a multiple-choice questionnaire regarding

212 the probability of occurrence of 17 events leading to the release of viruses in the environment

213 of captive birds in this specific outdoor bustards-breeding context. The response choices for

214 each question consisted of probability intervals. The experts were asked to select all of the

215 intervals that were considered as credible for a given probability. The final interval that was

216 considered for a given parameter was the concatenation of the smallest number of intervals

217 that were selected by at least 50% of respondents.

218 Finally, all parameters of the model were associated with a Pert distribution with lower,

219 median and upper limits of the interval as parameters to account for uncertainty in their value

220 (see Supplementary Materials and Table S1).

221

Model run

223 The distribution of the probabilities P_i was simulated by sampling randomly the parameter

224 values in their corresponding probability distributions (Table S1) and combining them as

225 detailed above. To do so, we ran 100,000 simulations using R software (R Core Team, 2019).

226 Figures were generated using the R software and the libraries *ggplot2* (Wickham H., 2016),

227 *readxl* (Wickham H and Bryan J., 2019), *stringr* (Wickham H., 2019) and *gridExtra* (Auguie

228 B., 2017).

229 Pairwise t-tests were used to analyse differences between the outcome probabilities, and a p-

230 value < 0.05 was used to determine significance.

231

232 Sensitivity analysis

233 Two sensitivity analyses were run to evaluate the effect of individual variations of the

234 parameters calibrated using the expert opinion elicitation on the outputs of the model. The

235 first sensitivity analysis considered the overall daily probabilities Pi to evaluate the effect of

236 the uncertain parameters on the relative contribution of the wild bird species. The second

237 considered the probabilities of exposure via the different exposure pathways for the riskiest

238 wild bird species to evaluate the effect of the uncertain parameters on the relative

239 contribution of the exposure pathways for that species. To do so, we changed the value of the

240 uncertain parameters one at a time to their minimal and maximal expected values as

241 presented in Table S2. Meanwhile, the other uncertain parameters were set to their median

242 values and those of the other parameters were sampled in their respective distributions as

243 defined in Table S1. We used 10,000 iterations for each parameter combination.

244

245 ## Results

246 ## Probability of exposure

247 Model results highlighted that the risk of exposure to NDV was on average 2.39 times (95%

248 CI: 2.37 – 2.41) higher than that of AIV, irrespective of the species. Indeed, the average daily

249 probability of exposure to NDV for at least one captive bustard by at least one wild bird was

250 estimated between $2.3*10^{-3}$ and $132.3*10^{-3}$, while for AIV this probability ranged between

251 $0.6*10^{-3}$ and $60.3*10^{-3}$.

252 For both viruses, the wild bird species representing the highest mean risk of exposure was the

253 House sparrow (PASDOM). This species was associated with an average daily probability of

254 exposure of at least one captive bustard of $8.2*10^{-2}$ (95% CI: $2.4*10^{-2}$ – $16.7*10^{-2}$) and

255 $3.6*10^{-2}$ (95% CI: $0.9*10^{-2}$ – $7.8*10^{-2}$) for NDV and AIV, respectively (Figure 4). The risk of

256 exposure to NDV was on average 2.66 (95% CI: 2.65 – 2.67), 3.07 (95% CI: 3.05- 3.08) and

257 11.21 (95% CI: 11.15 – 11.27) times lower in White-eared bulbuls, Laughing doves and

258 Collared doves compared to House sparrows, respectively. For AIV, this risk of exposure was

259 on average 2.48 (95% CI: 2.47 – 2.50), 3.92 (95% CI: 3.90- 3.95) and 19.54 (95% CI: 19.4 –

260 19.6) times lower in White-eared bulbuls, Laughing doves and Collared doves compared to

261 House sparrows, respectively. Observed inter-species differences were statistically significant

262 (p-value<0.001).

263

264 Figure 4.

265

Pathways of exposure

267 House sparrows were identified as the riskiest species for exposing captive bustards to both

268 AIV and NDV. For this species, the pathway of exposure that contributed the most to this risk

269 was the exposure from the faeces excreted by an infectious bird that got inside the aviary.

270 This pathway was associated with an average daily probability of $1.9*10^{-2}$ (95% CI: $0.5*10^{-2}$

271 – $3.8*10^{-2}$) for both viruses (Figure 5). The risk of exposure was on average 1.72 (95% CI:

272 1.71- 1.72), 1.95 (95% CI: 1.95 – 1.96), 3.77 (95% CI: 3.76- 3.79), 3.90 (95% CI: 3.89- 3.92)

273 and 53.3 (95% CI: 53.0 – 53.6) times lower through the faeces of an infectious bird perched

274 on the aviary, the aerosols of an infectious bird inside the aviary, the feathers of an infectious

275 bird perched on the aviary, the feathers of an infectious bird inside the aviary and the carcass

276 of an infectious bird inside the aviary, respectively. Observed differences between pathways

277 were statistically significant (p-value<0.001).

278 Delving more deeply, the pathway that contributed the most to the risk of exposure of a least

279 one captive bustard to both AIV and NDV was the exposure via the consumption of water

280 contaminated by the faeces of an infectious bird that got inside the aviary. This pathway was

281 associated with an average daily probability of $9.8*10^{-2}$ (95% CI: $2.6*10^{-2}$–$20.0*10^{-2}$) for both

282 viruses (Figure 5). The risk of exposure was on average 1.05 (95% CI: 1.04 – 1.06) and 3.50

283 (95% CI: 3.49 – 3.52) times lower through the consumption of contaminated food and the

284 consumption of faeces on the ground, respectively. Observed differences between pathways

285 were statistically significant (p-value<0.001).

286 For all others species, the pathway of exposure that contributed the most to the risk of

287 exposure of a least one captive bustard to both AIV and NDV was the indirect exposure via

288 the consumption on the ground of faeces excreted by an infectious bird perched on the aviary.

289

290   Figure 5.

291

292   Sensitivity analysis

293   The sensitivity analysis showed that the ranking of species according to their level of

294   exposure risk was not modified when the values of the parameters estimated from experts'

295   opinions varied between the lowest value and the highest. House sparrows remained the

296   species contributing the most to the risk of exposure to both viruses (Figures S1 and S2).

297   Moreover, the analysis showed that the variation of parameters values had little or no effect

298   on the ranking of the pathways of exposure for the riskiest species. Thus, indirect exposure

299   from the faeces of an infectious House sparrow that got inside the aviary contributed the most

300   to the risk of exposure for both viruses in almost all cases (Figure S3).

301   Similarly, indirect exposure from consumption of contaminated water contributed the most to

302   the risk of exposure in almost all cases (Figure S4).

303

304 Discussion

305 Overall, this analysis highlighted that captive bustards had a high risk of being exposed to

306 pathogens by wild birds. This risk was higher for Newcastle disease virus (NDV) than avian

307 influenza virus (AIV), and House sparrows represented the riskiest species for the

308 transmission of both viruses through indirect exposure from consumption of water

309 contaminated from the faeces of an infectious bird that got inside the aviary.

310 Exposure probabilities presented in this study are comparatively higher than the ones

311 presented in similar studies (Hernández-Jover et al., 2015; Scott et al., 2018). This can likely

312 be explained by the system considered, i.e., one in which a strong oasis effect converged with

313 a need for outdoor housing to prepare bustards for release into the wild. Indeed, outdoor

314 breeding is usually considered as a major risk factor for pathogens exposure (Gonzales,

315 Stegeman, Koch, de Wit, & Elbers, 2013; Scott et al., 2018; Sims, Weaver, & Swayne, 2016).

316 As demonstrated in similar studies, indirect exposure from consumption of contaminated

317 water is the riskiest pathway (Scott et al., 2018; Sims et al., 2016). However, direct contact

318 with infectious wild birds appears to be less significant in the present study, most likely

319 because bustards are housed in netted aviaries which protect them from direct contacts.

320 For this analysis, we had to make several assumptions. First, the estimated exposure

321 probabilities were considered as representative of an "average" AI and ND virus. However,

322 some of the experimental infection studies compiled to extract the probabilities of shedding

323 of the viruses in the different biological matrices (*p.fecalexcretion, p.featherexcretion,*

324 *p.respiexcretion, p.organexcretion*) mentioned important variations in shedding according to

325 the strain considered (sub-type, pathogenicity) (Hayashi et al., 2011; Hiono et al., 2016; Isoda

326 et al., 2006; Jia et al., 2008; Shriner et al., 2016; Susta et al., 2018; Xiang et al., 2017).

327 Considering the diversity of AIV and NDV would sharpen the analysis. This holds

328   particularly true with regard to AIV, as shedding probabilities in feathers and organs are

329   likely to vary according to the pathogenicity of the strain considered. This is because only

330   highly pathogenic strains present a systemic replication whereas low pathogenic strains are

331   restricted to the digestive and respiratory tracts (Swayne, Suarez, & Sims, 2017).

332   In this analysis, we can consider that data from the field are more likely related to low

333   pathogenic viruses, at least for AIV (absence of clinical signs, low viroprevalence and low

334   viral loads) (Hirschinger et al., 2019). In contrast, most of data from the literature are related

335   logically to highly pathogenic viruses. Finally, data drawn from experts' opinions depend

336   greatly on the field of expertise of each expert, but a bias toward highly pathogenic viruses

337   may be assumed. Therefore, it would be interesting to conduct separate analyses of low and

338   highly pathogenic viruses. Ideally, the analysis would target strains circulating in the UAE.

339   Moreover, the viral load shed is often linked with the inoculated one (Abolnik et al., 2018; J.

340   D. Brown et al., 2009; Kapczynski et al., 2006), and viral loads are usually higher in

341   experimental infection studies than the loads birds may face in the wild. Therefore, we may

342   have overestimated shedding probabilities in our epidemiological context and artificially

343   increased the exposure risk. The extrapolation of shedding data from related species, although

344   justified in our case, also may represent an important limitation for this analysis as some

345   studies mentioned important shedding variations according to the infected species, even with

346   regard to closely related species (Ayala et al., 2019; Carrasco et al., 2008; Dortmans et al.,

347   2011; Nemeth et al., 2010).

348   The estimation of virus excretion in the environment based on expert elicitation may be

349   considered to be subjective. However, the sensitivity analysis showed that neither the rank of

350   the species nor the rank of the pathways of exposure were significantly modified when the

351   input values of these parameters were varied along their estimated intervals, suggesting these

352   estimates were realistic.

353   Overall, outcomes of the analysis seem trustworthy and show a high exposure risk from wild

354   birds to captive bustards. However, despite this large exposure probability, the real number of

355   captive bustards clinically infected by AIV or NDV is very low (Hirschinger, 2020).

356   We ended this analysis at the exposure step, but exposure does not lead inevitably to

357   infection. To assess the risk of infection, one should consider a probability of transmission

358   (i.e., pathogen passing from contaminated matrix to bustard) and a probability of infection

359   (i.e., effective spread of the pathogen in the organism after transmission). Thus, the limited

360   number of diseased captive bustards may simply be the result of the efficient vaccine

361   protection set up, but it also may be due to the limited efficiency of the transmission and

362   infection as even in sentinel bustards (non-vaccinated birds), morbidity, mortality and

363   seroprevalence rates are very low (Hirschinger, 2020). This result suggests that even with a

364   strong exposure pressure, contamination is limited.

365   Several explanations are worth considering (Sims et al., 2016). First, environmental and

366   climatic conditions are clearly unfavourable to the environmental persistence of the viruses

367   (high temperatures, low humidity, high UV index) and likely prevent the contamination of

368   bustards (Stallknecht & Brown J., 2009). We can also assume a limited susceptibility of

369   bustards for the strains carried by wild birds, but this hypothesis seems unlikely as shared

370   strains have already been highlighted (Hirschinger et al., 2019). Nevertheless, in the case of

371   the circulation of a highly pathogenic strain in wild birds, exposure probabilities suggest that

372   an outbreak in captive bustards is of real concern.

373   Overall, the absolute values presented in this analysis may only have a relative significance

374   because they are directly associated with a specific epidemiologic context. However, they are

375 of great interest for the sanitary management of the breeding site presented in this study,

376 allowing a hierarchization of risk levels between viruses, species and pathways of exposure.

377 Specifically, this study has made it possible to target House sparrows for sanitary surveillance

378 of AIV and NDV, and water contamination by wild birds' faeces appears as a priority target

379 for sanitary control.

380 Thus, although the role of some peridomestic species in the transmission of AIV and NDV

381 has already be examined in numerous studies (Abolnik, 2014; Nemeth et al., 2013, 2010),

382 this analysis reveals that, at least in this specific environmental context, wild peridomestic

383 birds should not be neglected.

384 These results also confirm the importance of known pathways of exposure for outdoor

385 poultry (faeces-contaminated water) and reaffirm the need to implement sanitary measures to

386 limit contacts between wild and captive birds. They also highlight the need for further

387 research dedicated to the pathogens circulating in the Middle East. Finally, despite the current

388 uncertainties associated with probabilities, this study offers an efficient tool that may be used

389 by decision-makers to implement a sanitary management strategy.

390 To conclude, such a risk assessment, one based on the best data available with the use of a

391 multimodal approach merging ecological, epidemiological and virological data, although

392 resource and time-consuming, appears to be the most appropriate approach to assess the risk

393 of pathogen exposure at the interface between wildlife and domestic animals.

394

Data availability statement

The data that supports the findings of this study are available in the supplementary material of this article.

Ethics

The authors confirm that the ethical policies of the journal, as noted on the journal's author guidelines page, have been adhered to. All birds used in this study have been captured, handled and sampled by skilled ornithologists graduated from the Centre de Recherches par le Baguage des Populations d'Oiseaux (CRBPO, Natural History Museum Paris) and trained veterinarians from the NARC according to international ethical standards (Fair, J., E. Paul, and J.Jones, Eds. 2010. Guidelines to the Use of Wild Birds in Research.Washington,D.C.: Ornithological Council).

Conflict of interest

The authors declare no conflicts of interest.

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740 Figure 1. Satellite view of the United Arab Emirates. On the top right, the breeding sites of

741 the National Avian Research Center (NARC). This figure was produced on the basis of

742 satellite views from Google Earth.

743 Figure 2. Scenario tree representing all of the potential pathways by which at least one

744 captive bustard can be exposed to AIV and NDV by one wild bird. Details of the pathways

745 leading to the exposure of at least one captive bustard by one infectious bird perched on an

746 aviary are presented. Each black rectangle represents an event and each red wording

747 represents the probability of the event to occur (all probabilities are defined in Table S1).

748 Dark arrows represent the succession of events. Each coloured block represents a pathway of

749 exposure.

750 Figure 3. Scenario tree representing details of the pathways leading to the exposure of at least

751 one captive bustard by one wild bird inside an aviary. Each black rectangle represents an

752 event and each red wording represents the probability of the event to occur (all probabilities

753 are defined in Table S1). Dark arrows represent the succession of events. Each coloured

754 block represents a pathway of exposure.

755 Figure 4. Daily probability of exposure to NDV and AIV of at least one captive bustard by

756 one wild bird from the different species. PASDOM = House sparrow, PYCTIS = White-eared

757 bulbul, STRSEN = Laughing dove, STRDEC = Collared dove.

758 Figure 5. Daily probability of exposure of at least one captive bustard to NDV and AIV from

759 at least one House sparrow (Passer domesticus) according to the different exposure pathways.

760 feces.perch = exposure through the faeces of an infectious bird perched on an aviary,

761 feathers.perch = exposure through the feathers of an infectious bird perched on an aviary,

762 feces.in = exposure through the faeces of an infectious bird inside an aviary, feathers.in =

763 exposure through the feathers of an infectious bird inside an aviary, aerosols = exposure

764 through the aerosols of an infectious bird inside an aviary, carcass exposure through the

765 carcass of an infectious bird inside an aviary, water.feces.in = exposure from consumption of

766 contaminated water, food.feces.in = exposure from consumption of contaminated food,

767 ground.feces.in = exposure from consumption of faeces on the ground.

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769 Supporting Information

770 Supplementary Material.docx