

我国野生鸟类疫病传播风险及防范措施

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摘要: 众多疫病病毒来源于野生动物, 具有向人类传播的风险, 尤其是具有飞翔能力的鸟类不易控制, 所携带的病毒传播广泛, 威胁人畜安全。因此, 充分了解鸟类携带疫病情况以及鸟类迁徙路线中重点区域的疫病风险, 对疫病防控非常重要。本文总结了鸟类主要携带的病原类型, 如冠状病毒、流感病毒、寄生虫和新城疫病毒等。着重探讨鸟类携带病原对生物安全防范重点区域的人员和动物的疫病风险, 包括自然保护区、机场和禽类养殖场等, 并从加强候鸟迁徙的动态监测、加强栖息地检疫和保护、家禽定期疫苗接种等方面提出疫病防范措施。

关键词: 自然保护区; 生态湿地; 禽类养殖场; 机场; 疫病

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Analysis of Avian Disease Transmission Risk and Prevention Measures in China

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Abstract: Many zoonotic diseases are found in wild animals and present a serious risk to human health, in particularly the virus carried by birds flying freely around the world is hard to control. There are three main bird migration routes which cover the most areas of China. It is important to investigate and fully understand the types of avian transmitted diseases in key areas on the bird migration routines and its impacts on both birds and human health. However, no literature is available in how about the risk of virus carried by migrating birds, and how to predict and reduce this risk of virus spreading to human being so far. In this paper, we first reviewed the main pathogen types carried by birds, including coronaviruses, influenza viruses, parasites, Newcastle disease virus (NDV), etc., and then discussed the spread risk of avian viruses to human being and animals in key areas of biosafety prevention. We also analyzed and discussed the risk of cross-spread of diseases among different bird species in nature reserves located on bird migration routes which provide

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sufficient food sources for migratory birds and attract numerous birds. Diseases transmitted by wild birds pose a serious threat to poultry farms, where high density of poultry may become avian influenza virus (AIV) reservoirs, cause a risk of avian influenza outbreaks. Airports are mostly built in suburban areas or remote areas with good ecological environment. There are important transit places for bird migration and densely populated areas, which have serious risk of disease transmission. Finally, this paper puts forward the following prevention suggestions from three aspects. First, establish and improve the monitoring and prediction mechanism of migratory birds, and use laser technology to prevent contact between wild birds and poultry. Second, examine and identify virus types carried by birds in their habitats and carry out vaccination. Third, protect the ecological environment of bird habitat, and keep wild birds in their natural habitat, so as to reduce the contact between wild birds and human and poultry, and thus reduce the risk of virus transmission.

Key words: Nature reserves; Ecological wetland; Poultry farms; Airport; Epidemic

鸟类属温血动物, 具有高度的物种多样性、特有的行为(如筑巢、迁徙等)和独特的适应性免疫系统(Lee et al. 2014), 是病毒的天然宿主, 包括流感病毒、冠状病毒和腺病毒等(Chan et al. 2015)。野生鸟类跨洲际和国家的迁徙活动将全球各地联系在一起(Duff et al. 2021, Huang et al. 2021), 不同物种鸟类迁移模式具有一定差异, 但飞行路线产生重叠(Lycett et al. 2019), 鸟类集群和迁徙习性加大了病原交叉传播威胁(Parvez et al. 2017), 因此发生了不同病毒随野生鸟类迁徙交叉感染, 在洲际间传播疫病的情况(Bahl et al. 2013)。近年来, 全世界新出现或重新出现 20 余种病毒, 多数属人与动物共患病, 野生鸟类与人畜的接触是其中主要因素之一(Parvez et al. 2017)。

截至 2021 年, 我国发现鸟类 1 491 种, 排世界第六位, 迁徙鸟类占半数以上(刘阳等 2021)。我国鸟类迁徙路径主要有三条, 东部路线鸟类跨越黑龙江、吉林、辽宁三省和华北东部地区, 沿海岸线迁往华中和华南直至东南亚地区, 或迁往日本、澳大利亚等地, 涉及黄河三角洲、莫莫格、向海、辽河入海口和獾子洞水库等湿地和保护区; 中部路线鸟类由内蒙古中部及东部、华北西部和陕西中南部翻越秦岭迁至四川或以南越冬, 涉及河套平原、红碱淖和三门峡黄河公园等重要农产区和湿地保护区; 西部路线由内蒙古西部、甘肃等荒漠地区

或高原草甸地区迁至四川、云南和西藏等地。斑头雁(*Anser indicus*)等大型鸟类能够跨越喜马拉雅山系至尼泊尔越冬, 路线涉及雅鲁藏布江、青海湖、扎陵湖、羊卓雍错和鄂陵湖等湿地保护区, 3 条迁徙路线覆盖我国大部分地区(张孚允等 1997, 郑光美 2017)。野生鸟类具有极强的飞翔能力, 可进行上万千米的迁徙, 为各种病原向外界传播创造了条件(Somveille 2016)。雁鸭类、鸥类和鸬鹚类等鸟类跨国迁徙, 病毒在不同大陆板块间产生基因交流, 加快了病毒的传播和变异(Li et al. 2018)。自然保护区、生态湿地、机场、野生动物园和禽类养殖场等地的防疫管理对人畜安全和经济发展尤为重要(Lin et al. 2012, Balami et al. 2014, Bakran-Lebl et al. 2022), 保护区、湿地和机场等也是鸟类迁徙途中的重要栖息地(乌日罕等 2014, 程成等 2019)。因此, 为加强对鸟类疫病传播认知及防控, 本文着重探讨鸟类迁徙过程中对重点区域产生的疫病传播风险, 并提出相应的疫病防范策略, 以降低鸟类疫病对相关地域的威胁。

1 野生鸟类的疫病类型

1.1 冠状病毒

冠状病毒(Coronavirus, CoVs)包含一条相对较长的正极性单链 RNA, 由(27~32)×10³个核苷酸组成, 是已知最大的病毒 RNA

(ribonucleic acid) 分子 (Rajcani 2020)。冠状病毒可感染包括人类在内的多种动物, 导致生殖、呼吸和胃肠道疾病 (王安如等 2021)。根据分离株间的血清学差异以及它们的基因组系统发育, 目前国际病毒分类委员会 (The International Committee on Taxonomy of Viruses, ICTV) 将冠状病毒分为 4 个属, 分别是 Alpha-CoV、Beta-CoV、Delta-CoV 和 Gamma-CoV (Woo et al. 2007), Alpha-CoV 和 Beta-CoV 的成员感染蝙蝠、人类和其他哺乳动物, 而 Gamma-CoV 和 Delta-CoV 的成员主要感染鸟类, 但也有少数感染哺乳动物 (Woo et al. 2014, Lau et al. 2018, Wong et al. 2019)。

迄今为止, 已在 15 目 30 科 108 种野生鸟类中发现冠状病毒 (Wille et al. 2020)。这些病毒经常被发现的鸟类类群包括雁形目 (Anseriformes)、鸻形目 (Charadriiformes)、鹈形目 (Pelecaniformes) 和鲣鸟目 (Suliformes) 等水鸟, 与人类密切接触的有鸡形目 (Galliformes)、鸮形目 (Columbiformes) 和雀形目 (Passeriformes) (Chu et al. 2011, Wille et al. 2020)。2018 年在湖南省 415 只野生鸟类的粪便样本中鉴定出 8 份来自喜鹊 (*Pica pica*) 的 Delta-CoV 阳性样本, 通过贝叶斯系统地理学分析表明, 中国南部沿海地区可能是我国内陆地区禽类 Delta-CoV 的潜在来源 (Wang et al. 2021)。家禽冠状病毒在抗原上相似, 系统遗传学上相关, 野鸟和家禽的接触产生交叉感染风险 (Breslin et al. 1999, Cavanagh et al. 2001, 2002)。原鸡 (*Gallus gallus*) 传染性支气管炎病毒 (infectious bronchitis virus, IBV) 属鸡冠状病毒, 可引起鸡急性呼吸道疾病, 造成家禽业严重的经济损失, 影响肉禽和蛋禽的生产性能 (Cavanagh 2007)。IBV 病毒不仅在上、下呼吸道组织的上皮细胞中复制, 也可在消化道、肾、输卵管和睾丸等部位的组织中增殖 (Cavanagh 2007)。此前易感火鸡 (*Meleagris gallopavo*) 和环颈雉 (*Phasianus colchicus*) 等鸡形目的 IBV, 感染范围扩大, 现已造成鸭等的感染 (Mardani et al.

2006)。此外, 火鸡冠状病毒 (Turkey coronavirus, TCoV) 在火鸡中引起急性肠道疾病, 迄今为止尚无商业疫苗可用于控制该疾病 (Kang et al. 2021)。

1.2 流感病毒

甲型流感病毒 (Influenza A virus, IAV) 包括所有禽流感病毒 (Avian influenza virus, AIV), 属负义单链 RNA 病毒, 具有高突变率 (Chen et al. 2006)。野生水禽, 特别是雁形目, 如绿头鸭 (*Anas platyrhynchos*)、大天鹅 (*Cygnus cygnus*) 和灰雁 (*Anser anser*) 等, 以及鸻形目, 如普通海鸥 (*Larus canus*)、黑尾鸥 (*L. crassirostris*) 和普通燕鸥 (*Sterna hirundo*) 等被认为是 IAV 的天然宿主 (Olsen et al. 2006), 这些宿主物种的感染不仅通常是低致病性的, 而且可能是无症状的 (Kuiken 2013, Runstadler et al. 2013)。研究表明, 候鸟可以无症状地长距离携带禽流感病毒 (Jourdain et al. 2010), 而且鸟类 IAV 谱系可以沿着候鸟的飞行路线传播 (Lam et al. 2012, Scotch et al. 2014)。

随着测序技术和相应的系统发育方法的出现, 对流感流行的起源、进化和流行病学有了更多的了解 (Lycett et al. 2019)。遥感和系统发育分析表明, H5N1 病毒在东亚的分布遵循 2003 至 2012 年期间野生鸟类的迁徙路线 (Tian et al. 2015)。2014 年在我国四川和江西两省分别发现了 H5N8 和两种不同 H5N6 重组谱系, 这两种 H5N6 谱系均在迁徙鸟类中传播 (Bi et al. 2015, Erik et al. 2015)。经系统地理学分析发现, 该病毒最早起源于广东省, 随后经江苏省向北和向南传播 (Bi et al. 2016), 其中一个谱系获得了 H5N1/H7N9 谱系病毒的内部蛋白编码片段, 并导致人类感染 (Zhang et al. 2016a)。2016 年 5 月在青海湖的野生鸟类中发现了 H5N8 (QH-H5N8) 病毒毒株 (Li et al. 2017), 同期在乌布苏湖附近发现了类似的 H5N8 病毒 (Lee et al. 2017)。至 2016 年 11 月, 中东和欧洲发现与 QH-H5N8 高度相似病毒毒株, 秋季候鸟迁徙在病毒扩散传播中起到重要

作用(Ghafouri et al. 2017, Kleyheeg et al. 2017, Globig et al. 2018)。来自不同地区的候鸟聚集在西伯利亚湿地繁殖和换羽,此区域不同水鸟频繁的接触和迁徙路径的交叉可能是 AIV 传播扩散的重要因素。H5N8 禽流感在欧洲野鸟和家禽中造成历史上规模最大、传播最广的禽流感疫情,野鸟呼吸道和肠道上皮细胞中表达病毒抗原,病毒的传播方式由呼吸道向肠道转变,从而造成更大粪口传播几率,肠倾向增加意味着增加该病毒在野生水鸟病毒库中长期存在的可能性(Caliendo et al. 2020)。AIV 在野鸟间的传播和重组几乎不受地域限制,2017 年在江苏省某农场小麦地的野生豆雁(*Anser fabalis*)粪便中鉴定出 1 株 H6N1 亚型 AIV (J746),该毒株来源于不同国家和地区,属多元重组病毒(杨晓宇等 2020)。2018 年在渤海湾鸬鹚类粪便样品分离出 H2N7 和 H2N8 亚型禽流感病毒,均属低致病性禽流感病毒,与我国湖南以及日本、韩国、孟加拉国和越南的毒株同源性最高,遗传关系最近(孟维悦等 2019)。

自 1997 年我国香港特别行政区发生禽流感事件以来,多项研究强调了家禽(如火鸡和原鸡)在 AIV 传播中的重要作用(Zhou et al. 1999, Cameron et al. 2001)。2002 年,通过对意大利家禽和野生鸟类携带 H7N3 病毒基因序列比对,发现家禽中病毒完全来自于 1 年前野生水禽中传播的禽流感病毒株(Campitelli et al. 2004)。2020 年,在山西省发现 2 只大天鹅尸体携带 H5N8 病毒,随后在其他 10 种不同种类的野生鸟类和家禽中检测到该病毒。经遗传分析发现,有两种不同基因型的 H5N8 病毒由野生鸟类传入中国,其中一种基因型病毒在野生鸟类和家养水禽间广泛传播(Cui et al. 2022)。AIV 在野鸟和家禽间的相互传播,对养殖业造成了严重威胁,同时 AIV 的传播对人类安全造成的影响也不容小觑。在我国, AIV 的传播与人类活动关系密切,其中包括家禽产品的运输和贸易(Kilpatrick et al. 2006, Bahl et al. 2016,

Lu et al. 2017)。在活禽市场监测中发现了低致病性禽流感 H7N9 病毒,家鸡为无症状或轻度症状(Pantin-Jackwood et al. 2014, Jiao et al. 2018),但在人类中引起了一系列症状,造成严重呼吸困难甚至死亡(Gao et al. 2013)。IAV 中 H1N1、H5N1、H7N4、H7N7 和 H7N9 等多种禽流感病毒亚型直接感染人类(Liu et al. 2013, 杨正时等 2014, Bui et al. 2017),这些感染在人类中将产生严重后果,如 1918 年,由 H1N1 流感病毒引起的西班牙流感大流行,造成大约 5 000 万人死亡(Johnson et al. 2002); 2013 年 2 月,中国上海和安徽发现了首例人感染 H7N9 病毒病例,经证实为人畜共患病(Chen et al. 2013, Gao et al. 2013); 2016 年 12 月,在家鸡和人的病例中发现了高致病性禽流感 H7N9 病毒(Zhou et al. 2017)。因此,应持续关注潜在的人感染禽流感风险。

1.3 寄生性传染病

鸟类寄生虫分为体内寄生和体表寄生两类,体内寄生包括肠道内寄生和细胞内寄生,体表寄生主要以蜱虫为主,两类寄生虫均具有传染性(de la Fuente et al. 2015)。禽疟(Avian malaria)是一种蚊虫传播的鸟类体内寄生虫病,由疟原虫(*Plasmodium relictum*)引起并在全球传播,此疾病已被确定为鸟类急剧减少和灭绝的主要原因(Dahlin et al. 2019)。鸟类是蜱虫最主要的宿主之一,约 60 种硬蜱将鸟类作为宿主,寄生蜱在吸食血液过程传播多种病毒,并随鸟类的迁飞扩散传播(Kolonin 2008, de la Fuente et al. 2015)。雀形目鸟类携带蜱虫的种类最多,其中留鸟携带蜱虫的几率大于候鸟,且鸟类集群的特性给蜱虫提供充足寻找新宿主的机,不同病原在候鸟和留鸟间交叉传染(Loss et al. 2016)。我国鸟类寄生蜱传播人畜共患病病毒案例多发,如广西灰斑鸠(*Streptopelia decaocto*)体内携带伯氏疏螺旋体(*Borrelia garinii*),引发莱姆病(Lyme disease)(杨吉飞等 2010, Yang et al. 2015); 雕鸮(*Bubo bubo*)体内携带嗜吞噬细胞无形体(*Anaplasma*

phagocytophilum), 引起无形体病(*Anaplasmosis*), 严重时导致多器官受损甚至死亡(Li et al. 2011)。不仅如此, 鹦鹉热(*Psittacosis*)(Williams et al. 1998)、墨累河谷脑炎(Murray Valley encephalitis, MVE)(Mackenzie et al. 2017)和克里米亚-刚果出血热(Crimean-Congo hemorrhagic fever)(Mancuso et al. 2019)通过衣原体、蜱虫传播, 感染鸟类和人类。候鸟的长途迁徙对蜱传播病毒具有重要作用, 一种由长角血蜱(*Haemaphysalis longicornis*)传播的新型布尼亚病毒在中国发现后出现于日本和韩国, 研究发现长角血蜱的分布与4种候鸟在中、日、韩三国间的迁徙路线一致(Yun et al. 2015, Zhang et al. 2016b)。此外, 对我国江苏省由蜱传播病毒引起的发热伴血小板减少综合征(severe fever with thrombocytopenia syndrome, SFTS)的研究发现, 鸿雁(*Anser cygnoides*)和珠颈斑鸠(*Streptopelia chinensis*)两种候鸟中具有抗该病毒抗体, 表明野生鸟类被蜱虫寄生后可以经飞行线路远距离传播, 进而揭示该蜱传播病毒在中、日两国较高同源性的原因(Li et al. 2016)。因此, 鸟类是蜱等寄生性疾病传播重要的一环, 防范工作不容忽视。

1.4 其他风险

历史上由鸟类扩散传播而暴发的流行病众多, 除上述严重疫病风险, 其他传染病也应充分关注。西尼罗河病毒(West Nile virus, WNV)和乌苏图病毒(Usutu virus, USUV)造成人畜共患病, 鸟类是主要携带者(Kvapil et al. 2021), 可感染人、马等哺乳动物, 使宿主出现发热、脑炎等症状(Vilibić-Cavlek et al. 2019), 病死率约为3%~5%(童明龙等 2005)。2018年以来, WNV在欧洲各地暴发, 人类和动物感染数量急剧增加(Kvapil et al. 2021)。USUV对乌鸫(*Turdus merula*)和乌林鸮(*Strix nebulosa*)等鸟类具有高致病性, 传播范围有扩大趋势(Vilibić-Čavlek et al. 2020)。被称为亚洲鸡瘟病毒的新城疫病毒(Newcastle disease virus, NDV), 在野鸟中传播和储存(Ababneh

et al. 2012), 可通过排泄物传染给家禽(Solomon et al. 2012)。在我国东北地区湿地和活禽市场监测中分离出10株NDV, 其中4株来自野生鸟类, 该流行趋势表明NDV可能在野鸟和家禽间传播(Zhang et al. 2016c)。新城疫由于其高传染性已被我国列为重点防疫疾病。

2 疫病威胁的重点区域

2.1 自然保护区

鸟类的种类及数量是评价生态环境质量的重要指标, 目前我国已经成立82处以保护鸟类为主的国家级自然保护区(生态环境部 2019)。湿地给迁徙鸟类提供充足的食物来源, 吸引大量鸟类越冬栖息(程成等 2019)。栖息地中不同鸟群密切接触, 病毒在鸟群中交叉传播, 并随鸟类迁飞传入新的区域(Olsen et al. 2006)。在三江保护区的绿头鸭、白额雁(*Anser albifrons*)和鸳鸯(*Aix galericulata*)等5种野生迁徙水禽中分离出20株禽流感病毒和13株新城疫病毒, 绿头鸭在世界分布广泛, 种群数量庞大, 在病毒的传播中起重要作用(曾祥伟等 2008)。青海湖是东南亚、西藏、印度等地区候鸟的重要越冬和栖息地之一, 2005年暴发的高致病性H5N1病毒感染斑头雁、棕头鸥(*Larus brunnicephalus*)和渔鸥(*Larus ichthyaetus*)等鸟类(Liu et al. 2005); 2016年H5N8病毒导致了斑头雁、棕头鸥和渔鸥3种鸟类死亡(Li et al. 2017)。研究表明, 候鸟是众多疫病引入并在全球传播的重要媒介(Verhagen et al. 2015, Lycett et al. 2016), 多数保护区是候鸟重要繁殖地并处在迁徙路线上(Debela et al. 2020), 对于不同鸟类间疫病交叉传播风险应得到充分重视。

2.2 养殖场及动物园

野生鸟类传播的疾病给禽类养殖场带来严重威胁, 候鸟可能是疫病传播良好媒介, 但部分传播是通过受感染家禽的贸易产生的(Bahl et al. 2016)。养殖场中高聚集度的禽类可能成为AIV储存库, 存在暴发禽流感风险(Butler

2006)。2005 年南非第二大省西开普省约六分之一的非洲鸵鸟 (*Struthio camelus*) 养殖场检查出 H5 型禽流感病毒, 发生禽流感的风险与养殖场鸵鸟数量、饲料槽清洗频率和鸵鸟运输车清洁消毒频率显著相关 (Thompson et al. 2008)。此外, H5 型禽流感感染风险与白鹳 (*Ciconia ciconia*)、鸥 (*Larus spp.*)、埃及雁 (*Alopochen aegyptiaca*) 等野生鸟类接触的频率相关 (Thompson et al. 2008)。野生鸟类给家禽养殖带来疫病威胁的同时, 家禽同样影响野生鸟类。通过对比全球 75 个地区 11 年的 AIV 数据, 发现野生鸟类和家禽的 AIV 基因遗传多样性差异不显著, AIV 的传播途径很可能是双向性 (Zhang et al. 2019)。因此, 加强对家禽养殖场的疫病防控, 将减少野生鸟类的疫病风险。

野生鸟类与动物园中动物直接或间接接触, 产生疫病传入和传出风险, 如通过蚊虫媒介, 野生鸟类携带西尼罗河病毒可传播给人类、马和其他动物 (童明龙等 2005)。在安徽皖南野生动物急救中心出现了鸟类和哺乳动物跨物种感染戊型肝炎病毒 (Hepatitis E virus, HEV) 的案例, 急救中心的 22 种动物中白鹈 (*Lophura nycthemera*)、冠鹤 (*Balaerica regulorum*)、梅花鹿 (*Cervus nippon*)、毛冠鹿 (*Elaphodus cephalophus*)、亚洲黑熊 (*Ursus thibetanus*)、云豹 (*Neofelis nebulosa*) 等 7 种动物被感染, 并且在 7 名饲养员的血清检测中 5 名呈阳性 (Zhang et al. 2008)。因此, 定时对动物园进行全面病毒检测, 以对人畜共患病进行预警, 从而有效阻止病毒传播, 保障人类和动物安全。

2.3 机场

机场多建于城郊或偏远地区, 生态环境良好, 植被丰茂, 草坪绿地面积广, 蚊虫繁盛, 吸引大量留鸟进行栖息和捕食, 同时吸引候鸟停歇和觅食, 是鸟类迁徙过程的重要中转地 (乌日罕等 2014, 刘振江等 2021a)。此外, 我国具有众多临海机场, 大多处于鸟类迁徙的东部路线, 同时栖息水鸟及陆鸟 (刘振江等 2021b)。而日益全球化造成的国际运输量增长使机场成

为虫媒病毒活动的焦点, 鸟类是潜在的放大宿主。2018 年在中欧的一个国际机场检测到 WNV 和 USUV, 这两种病毒涉及机场内活动的特定鸟类宿主, 使病毒扩散传播 (Bakran-Lebl et al. 2022)。此外, 频繁的鸟类活动产生鸟击风险, 机场人员防鸟击作业时将在重点区域布设鸟网, 鸟类移除救助和死亡鸟类解剖研究过程中给工作人员带来病毒感染和传播风险 (Slota et al. 2011, Cyranoski 2017)。为减少机场人员接触病毒机会, 应通过食物链减少鸟类密度, 运用雷达、激光等措施替代杀伤性器材, 同时减轻对鸟类的伤害 (陈唯实等 2017, 刘振江等 2021c)。机场属于人员密集区域, 疫病传播风险严重, 对鸟类和虫媒病毒应实时监控。

3 野生鸟类的疫病防范

3.1 加强候鸟迁徙动态监测

野生动物疫病具有传播速度快, 扩散范围广, 阻隔消灭难等特点 (Beltran-Alcrudo et al. 2008)。影响鸟类迁徙轨迹的因素是复杂的, 大多数候鸟每年都会返回一些已知的中途停留地、繁殖地和越冬地 (Akesson et al. 2007), 构建传染病数学模型对了解鸟类迁徙动态和病毒传播的动态变化具有重要作用 (Bourouiba et al. 2010)。如易感-感染-治愈模型 (susceptible-infectious-recovered, SIR) (Kumar et al. 2020)、易感-感染-易感模型 (susceptible-infected-susceptible, SIS) (Zhu et al. 2019) 和易感-潜伏-感染-恢复模型 (susceptible-exposed-infectious-recovered, SEIR) (Liu et al. 2020) 等, 已经成为预测疫病传播规律的重要工具。各重点监控地区应联合科研院所、高校, 使用遥感 (remote sensing, RS)、地理信息系统 (geographic information system, GIS)、全球定位系统 (global position system, GPS) 等技术, 建立、健全鸟类迁徙大数据监控平台, 提升监控水平。病毒在不同地区和不同物种之间的传播可以通过系统动力学和系统地理学来推断分析 (Lemey et al. 2009, Pybus et al. 2009), 这些技术利用快速进

化的病毒序列数据来揭示扩散模式, 以此了解疫病病毒的进化和分布。系统地理学技术也用于显示亚洲不同鸟类传播高致病性 AIV 的影响路线和区域 (Trovão et al. 2015)。鸟类迁徙受到环境、气温和食物等因素的影响, 调整迁徙时间 (Hickling et al. 2006, Thackeray et al. 2010)。在全球环境变暖背景下, 各地的保护区和机场等难以准确预测鸟类迁徙的途经时间。因此, 全国各保护区和机场间应建立联动机制, 共享鸟类迁徙数据, 提供鸟类动态情报, 减轻疫病对人畜的危害。

禽类养殖场等重要区域受到野生鸟类携带病毒威胁大, 需对野生鸟类进行控制, 避免其与人畜接触。通过激光手段可有效阻止野生鸟类进入此类区域, 研究证明, 激光在家禽养殖区对野生鸟类的抑制率在 98% 以上, 能够极大降低野生鸟类与家禽间疫病的交互传播概率 (Elbers et al. 2021)。持续防控野生鸟类, 特别是候鸟, 对可能发生的疫病流行提供早期预警和了解病毒生态学具有重要意义。

3.2 鸟类检疫及疫苗接种

除监控鸟类动态, 对野生鸟类中存在的病毒类型进行监测在疫情预防中同等重要。快速诊断疫病病毒有利于对疫情动态实时监控, 提早发现和控制疫情。目前, 高通量测序技术, 如 DNBSEQ-T7 和 Illumina HiSeq 等测序平台可精确检测病毒逆转录 DNA (Wang et al. 2019, Lu et al. 2020)。病毒监测工作主要集中于检测已死亡或捕获的鸟类, 但很少提供危险毒株的预警 (Kuchinski et al. 2020)。为全面监测野生鸟类病毒传播情况, 可以通过采集野生鸟类栖息地的遗留样本, 如巢中羽毛、粪便等, 其中包含本地传播病毒的遗传信息, 利用基因测序技术对病毒进行鉴定 (Kuchinski et al. 2020)。

野生鸟类和家禽的交叉传播是 AIV 流行面临的重要挑战 (Zhang et al. 2019), 家禽的防疫为减少野生鸟类传播疫病提供屏障作用。禽流感疫苗治疗是一种常用的控制疾病的方法,

Kharis 等 (2018) 通过数学建模工具分析易感鸟类, 制定疫苗接种最佳比例防止疫病在鸟类间传播。因此, 提高鸟类的生物安全性和对家禽进行免疫接种是将疫情控制在最低限度的重要策略。禽流感病毒持续向人类传播, 表明人畜共患禽流感对人类健康构成持续威胁。2017 年, 中国 H7N9 疫苗接种计划的成效表明, 接种疫苗能够极大减少家禽感染禽流感病毒, 以及人类感染的数量和持续传播的风险 (Lycett et al. 2019)。禽类养殖场感染禽流感的主要因素有开放水源、附近养殖场、其他牲畜以及养殖场消毒情况 (Wang et al. 2014)。以往的经验表明, 病毒一旦在家禽种群中蔓延, 难以控制和封锁 (Chen et al. 2005)。因此, 定期对保护区和养殖场等高危区域检疫, 加强对环境和鸟类的监测, 定期接种疫苗对鸟类疫病防控具有重要作用。

3.3 栖息地保护

人类活动对生态环境的破坏是引发野生动物疫病暴发的重要因素 (赛日克·居马地力等 2015), 生境破坏导致鸟类离开原有栖息地进入人类生活区, 减少生态环境破坏是防范疫病的基础。充分了解鸟类栖息地中水体、植被和地理条件, 对鸟类多样性保护和湿地管理具有重要意义 (Yang et al. 2016)。在鸟类栖息地对影响鸟类安全的人类设备进行改造, 如设置人工栖架等 (王超等 2020), 并着力恢复植被森林绿化, 增加生物多样性, 保障食物来源, 将鸟类留在自然栖息环境中。

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