

1 Winds of change: Charting a pathway to ecosystem monitoring using
2 airborne environmental DNA

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35

36 **Abstract**

37 Airborne environmental DNA (airborne eDNA) analysis leverages the globally ubiquitous
38 medium of air to deliver broad species distribution data and support ecosystem monitoring across
39 diverse environments. As this emerging technology matures, addressing critical challenges and
40 seizing key opportunities will be essential to fully realise its potentially transformative impact. In
41 June 2024, the Southern eDNA Society convened over 100 researchers, industry leaders, and
42 biodiversity management stakeholders in a landmark workshop to evaluate the current state of
43 airborne eDNA research and chart a course for future development. Participants explored
44 opportunities for integrating airborne eDNA into existing monitoring systems, but they
45 unanimously agreed that research must first be applied to improving understanding of airborne
46 eDNA ecology. The workshop emphasised the importance of collaborative engagement with
47 stakeholders – including government agencies, Indigenous communities, and citizen scientists –
48 to ensure practical and ethical implementation. This summary highlights actionable
49 recommendations from the workshop, such as addressing outstanding questions about airborne
50 eDNA ecology, refining sampling strategies, and fostering early, sustained stakeholder
51 collaboration. By addressing these challenges, airborne eDNA analysis can become a
52 transformative tool for biodiversity, biosecurity, and conservation monitoring on a global scale.
53 Its ability to detect diverse taxonomic groups—including fungi, plants, arthropods, microbes, and
54 vertebrates—positions airborne eDNA as a pivotal technology for holistic terrestrial biodiversity
55 assessments that transcend traditional, species-focused monitoring approaches.

56 **Keywords:** airborne eDNA, biodiversity, biosecurity, monitoring, terrestrial, Southern eDNA
57 Society, implementation, aerobiology, aeolian, conservation

58 Introduction

59 Amid a growing global biodiversity crisis, decision-makers require accurate and timely species
60 distribution and occurrence data. Over the last decade, environmental DNA (eDNA) analysis has
61 become a widely used surveillance tool, particularly within aquatic ecosystems. Sequencing DNA
62 shed by organisms in the environment has enabled time- and cost-effective, non-invasive
63 biodiversity assessments ([Ficetola et al., 2008](#); [Pawlowski et al., 2020](#); [Rodriguez-Ezpeleta et al.,
64 2021](#)). As the field evolves, new eDNA methods continue to emerge, with airborne eDNA analysis
65 being one of the latest additions ([Bohmann & Lynggaard, 2023](#); [Johnson & Barnes, 2024](#)).
66 Airborne eDNA is derived from bioaerosols, which encompass a diverse array of organic
67 materials. These include (1) microorganisms such as viruses, bacteria, microalgae, and unicellular
68 fungi; (2) propagules like pollen and spores released by plants and fungi; and (3) biological
69 fragments, including excretions, cells, and tissue pieces from plants, animals, and microbes
70 ([Després et al., 2012](#)). While the definition of “airborne eDNA” remains an unresolved point in
71 the field, for practical purposes, we define it here as DNA extracted from any biological material
72 captured in air samples. This broad definition acknowledges the methodological consistency
73 required across different bioaerosol sources. Given its ability to capture DNA from diverse
74 sources, airborne eDNA analysis has been applied across multiple fields, including biodiversity
75 assessments ([Clare et al., 2022](#)), detection of rare or elusive species ([N. Garrett et al., 2023b](#)),
76 monitoring of GMOs and invasive species ([Trujillo-González et al., 2022](#)), tracking of allergenic
77 pollen ([Kraaijeveld et al., 2015](#)), and pathogen surveillance ([Sanders et al., 2023](#)). Together, these
78 applications facilitate cross-disciplinary ecological and evolutionary research enabling
79 comprehensive ecosystem health monitoring.

80 Airborne eDNA analysis holds immense promise for monitoring applications across diverse
81 ecosystems, capturing genetic material from air to complement substrate-restricted eDNA
82 methods. This unique potential could enable broad-scale biodiversity assessments in locations
83 where other monitoring methods are impractical. However, the methodology remains nascent,
84 sharing many challenges with established eDNA sources like water, such as imperfect detection
85 and sensitivity to environmental conditions ([Johnson, Cox, et al., 2021](#); [Rowney et al., 2021](#)).
86 Rather than deterring progress, these challenges underscore the need for targeted research and
87 methodological innovation. Variation in sample collection and analysis, although expected in an
88 emerging field, has prompted studies on sampling method effects ([Mark D Johnson et al., 2019](#)),
89 detection limits ([Foster et al., 2023](#)), and source estimation for airborne eDNA ([Gusareva et al.,
90 2022](#); [Lennartz et al., 2021](#)), emphasising the importance of quantifying methodological impacts
91 on data robustness, repeatability, and reliability. Recognising this momentum, Johnson & Barnes
92 (2024) recently reviewed the field’s growth, challenges, and potential future directions, identifying
93 key hurdles still to be addressed ([Johnson & Barnes, 2024](#)).

94 In June 2024, over 100 researchers, industry leaders and management stakeholders convened in
95 Canberra, Australia, both in person and virtually, for a pivotal two-day workshop hosted by the
96 Southern eDNA Society (SeDNAS, <https://sednasociety.com/>, accessed 13 September 2024).
97 Participants from 30 institutions and eight countries evaluated the current state of airborne eDNA
98 research, identified key challenges, and outlined strategic pathways for future development. While
99 acknowledging the long-standing use of eDNA metabarcoding and targeted species detection in
100 airborne microbial community and pollen and fungal spore studies, the workshop primarily
101 focussed on the use of airborne eDNA for detecting macro-organisms. The workshop revealed that
102 many challenges faced by airborne eDNA analysis are shared with other forms of eDNA, such as
103 aquatic or soil-based methods, but a subset of challenges – such as accounting for exceptionally
104 low DNA concentrations and establishing appropriate field controls – are unique to the medium of
105 air. Key discussions at the workshop centred around four key questions: (1) What might airborne
106 eDNA data be used for? (2) How is airborne eDNA currently collected and processed? (3) What
107 are key questions about airborne eDNA ecology that need to be answered? (4) How do we as
108 researchers engage effectively with airborne eDNA stakeholders? Here, we summarise the
109 workshop outputs, provide insights into the advances and future directions of airborne eDNA
110 technology, and offer a workshop statement to summarise current community consensus on the
111 emerging field (see Box 1).

112

113 **Box 1. Southern eDNA Society Airborne eDNA Workshop Joint Statement**

114 *“Airborne eDNA analysis is a potentially powerful biomonitoring tool, however we must*
115 *improve our understanding of airborne eDNA ecology, sampling strategy impacts, signal*
116 *variability and sensitivity. With validation, airborne eDNA tools may become standard in*
117 *biodiversity, biosecurity and conservation applications.”*

118 Airborne eDNA applications

119 Interest in airborne eDNA has grown rapidly following proof-of-concept studies demonstrating its
120 utility in detecting vertebrates ([Clare et al., 2021](#)) and plants that rely on insect or animal
121 pollination rather than wind dispersal ([M. D. Johnson et al., 2019](#)). These studies paved the way
122 for early applications of airborne eDNA analysis in terrestrial biodiversity assessments ([Bohmann
123 & Lynggaard, 2023](#); [Clare et al., 2022](#); [Lynggaard et al., 2022](#); [Lynggaard et al., 2024](#)). The utility
124 of airborne eDNA extends beyond targeted species detection to monitoring across the tree of life.
125 Its ability to simultaneously identify microorganisms, plants, and animals enables a broader
126 understanding of ecosystem dynamics and facilitates the development of comprehensive
127 biodiversity baselines. In addition, its potential for broad-scale taxonomic monitoring offers
128 unparalleled opportunities to detect shifts in community composition and biodiversity health.
129 When paired with traditional survey techniques such as camera traps, manual handling, and visual
130 surveys ([Johnson, Fokar, et al., 2021](#); [Roger et al., 2022](#)), as well as complementary forms of
131 eDNA ([Runnel et al., 2024](#)), airborne eDNA may improve detection of terrestrial and arboreal
132 species that may otherwise be underrepresented or undetected ([Banchi et al., 2020](#)).

133 In the context of a changing climate and increasingly interconnected world, airborne eDNA
134 analysis enables rapid detection of plant and animal pests and identification of incursion pathways,
135 offering valuable data for biosecurity applications ([Kestel et al., 2022](#); [Sanders et al., 2023](#);
136 [Trujillo-González et al., 2022](#)). Its potential spans all phases of the invasion curve – from pre-
137 biosecurity breach and early detection to containment and eradication monitoring – highlighting
138 its future role as a critical tool in biosecurity monitoring ([Bell et al., 2024](#)). For example, airborne
139 eDNA has been shown to complement visual monitoring approaches for detecting pest species
140 incursions, such as the successful detection of the invasive hemlock woolly adelgid in North
141 America, a species native to Japan ([Geller & Partridge, 2025](#)).

142 Airborne eDNA collection offers an opportunity to sample in inaccessible regions and at
143 previously unattainable scales. Not unlike other eDNA approaches, airborne eDNA analysis may
144 allow for access to remote or challenging locations, including burrows and mountain-tops and
145 enhance monitoring of sensitive or cryptic species ([Lynggaard et al., 2024](#)). The possible
146 simplicity of airborne eDNA capture lends kindly to the expansion of sampling density through
147 citizen scientist initiatives ([Madden et al., 2016](#)), mirroring those currently in use in aquatic
148 systems ([Biggs et al., 2014](#)). To increase sampling scale affordably, an opportunity is emerging in
149 repurposing existing sample collection infrastructure – such as pollen, spore or pollution
150 monitoring stations ([Littlefair et al., 2023](#)).

151 Airborne eDNA collection

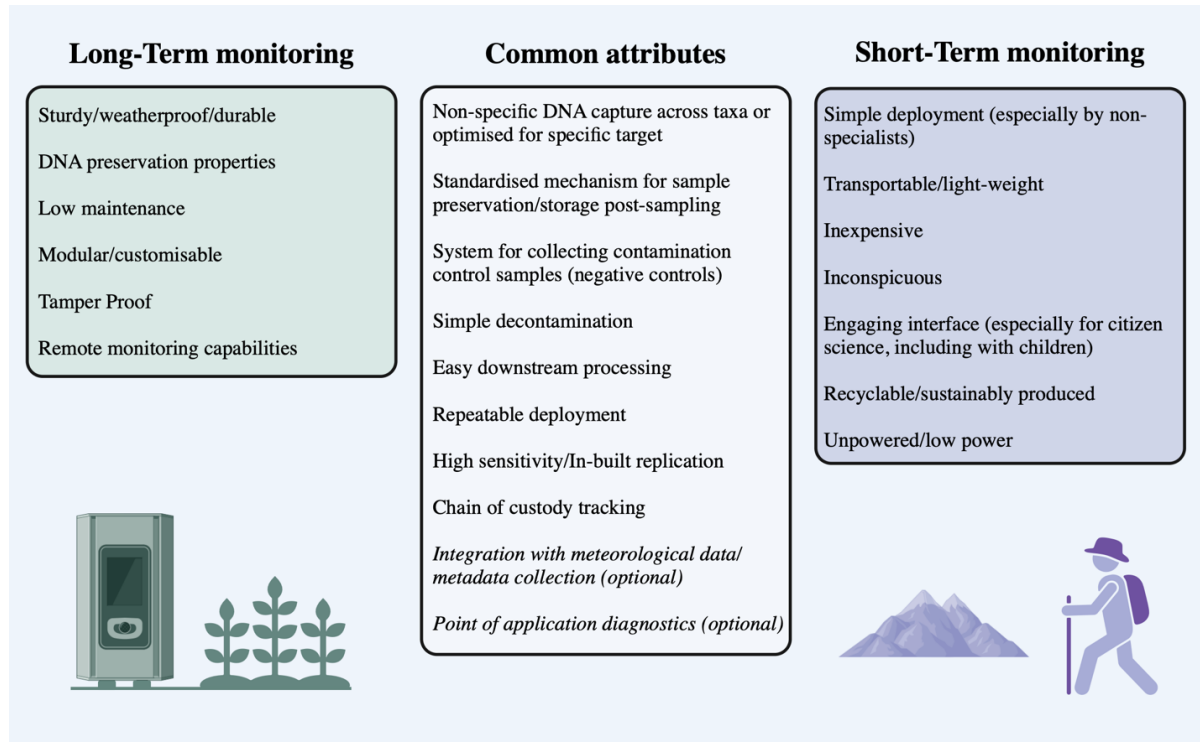
152 Platforms used to collect airborne eDNA vary widely in design and material composition,
153 generally falling into two categories: passive or active samplers. The choice between these

154 methods depends equally on monitoring goal and project resources, as passive samplers are
155 typically simpler and more cost-effective, while active samplers tend to be more complex and
156 expensive.

157 Passive samplers rely on natural air movement to collect eDNA. With simpler designs requiring
158 lower maintenance, passive sampling can be deployed at higher density to increase temporal and
159 spatial replication, leading to more precise detection probability and occupancy estimates, and
160 reducing the effect of random variation due to fluctuating environmental conditions ([Burian et al.,
2021](#); [Whittington et al., 2015](#)). Examples of passive samplers include Big Spring Number Eight
161 dust traps ([Johnson et al., 2023](#); [Mark D Johnson et al., 2019](#)), modified Wilson and Cooke towers,
162 marble-filled pan traps ([Mark D Johnson et al., 2019](#)), filter and funnel sedimentation traps
163 ([Schlegel et al., 2024](#)), and sticky traps ([Runnel et al., 2024](#)). Some studies have also explored
164 opportunistic passive sampling methods, such as collecting spiderwebs to capture airborne eDNA
165 ([Gregoric et al., 2022](#); [Newton et al., 2024](#); [Xu et al., 2015](#)).

167 In contrast, active samplers use powered equipment, such as fans, to intentionally draw air through
168 or onto a particle collection system, including filters, impingers, or cyclonic separators. This
169 method may increase the volume of air sampled over a given time period, which would impact the
170 effective test area and detection probability, though further research is needed to quantify this
171 effect. Examples of active samplers include cyclonic air-samplers ([Brennan et al., 2019](#); [Roger et
al., 2022](#)), dry cyclone samplers ([Brennan et al., 2019](#)), computer fan-powered 3D-printed filter
172 frames ([N. Garrett et al., 2023b](#); [Lynggaard et al., 2022](#)), and repurposed pollution monitoring
173 stations ([Littlefair et al., 2023](#)).

175 As new systems are developed and tested, variation in platform design is expected to increase. To
176 guide this innovation, workshop attendees identified key attributes for airborne eDNA samplers
177 (Figure 1). The desired features of a sampling platform directly relate to the scale and longevity of
178 the monitoring objectives. Broadly, we have classified collection platforms into those suitable for
179 long-term and short-term monitoring. Long-term monitoring platforms would be designed to
180 deliver repeated sampling tailored to a target site or application (e.g., pest monitoring in
181 agricultural systems or biodiversity assessments at long-term research sites). Conversely, short-
182 term monitoring platforms would be designed to deliver mobile and flexible sampling appropriate
183 for a wider variety of research questions (e.g., establishing invasion fronts in biosecurity controls
184 efforts or supporting citizen science initiatives). Long-term monitoring platforms might emphasise
185 durability, automation, and robust data management while short-term platforms might prioritise
186 portability, simplicity, and affordability to enhance accessibility. Regardless of the approach,
187 attendees underscored that before any method or device can be widely adopted for monitoring
188 purposes, critical sampling parameters must be validated to ensure reliable and accurate data
189 generation.



190

191 **Figure 1. Key attributes of airborne eDNA collection platforms**

192 Ideal airborne eDNA collection devices will balance critical common attributes with fit-for-purpose design. For long-
 193 term monitoring, platforms should prioritise durability, sample integrity, and seamless integration into existing
 194 infrastructure while minimising maintenance. Short-term monitoring platforms, particularly for citizen science
 195 initiatives, should emphasise simplicity, cost-effectiveness, and user-friendly interfaces. Both types of devices should
 196 incorporate features that ensure reliable sampling and downstream processing.

197 **Advancing understanding of factors influencing airborne eDNA**
 198 **detection**

199 A comprehensive understanding of environmental and technical parameters is critical for effective
 200 airborne eDNA monitoring. It is broadly understood that eDNA generation, persistence and
 201 degradation (i.e., eDNA ecology) can be impacted by temperature, humidity, and other
 202 environmental factors and introduces variability in species detection ([Barnes et al., 2021](#); [Barnes](#)
 203 [et al., 2014](#); [Harrison et al., 2019](#); [Jo & Minamoto, 2021](#); [Shogren et al., 2017](#)). Additionally, a
 204 broad range of technical factors, such as sampling and analytical methodology, influence data
 205 composition. While we cannot eliminate all sources of variability in airborne eDNA datasets, we
 206 can characterise and account for them. Insights into factors influencing detection variability from
 207 other substrates, such as soil and water, may be applicable to DNA carried in the air, however, not
 208 all features may be mirrored across eDNA sources. Airborne eDNA also presents unique
 209 challenges, such as potentially very low DNA concentrations, rapid particle sedimentation, and the
 210 influence of complex air currents, all of which necessitate specific investigation. Without insight

211 into these factors, conservation or biosecurity actions informed by airborne eDNA data may risk
212 misinterpretation and inefficiency due to the introduction of detection error. Thus, investigation
213 and validation of a diverse range of parameters will be essential for progressing the utility of
214 airborne eDNA analysis ([Atkinson & Roy, 2023](#); [Bohmann & Lynggaard, 2023](#)).

215 Recognising the significance of factors impacting species detection, workshop attendees compiled
216 a list of critical parameters that may require validation (Table 1), noting that the need for validation
217 will depend on study objectives. While the field works toward understanding these factors, it will
218 be important to communicate study limitations when reporting results to account for
219 uncharacterised sources of detection variability. Importantly, airborne eDNA studies should
220 clearly articulate their experimental design, use of controls, and data analysis approach to facilitate
221 identification of potential sources of detection error.

222 While not unique to air sampling, eDNA-derived biodiversity data is prone to error from several
223 major sources, including, contamination of DNA in the workflow, inefficient DNA capture,
224 misidentification of DNA, and changing taxonomies ([Burian et al., 2021](#); [Furlan et al., 2020](#); [N.
225 Garrett et al., 2023a](#); [N. R. Garrett et al., 2023](#)). Based on discussions at the Workshop, we have
226 developed a four-part framework for articulating sources of error in eDNA datasets (Figure 2). In
227 this framework, errors are divided into four categories: (1) false negative detections, where DNA
228 present in the environment is not captured; (2) false negative identifications, where captured DNA
229 cannot be accurately identified; (3) false positive detections, where DNA is correctly identified
230 but should not be present in the sample; and (4) false positive identifications, where DNA is
231 misidentified. Each of these errors stems from different sources, including data collection and
232 assignment, and therefore requires tailored mitigation strategies. For example, improving detection
233 methods may address false negatives, while enhanced bioinformatic pipelines and reference
234 databases can reduce the likelihood of false positive identifications.

235 eDNA datasets are often complicated by false positive detections from laboratory contaminants
236 and ubiquitous signals from humans, agricultural plants and animals, and common fungi. While
237 detection of common contaminants is not unique to airborne eDNA ([Sepulveda, Hutchins, et al.,
238 2020](#)), sampling air presents a unique challenge in that every step of the collection and analysis
239 process is unavoidably conducted in the presence of potentially contaminating air sources. For this
240 reason, it is critical to establish appropriate controls for field sampling and laboratory processing
241 as current methodologies may not adequately address contamination issues specific to airborne
242 eDNA. While most studies include standard blank extraction controls, some have instituted
243 negative filter controls (e.g., filters not exposed to air in the field) see ([Roger et al., 2022](#)), and
244 others also include laboratory air controls (e.g., filters exposed to laboratory air) see ([Littlefair et
245 al., 2023](#)). By using controls to remove background signals, airborne eDNA datasets will be more
246 informative and reliable for management questions.

247 Sources of error stemming from DNA identification can have broad-reaching impacts on
248 management decisions made from eDNA data. For example, biodiversity estimates can be skewed
249 by both forms of false identification. The complexity of this problem was illustrated in a recent
250 study surveying bat biodiversity using airborne eDNA ([N. Garrett et al., 2023b](#); [N. R. Garrett et
251 al., 2023](#)). In this study, Garrett et al (2023a/b) attempted to trace reference sequence provenance
252 and manually curate their identifications using taxon-specific expert advice to confirm species
253 identification but still could not conclusively confirm all detections. Continued improvement of
254 bioinformatics pipelines and reference databases will reduce the likelihood of false identifications.
255 Advanced data processing tools can enhance the reliability of eDNA data interpretation,
256 accounting for error which cannot otherwise be eliminated through control of characterised
257 variables ([Burian et al., 2021](#)). Data processing tools which apply hierarchical occupancy or
258 process-based models have been shown to mitigate the impact of error sources through the
259 estimation of uncertainty related to species detection ([McClenaghan et al., 2020](#)).

260 While best practices in field and laboratory protocols and data interpretation remain important,
261 they are insufficient on their own to negate all sources of error. However, as has been observed in
262 aquatic ecosystem monitoring, data error should not deter managers from utilising eDNA data
263 when eDNA monitoring stands to deliver a means of cost-effective non-invasive species detection
264 ([Jerde, 2021](#)).

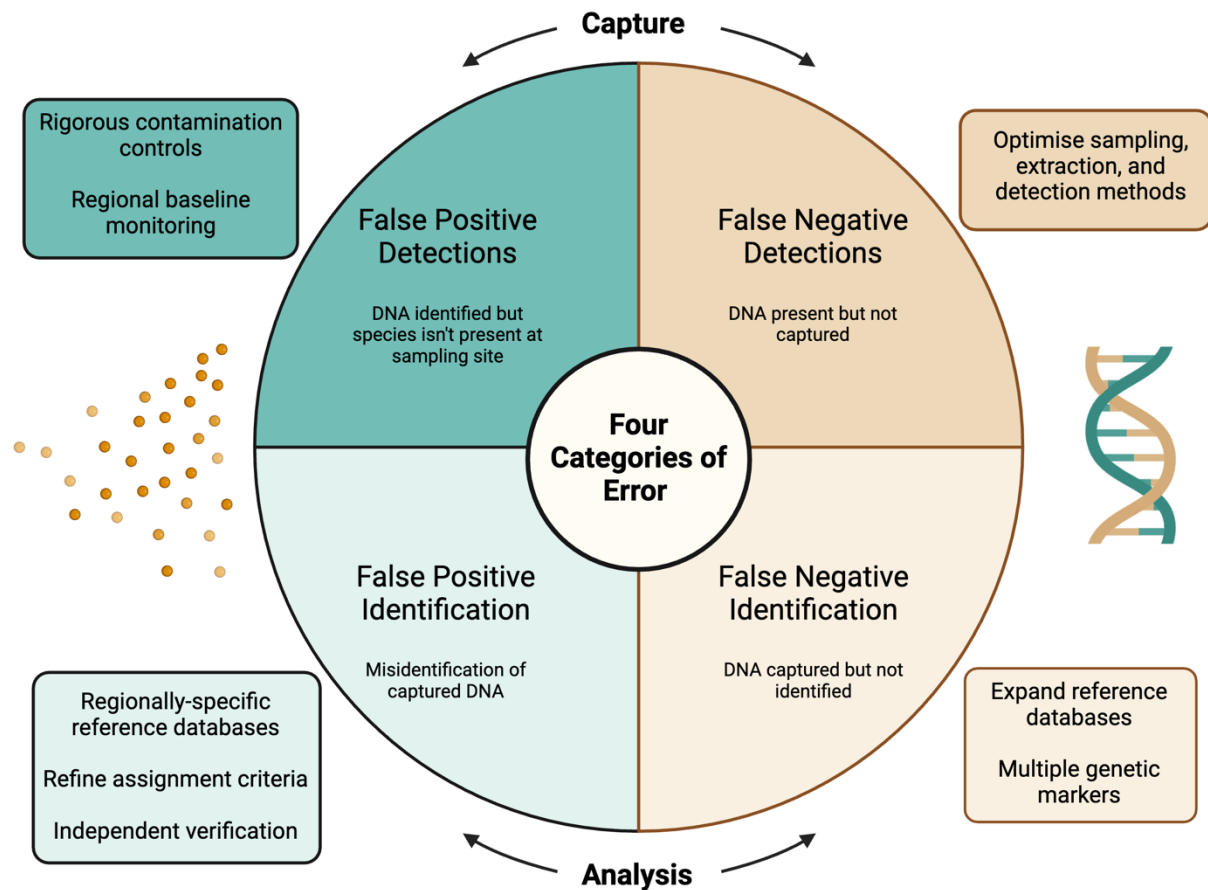
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266

267 **Table 1. Key parameters requiring validation for reliable airborne environmental DNA**
 268 **(eDNA) monitoring**

269 A non-exhaustive list of critical parameters requiring validation to ensure the reliability of airborne eDNA monitoring.
 270 Parameters are grouped into four categories: Technical/experimental, Environmental factors, Ecology of target
 271 species, and Detection limits. For each category, specific parameters, the validation required, and examples of relevant
 272 studies are provided. The δ symbol indicates studies or recommendations made for aquatic eDNA, highlighting
 273 transferable knowledge from existing eDNA research.

Category	Parameters	Validation Required	Examples
Technical/experimental	<ul style="list-style-type: none"> • Sampling methods • Sampling density • Replication • Sample preservation • Bioinformatics • Controls 	<p>Comparisons of sampling methods (e.g., active versus passive).</p> <p>Optimisation of sampling materials.</p> <p>Effects of sampling design (e.g., height of sampler, sampling duration, air volume), DNA preservation solutions and contamination.</p> <p>Selection of bioinformatic cutoffs.</p> <p>Identification of appropriate controls.</p>	<p>Sampling and processing effects on terrestrial plant detection (Mark D Johnson et al., 2019)</p> <p>Sampling impacts on airborne viral detection (Chang et al., 2023)</p> <p>Aquatic study recommendations (Goldberg et al., 2016)^{δ}</p> <p>Sampling and extraction effects in freshwater systems (Deiner et al., 2015)^{δ}</p>
Environmental factors	<ul style="list-style-type: none"> • Weather • UV irradiance • Human activity 	<p>Impact of humidity, temperature, wind direction and speed, UV index, precipitation, air pressure, and local human activity on DNA transport and persistence.</p>	<p>Seasonal weather impact on tree species detection (Hanson et al., 2024)</p> <p>Combined influence of seasonality and human activity on plant detection (Johnson, Cox, et al., 2021)</p> <p>Environmental influence over eDNA particle size in freshwater systems (Barnes et al., 2021)^{δ}</p> <p>eDNA persistence in controlled freshwater system (Barnes et al., 2014)^{δ}</p>
Ecology of target species	<ul style="list-style-type: none"> • Habitat • Behaviour • Life cycle • Species mobility • DNA shedding rates • Shed DNA form 	<p>Influence of species biology on DNA shedding, DNA distribution and detection.</p>	<p>Source locations of eukaryotic species detected in atmospheric dust (Aalismail et al., 2021)</p> <p>Influence of tree species biology on detection (M. D. Johnson et al., 2019)</p> <p>Influence of land-use type and seasonality on airborne bacterial and fungal community composition (Anees-Hill et al., 2022; Bowers et al., 2011; Caliz et al., 2018)</p>
Detection limits	<ul style="list-style-type: none"> • Sensitivity • Inhibition • Error Estimation 	<p>Minimum detection thresholds.</p> <p>Identification of likely inhibitors.</p> <p>Estimating and accounting for error using analysis tools.</p>	<p>qPCR inhibition in indoor air samples (McDevitt et al., 2007)</p> <p>Defining detection limits (Klymus et al., 2020)</p> <p>PCR inhibition in freshwater systems (Buxton et al., 2017; Jane et al., 2015)^{δ}</p> <p>Improving reliability of eDNA data interpretation using statistical models (Burian et al., 2021)</p>



274

275 **Figure 2. Framework for addressing errors in airborne eDNA analysis**

276 Framework for understanding error in eDNA analysis, highlighting four distinct error categories and distinct mitigation strategies.
277 Green and tan indicate positive and negative conclusions, respectively, with the upper and lower halves describing detection and
278 identification errors, respectively.

279

280 Building partnerships and trust in airborne eDNA

281 As airborne eDNA research matures, models of stakeholder engagement used in water and soil
282 eDNA sampling can be adopted to encourage successful implementation ([Morissette et al., 2021](#)).
283 To facilitate stakeholder engagement, early and sustained collaboration with agencies, industries,
284 academic institutions, citizen scientists, and Indigenous communities will be required ([Bonicalza
285 et al., 2024](#)). Given the complexity of integrating genetic data with climatic and ecological
286 information, engaging stakeholders from the outset ensures that research approaches are fit-for-

287 purpose and ethically sound. Best practices should prioritise co-designing studies with Indigenous
288 communities, respecting local contexts and protocols, and adhering to FAIR and CARE data
289 governance principles (www.gida-global.org/care) ([Hutchins et al., 2023](#); [Kukutai & Black, 2024](#)).
290 Frameworks such as the Te Mata Ira and Te Nohonga Kaitiaki Guidelines for Genomic Research
291 with Māori and on Taonga Species from Genomics Aotearoa ([Hudson et al., 2021](#)) and the United
292 States' National Aquatic eDNA Strategy ([Goodwin et al., 2024](#)) provide guidance on Indigenous
293 engagement and should inform study development. Early and intentional engagement with
294 Indigenous communities and management agencies can align scientific goals with practical needs,
295 fostering mutually beneficial and culturally respectful outcomes ([Handsley-Davis et al., 2021](#);
296 [Newton et al., 2025](#); [Wilcox et al., 2008](#)).

297 Stakeholders may approach airborne eDNA analysis with cautious optimism, given its relative
298 early stage as a monitoring tool ([Polling et al., 2024](#)) and the need to build confidence in the
299 reliability of eDNA data for biosecurity and conservation management ([Sepulveda, Nelson, et al.,
300 2020](#)). Effective stakeholder engagement requires researchers to clearly communicate current
301 limitations, set realistic expectations, and emphasise the technology's role as a complementary
302 tool rather than a substitute for traditional methods. Integrating airborne eDNA analysis with
303 established sampling techniques such as camera traps ([Polling et al., 2024](#)), visual surveys
304 ([Johnson, Fokar, et al., 2021](#)), and acoustic monitoring ([N. Garrett et al., 2023b](#)), provides an
305 opportunity to build confidence through corroborative evidence. To facilitate adoption, it is
306 essential to co-design protocols with stakeholders, ensuring alignment with regulatory processes
307 and practical applications. Developing well-defined sampling protocols and robust controls,
308 modelled on those established in aquatic eDNA studies ([Deiner et al., 2018](#); [Deiner et al., 2015](#);
309 [Goldberg et al., 2016](#); [Minamoto et al., 2016](#)), will ultimately contribute to end-user adoption of
310 airborne eDNA methods.

311 The simplicity and accessibility of air sampling provides a powerful opportunity to engage
312 communities in citizen science initiatives, expanding monitoring capabilities ([Palmer et al., 2017](#))
313 while fostering environmental awareness and education ([Isley et al., 2022](#); [Sbrocchi, 2015](#)). By
314 involving citizen science in data collection, programs can leverage public interest and participation
315 to enhance sampling density and geographic coverage. To ensure the success and sustainability of
316 these program, it is essential to follow established frameworks for citizen-scientist engagement
317 that emphasise clear goals, transparent data management, and adaptable protocols ([Kieslinger et
318 al., 2017](#)). An additional benefit of such initiatives is the potential to create biobanking repositories
319 of samples collected by citizen scientists, generating valuable time-series data for future research
320 ([Jarman et al., 2018](#)). Ultimately, effective communication and ongoing collaboration between
321 scientists and participants will be pivotal in building trust and maximising the impact of airborne
322 eDNA initiatives, fostering a shared commitment to biodiversity monitoring and conservation.

323

324 Clear skies ahead?

325 Advancing airborne eDNA analysis as a monitoring tool may transform biodiversity and
326 biosecurity management through the provision of rapid, non-invasive insights into ecosystems at
327 previously unattainable scales. Realising its potential is reliant on overcoming numerous
328 challenges, particularly those concerned with evaluating collection methods, addressing the
329 complexities of airborne eDNA ecology, and accounting for data error. Through focused
330 collaborative research, the field will transition from experimental research to practical application
331 – which is required to bridge the gap between eDNA research and policy ([Lodge, 2022](#)).

332 Integrating airborne eDNA with other monitoring methods, such as remote sensing and traditional
333 field surveys, could expand the scope and resolution of ecosystem assessments, aligning with
334 broader 'one health' approaches that link environmental, animal, and human health ([Childress et
335 al., 2024](#); [Farrell et al., 2021](#)). Using airborne eDNA analysis as a complementary tool broadens
336 understanding of ecosystems, improving our capacity to detect biodiversity loss and biosecurity
337 threats that otherwise go unnoticed. In the future, data generated through airborne eDNA analysis
338 has the potential to become a cornerstone of large-scale monitoring networks, similar to
339 wastewater surveillance for tracking disease outbreaks like COVID-19 ([Bogler et al., 2020](#)).
340 Integration of this monitoring tool into global initiatives like GBiOS could revolutionise how
341 biodiversity is monitored through the provision of standardised data to inform rapid, evidence-
342 based management decisions ([Gonzalez et al., 2024](#)). The capacity of airborne eDNA to integrate
343 genetic information from a wide range of taxonomic groups makes it an ideal candidate for such
344 global initiatives. By providing a unified framework for biodiversity monitoring, airborne eDNA
345 can facilitate the development of global datasets that support comparative ecological research and
346 guide policy at an international scale.

347 If the significant challenges are overcome, airborne eDNA analysis has the potential to
348 revolutionise environmental monitoring, offering innovative ways to observe and protect
349 ecosystems. To realise the potential of this emerging tool, sampling methods should be refined,
350 and robust parameter validation established. Insights gained using airborne eDNA analysis could
351 set new benchmarks in biodiversity, biosecurity, and conservation practices, seeing the technology
352 integrated as a routine part of ecosystem management. As the field matures, airborne eDNA
353 analysis has the potential to transition from an experimental approach to a reliable tool, guiding
354 decision-making at local, national, and global scales and safeguarding natural resources for future
355 generations.

356 References

357 Aalismail, N. A., Díaz-Rúa, R., Geraldi, N., Cusack, M., & Duarte, C. M. (2021). Diversity and Sources
358 of Airborne Eukaryotic Communities (AEC) in the Global Dust Belt over the Red Sea. *Earth
359 Systems and Environment*, 5(2), 459-471. <https://doi.org/10.1007/s41748-021-00219-4>

- 360 Anees-Hill, S., Douglas, P., Pashley, C. H., Hansell, A., & Marczylo, E. L. (2022). A systematic review
361 of outdoor airborne fungal spore seasonality across Europe and the implications for health.
362 *Science of the Total Environment*, 818. <https://doi.org/10.1016/j.scitotenv.2021.151716>
- 363 Atkinson, C. T., & Roy, K. (2023). Environmental monitoring for invasive fungal pathogens of ‘Ōhi‘a
364 (*Metrosideros polymorpha*) on the Island of Hawai‘i. *Biological Invasions*, 25(2), 399-410.
365 <https://doi.org/10.1007/s10530-022-02922-3>
- 366 Banchi, E., Ametrano, C. G., Tordoni, E., Stanković, D., Ongaro, S., Tretiach, M., Pallavicini, A.,
367 Muggia, L., Verardo, P., Tassan, F., Trobiani, N., Moretti, O., Borney, M. F., & Lazzarin, S.
368 (2020). Environmental DNA assessment of airborne plant and fungal seasonal diversity. *The*
369 *Science of the total environment*, 738, 140249-140249.
370 <https://doi.org/10.1016/j.scitotenv.2020.140249>
- 371 Barnes, M. A., Chadderton, W. L., Jerde, C. L., Mahon, A. R., Turner, C. R., & Lodge, D. M. (2021).
372 Environmental conditions influence eDNA particle size distribution in aquatic systems.
373 *Environmental DNA*, 3(3), 643-653.
- 374 Barnes, M. A., Turner, C. R., Jerde, C. L., Renshaw, M. A., Chadderton, W. L., & Lodge, D. M. (2014).
375 Environmental conditions influence eDNA persistence in aquatic systems. *Environmental Science*
376 *& Technology*, 48(3), 1819-1827. <https://doi.org/10.1021/es404734p>
- 377 Bell, K. L., Campos, M., Hoffmann, B. D., Encinas-Viso, F., Hunter, G. C., & Webber, B. L. (2024).
378 Environmental DNA methods for biosecurity and invasion biology in terrestrial ecosystems:
379 Progress, pitfalls, and prospects. *Science of the Total Environment*, 926, 171810.
380 <https://doi.org/10.1016/j.scitotenv.2024.171810>
- 381 Biggs, J., Ewald, N., Valentini, A., Gaboriaud, C., Griffiths, R., Foster, J., Wilkinson, J., Arnett, A.,
382 Williams, P., & Dunn, F. (2014). Analytical and methodological development for improved
383 surveillance of the Great Crested Newt. *Defra Project WC1067*.
- 384 Bogler, A., Packman, A., Furman, A., Gross, A., Kushmaro, A., Ronen, A., Dagot, C., Hill, C., Vaizel-
385 Ohayon, D., Morgenroth, E., Bertuzzo, E., Wells, G., Kiperwas, H. R., Horn, H., Negev, I.,
386 Zucker, I., Bar-Or, I., Moran-Gilad, J., Balcazar, J. L.,...Bar-Zeev, E. (2020). Rethinking
387 wastewater risks and monitoring in light of the COVID-19 pandemic. *Nature Sustainability*,
388 3(12), 981-990. <https://doi.org/10.1038/s41893-020-00605-2>
- 389 Bohmann, K., & Lynggaard, C. (2023). Transforming terrestrial biodiversity surveys using airborne
390 eDNA. *Trends in ecology & evolution*, 38(2), 119-121. <https://doi.org/10.1016/j.tree.2022.11.006>
- 391 Bonicalza, S., Valsecchi, E., Coppola, E., Catapano, V., & Thatcher, H. (2024). Citizen science in eDNA
392 monitoring for Mediterranean monk seal conservation. *BMC Ecology and Evolution*, 24(1), 148.
393 <https://doi.org/10.1186/s12862-024-02338-8>
- 394 Bowers, R. M., McLetchie, S., Knight, R., & Fierer, N. (2011). Spatial variability in airborne bacterial
395 communities across land-use types and their relationship to the bacterial communities of potential
396 source environments. *ISME J*, 5(4), 601-612. <https://doi.org/10.1038/ismej.2010.167>
- 397 Brennan, G. L., Potter, C., de Vere, N., Griffith, G. W., Skjoth, C. A., Osborne, N. J., Wheeler, B. W.,
398 McInnes, R. N., Clewlow, Y., Barber, A., Hanlon, H. M., Hegarty, M., Jones, L., Kurganskiy, A.,
399 Rowney, F. M., Armitage, C., Adams-Groom, B., Ford, C. R., Petch, G. M.,...Creer, S. (2019).

- 400 Temperate airborne grass pollen defined by spatio-temporal shifts in community composition.
401 *Nat Ecol Evol*, 3(5), 750-754. <https://doi.org/10.1038/s41559-019-0849-7>
- 402 Burian, A., Mauvisseau, Q., Bulling, M., Domisch, S., Qian, S., & Sweet, M. (2021). Improving the
403 reliability of eDNA data interpretation. *Molecular ecology resources*, 21(5), 1422-1433.
404 <https://doi.org/10.1111/1755-0998.13367>
- 405 Buxton, A. S., Groombridge, J. J., & Griffiths, R. A. (2017). Is the detection of aquatic environmental
406 DNA influenced by substrate type? *PloS one*, 12(8), e0183371.
407 <https://doi.org/10.1371/journal.pone.0183371>
- 408 Caliz, J., Triado-Margarit, X., Camarero, L., & Casamayor, E. O. (2018). A long-term survey unveils
409 strong seasonal patterns in the airborne microbiome coupled to general and regional atmospheric
410 circulations. *Proceedings of the National Academy of Sciences USA*, 115(48), 12229-12234.
411 <https://doi.org/10.1073/pnas.1812826115>
- 412 Chang, Y., Wang, Y., Li, W., Wei, Z., Tang, S., & Chen, R. (2023). Mechanisms, Techniques and
413 Devices of Airborne Virus Detection: A Review. *International Journal of Environmental*
414 *Research and Public Health*, 20(8). <https://doi.org/10.3390/ijerph20085471>
- 415 Childress, J., Faust, C. L., & Deiner, K. (2024). Introduction to special issue: Advancing disease ecology
416 through eDNA monitoring of infectious agents. *Environmental DNA*, 6(1).
417 <https://doi.org/10.1002/edn3.502>
- 418 Clare, E. L., Economou, C. K., Bennett, F. J., Dyer, C. E., Adams, K., McRobie, B., Drinkwater, R., &
419 Littlefair, J. E. (2022). Measuring biodiversity from DNA in the air. *Current biology*, 32(3), 693-
420 700.e695. <https://doi.org/10.1016/j.cub.2021.11.064>
- 421 Clare, E. L., Economou, C. K., Faulkes, C. G., Gilbert, J. D., Bennett, F., Drinkwater, R., & Littlefair, J.
422 E. (2021). eDNAir: proof of concept that animal DNA can be collected from air sampling. *PeerJ*,
423 9, e11030-e11030. <https://doi.org/10.7717/peerj.11030>
- 424 Deiner, K., Lopez, J., Bourne, S., Holman, L. E., Seymour, M., Grey, E. K., Lacoursière-Roussel, A., Li,
425 Y., Renshaw, M. A., & Pfrender, M. E. (2018). Optimising the detection of marine taxonomic
426 richness using environmental DNA metabarcoding: the effects of filter material, pore size and
427 extraction method. *Metabarcoding and Metagenomics*, 2, e28963.
- 428 Deiner, K., Walser, J. C., Mächler, E., & Altermatt, F. (2015). Choice of capture and extraction methods
429 affect detection of freshwater biodiversity from environmental DNA. *Biological Conservation*,
430 183, 53-63. <https://doi.org/10.1016/j.biocon.2014.11.018>
- 431 Després, V. R., Huffman, J. A., Burrows, S. M., Hoose, C., Safatov, A. S., Buryak, G., Fröhlich-
432 Nowoisky, J., Elbert, W., Andreae, M. O., Pöschl, U., & Jaenicke, R. (2012). Primary biological
433 aerosol particles in the atmosphere: a review. *Tellus Series B-Chemical and Physical*
434 *Meteorology*, 64. <https://doi.org/ARTN10.3402/tellusb.v64i0.15598>
- 435 Farrell, J. A., Whitmore, L., & Duffy, D. J. (2021). The Promise and Pitfalls of Environmental DNA and
436 RNA Approaches for the Monitoring of Human and Animal Pathogens from Aquatic Sources.
437 *Bioscience*, 71(6), 609-625. <https://doi.org/10.1093/biosci/biab027>

- 438 Ficetola, G. F., Miaud, C., Pompanon, F., & Taberlet, P. (2008). Species detection using environmental
439 DNA from water samples. *Biology Letters*, 4(4), 423-425. <https://doi.org/10.1098/rsbl.2008.0118>
- 440 Foster, N. R., Martin, B., Hoogewerff, J., Aberle, M. G., de Caritat, P., Roffey, P., Edwards, R., Malik,
441 A., Thwaites, P., Waycott, M., & Young, J. (2023). The utility of dust for forensic intelligence:
442 Exploring collection methods and detection limits for environmental DNA, elemental and
443 mineralogical analyses of dust samples. *Forensic science international*, 344, 111599-111599.
444 <https://doi.org/10.1016/j.forsciint.2023.111599>
- 445 Furlan, E. M., Davis, J., & Duncan, R. P. (2020). Identifying error and accurately interpreting
446 environmental DNA metabarcoding results: A case study to detect vertebrates at arid zone
447 waterholes. *Molecular Ecology Resources*, 20(5), 1259-1276. [https://doi.org/10.1111/1755-
448 0998.13170](https://doi.org/10.1111/1755-0998.13170)
- 449 Garrett, N., Watkins, J., Francis, C. M., Simmons, N. B., Ivanova, N., Naaum, A., Briscoe, A.,
450 Drinkwater, R., & Clare, E. L. (2023a). Out of thin air: surveying tropical bat roosts through air
451 sampling of eDNA. *PeerJ (San Francisco, CA)*, 11, e14772-e14772.
452 <https://doi.org/10.7717/peerj.14772>
- 453 Garrett, N., Watkins, J., Francis, C. M., Simmons, N. B., Ivanova, N., Naaum, A., Briscoe, A.,
454 Drinkwater, R., & Clare, E. L. (2023b). Out of thin air: surveying tropical bat roosts through air
455 sampling of eDNA. *PeerJ*, 11, e14772-e14772. <https://doi.org/10.7717/peerj.14772>
- 456 Garrett, N. R., Watkins, J., Simmons, N. B., Fenton, B., Maeda-Obregon, A., Sanchez, D. E., Froehlich,
457 E. M., Walker, F. M., Littlefair, J. E., & Clare, E. L. (2023). Airborne eDNA documents a diverse
458 and ecologically complex tropical bat and other mammal community. *Environmental DNA*, 5(2),
459 350-362.
- 460 Geller, K., & Partridge, C. (2025). Evaluation of two environmental DNA (eDNA) approaches for
461 monitoring hemlock woolly adelgid (HWA). *MicroPubl Biol*, 2025.
462 <https://doi.org/10.17912/micropub.biology.001346>
- 463 Goldberg, C. S., Turner, C. R., Deiner, K., Klymus, K. E., Thomsen, P. F., Murphy, M. A., Spear, S. F.,
464 McKee, A., Oyler-McCance, S. J., Cornman, R. S., Laramie, M. B., Mahon, A. R., Lance, R. F.,
465 Pilliod, D. S., Strickler, K. M., Waits, L. P., Fremier, A. K., Takahara, T., Herder, J. E., &
466 Taberlet, P. (2016). Critical considerations for the application of environmental DNA methods to
467 detect aquatic species. *Methods in Ecology and Evolution*, 7(11), 1299-1307.
468 <https://doi.org/10.1111/2041-210x.12595>
- 469 Gonzalez, A., Vihervaara, P., Balvanera, P., Bates, A. E., Bayraktarov, E., Bellingham, P. J., Bruder, A.,
470 Campbell, J., Catchen, M. D., Cavender-Bares, J., Chase, J., Coops, N., Costello, M. J., Czucz,
471 B., Delavaud, A., Dornelas, M., Dubois, G., Duffy, E. J., Eggermont, H.,...Torrelío, C. Z. (2024).
472 A global biodiversity observing system to unite monitoring and guide action. *Nature Ecology &*
473 *Evolution*, 8(1), 175-175. <https://doi.org/10.1038/s41559-023-02263-x>
- 474 Goodwin, K. D., Aiello, C. M., Weise, M., Edmondson, M., Fillingham, K., Allen, D., Amerson, A.,
475 Barton, M. L., Benson, A., Canonico, G., Gold, Z., Gumm, J., Hunter, M., Joffe, N., Lance, R.,
476 Larkin, A., Letelier, R., Lipsky, C., McCoskey, D.,...White, T. (2024). *National Aquatic*
477 *Environmental DNA Strategy*. T. White House Office of Science, and Policy (OSTP).

- 478 Gregoric, M., Kutnjak, D., Bacnik, K., Gostincar, C., Pecman, A., Ravnikar, M., & Kuntner, M. (2022).
479 Spider webs as eDNA samplers: Biodiversity assessment across the tree of life. *Mol Ecol Resour*,
480 22(7), 2534-2545. <https://doi.org/10.1111/1755-0998.13629>
- 481 Gusareva, E. S., Gaultier, N. E., Uchida, A., Premkrishnan, B. N. V., Heinle, C. E., Phung, W. J., Wong,
482 A., Lau, K. J. X., Yap, Z. H., Koh, Y., Ang, P. N., Putra, A., Panicker, D., Lee, J. G. H., Neves,
483 L. C., Drautz-Moses, D. I., & Schuster, S. C. (2022). Short-range contributions of local sources to
484 ambient air. *PNAS nexus*, 1(2). <https://doi.org/10.1093/pnasnexus/pgac043>
- 485 Handsley-Davis, M., Kowal, E., Russell, L., & Weyrich, L. S. (2021). Researchers using environmental
486 DNA must engage ethically with Indigenous communities. *Nature Ecology & Evolution*, 5(2),
487 146-148. <https://doi.org/10.1038/s41559-020-01351-6>
- 488 Hanson, M., Petch, G., Adams-Groom, B., Ottosen, T. B., & Skjoth, C. A. (2024). Storms facilitate
489 airborne DNA from leaf fragments outside the main tree pollen season. *Aerobiologia*.
490 <https://doi.org/10.1007/s10453-024-09826-w>
- 491 Harrison, J. B., Sunday, J. M., & Rogers, S. M. (2019). Predicting the fate of eDNA in the environment
492 and implications for studying biodiversity. *Proceedings of the Royal Society B*, 286(1915),
493 20191409. <https://doi.org/10.1098/rspb.2019.1409>
- 494 Hudson, M., Thompson, A., Wilcox, P., Mika, J., Battershill, C., Stott, M., Brooks, R. T., & Warbrick, L.
495 (2021). *Te Nohonga Kaitiaki guidelines for genomic research on Taonga species*. Te Kotahi
496 Research Institute.
- 497 Hutchins, L., Mc Cartney, A., Graham, N., Gillespie, R., & Guzman, A. (2023). Arthropods are kin:
498 Operationalizing Indigenous data sovereignty to respectfully utilize genomic data from
499 Indigenous lands. *Molecular ecology resources*. <https://doi.org/10.1111/1755-0998.13822>
- 500 Isley, C. F., Fry, K. L., Sharp, E. L., & Taylor, M. P. (2022). Bringing citizen science to life: Evaluation
501 of a national citizen science program for public benefit. *Environmental Science & Policy*, 134,
502 23-33. <https://doi.org/10.1016/j.envsci.2022.03.015>
- 503 Jane, S. F., Wilcox, T. M., McKelvey, K. S., Young, M. K., Schwartz, M. K., Lowe, W. H., Letcher, B.
504 H., & Whiteley, A. R. (2015). Distance, flow and PCR inhibition: eDNA dynamics in two
505 headwater streams. *Molecular ecology resources*, 15(1), 216-227. <https://doi.org/10.1111/1755-0998.12285>
- 507 Jarman, S. N., Berry, O., & Bunce, M. (2018). The value of environmental DNA biobanking for long-
508 term biomonitoring. *Nature Ecology & Evolution*, 2(8), 1192-1193.
509 <https://doi.org/10.1038/s41559-018-0614-3>
- 510 Jerde, C. L. (2021). Can we manage fisheries with the inherent uncertainty from eDNA? *Journal of Fish*
511 *Biology*, 98(2), 341-353. <https://doi.org/https://doi.org/10.1111/jfb.14218>
- 512 Jo, T., & Minamoto, T. (2021). Complex interactions between environmental DNA (eDNA) state and
513 water chemistries on eDNA persistence suggested by meta-analyses. *Molecular Ecology*
514 *Resources*, 21(5), 1490-1503. <https://doi.org/10.1111/1755-0998.13354>

- 515 Johnson, M., & Barnes, M. A. (2024). Macrobial airborne environmental DNA analysis: A review of
516 progress, challenges, and recommendations for an emerging application. *Molecular ecology*
517 *resources*, 24(7), e13998. <https://doi.org/10.1111/1755-0998.13998>
- 518 Johnson, M. D., Barnes, M. A., Garrett, N. R., & Clare, E. L. (2023). Answers blowing in the wind:
519 Detection of birds, mammals, and amphibians with airborne environmental DNA in a natural
520 environment over a yearlong survey. *Environmental DNA*, 5(2), 375-387.
521 <https://doi.org/10.1002/edn3.388>
- 522 Johnson, M. D., Cox, R. D., & Barnes, M. A. (2019). Analyzing airborne environmental DNA: A
523 comparison of extraction methods, primer type, and trap type on the ability to detect airborne
524 eDNA from terrestrial plant communities. *Environmental DNA*, 1(2), 176-185.
- 525 Johnson, M. D., Cox, R. D., & Barnes, M. A. (2019). The detection of a non-anemophilous plant species
526 using airborne eDNA. *PLoS One*, 14(11), e0225262.
527 <https://doi.org/10.1371/journal.pone.0225262>
- 528 Johnson, M. D., Cox, R. D., Grisham, B. A., Lucia, D., & Barnes, M. A. (2021). Airborne eDNA Reflects
529 Human Activity and Seasonal Changes on a Landscape Scale. *Frontiers in Environmental*
530 *Science*, 8. <https://doi.org/10.3389/fenvs.2020.563431>
- 531 Johnson, M. D., Fokar, M., Cox, R. D., & Barnes, M. A. (2021). Airborne environmental DNA
532 metabarcoding detects more diversity, with less sampling effort, than a traditional plant
533 community survey. *BMC Ecology and Evolution*, 21(1), 218. [https://doi.org/10.1186/s12862-021-](https://doi.org/10.1186/s12862-021-01947-x)
534 [01947-x](https://doi.org/10.1186/s12862-021-01947-x)
- 535 Kestel, J. H., Field, D. L., Bateman, P. W., White, N. E., Allentoft, M. E., Hopkins, A. J. M., Gibberd,
536 M., & Nevill, P. (2022). Applications of environmental DNA (eDNA) in agricultural systems:
537 Current uses, limitations and future prospects. *Science of the Total Environment*, 847, 157556.
538 <https://doi.org/10.1016/j.scitotenv.2022.157556>
- 539 Kieslinger, B., Schäfer, T., Heigl, F., Dörler, D., Richter, A., & Bonn, A. (2017). The challenge of
540 evaluation: An open framework for evaluating citizen science activities. *SocArXiv*.
541 <https://doi.org/10.31235/osf.io/enzc9>
- 542 Klymus, K. E., Merkes, C. M., Allison, M. J., Goldberg, C. S., Helbing, C. C., Hunter, M. E., Jackson, C.
543 A., Lance, R. F., Mangan, A. M., & Monroe, E. M. (2020). Reporting the limits of detection and
544 quantification for environmental DNA assays. *Environmental DNA*, 2(3), 271-282.
- 545 Kraaijeveld, K., de Weger, L. A., Ventayol García, M., Buermans, H., Frank, J., Hiemstra, P. S., & den
546 Dunnen, J. T. (2015). Efficient and sensitive identification and quantification of airborne pollen
547 using next-generation DNA sequencing. *Molecular ecology resources*, 15(1), 8-16.
548 <https://doi.org/10.1111/1755-0998.12288>
- 549 Kukutai, T., & Black, A. (2024). CARE-ing for Indigenous nonhuman genomic data—rethinking our
550 approach. *Science*, 385(6708), eadr2493.
- 551 Lennartz, C., Kurucar, J., Coppola, S., Cramer, J., Bobrow, J., Bortolin, L., & Comolli, J. (2021).
552 Geographic source estimation using airborne plant environmental DNA in dust. *Scientific reports*,
553 11(1), 16238-16212. <https://doi.org/10.1038/s41598-021-95702-3>

- 554 Littlefair, J. E., Allerton, J. J., Brown, A. S., Butterfield, D. M., Robins, C., Economou, C. K., Garrett, N.
555 R., & Clare, E. L. (2023). Air-quality networks collect environmental DNA with the potential to
556 measure biodiversity at continental scales. *Current Biology*, 33(11), R426-R428.
557 <https://doi.org/10.1016/j.cub.2023.04.036>
- 558 Lodge, D. M. (2022). Policy action needed to unlock eDNA potential. *Frontiers in Ecology and the*
559 *Environment*, 20(8), 448-449. <https://doi.org/10.1002/fee.2563>
- 560 Lynggaard, C., Bertelsen, M. F., Jensen, C. V., Johnson, M. S., Frøslev, T. G., Olsen, M. T., & Bohmann,
561 K. (2022). Airborne environmental DNA for terrestrial vertebrate community monitoring.
562 *Current biology*, 32(3), 701-707.e705. <https://doi.org/10.1016/j.cub.2021.12.014>
- 563 Lynggaard, C., Frøslev, T. G., Johnson, M. S., Olsen, M. T., & Bohmann, K. (2024). Airborne
564 environmental DNA captures terrestrial vertebrate diversity in nature. *Molecular ecology*
565 *resources*, 24(1), e13840-n/a. <https://doi.org/10.1111/1755-0998.13840>
- 566 Madden, A. A., Barberan, A., Bertone, M. A., Menninger, H. L., Dunn, R. R., & Fierer, N. (2016). The
567 diversity of arthropods in homes across the United States as determined by environmental DNA
568 analyses. *Mol Ecol*, 25(24), 6214-6224. <https://doi.org/10.1111/mec.13900>
- 569 McClenaghan, B., Compson, Z. G., & Hajibabaei, M. (2020). Validating metabarcoding-based
570 biodiversity assessments with multi-species occupancy models: A case study using coastal marine
571 eDNA. *PloS one*, 15(3), e0224119-e0224119. <https://doi.org/10.1371/journal.pone.0224119>
- 572 McDevitt, J. J., Lees, P. S. J., Merz, W. G., & Schwab, K. J. (2007). Inhibition of quantitative PCR
573 analysis of fungal conidia associated with indoor air particulate matter. *Aerobiologia*, 23(1), 35-
574 45. <https://doi.org/10.1007/s10453-006-9047-6>
- 575 Minamoto, T., Naka, T., Moji, K., & Maruyama, A. (2016). Techniques for the practical collection of
576 environmental DNA: filter selection, preservation, and extraction. *Limnology*, 17(1), 23-32.
577 <https://doi.org/10.1007/s10201-015-0457-4>
- 578 Morisette, J., Burgiel, S., Brantley, K., Daniel, W. M., Darling, J., Davis, J., Franklin, T., Gaddis, K.,
579 Hunter, M., Lance, R., Leskey, T., Passamaneck, Y., Piaggio, A., Rector, B., Sepulveda, A.,
580 Smith, M., Stepien, C. A., & Wilcox, T. (2021). Strategic considerations for invasive species
581 managers in the utilization of environmental DNA (eDNA): steps for incorporating this powerful
582 surveillance tool. *Manag Biol Invasion*, 12(3), 747-775. <https://doi.org/10.3391/mbi.2021.12.3.15>
- 583 Newton, J. P., Allentoft, M. E., Bateman, P. W., van der Heyde, M., & Nevill, P. (2025). Targeting
584 Terrestrial Vertebrates With eDNA: Trends, Perspectives, and Considerations for Sampling.
585 *Environmental DNA*, 7(1), e70056. <https://doi.org/10.1002/edn3.70056>
- 586 Newton, J. P., Nevill, P., Bateman, P. W., Campbell, M. A., & Allentoft, M. E. (2024). Spider webs
587 capture environmental DNA from terrestrial vertebrates. *Isience*, 27(2).
588 <https://doi.org/10.3402/tellusb.v64i0.15598>
- 589 Palmer, J. R. B., Oltra, A., Collantes, F., Delgado, J. A., Lucientes, J., Delacour, S., Bengoa, M., Eritja,
590 R., & Bartumeus, F. (2017). Citizen science provides a reliable and scalable tool to track disease-
591 carrying mosquitoes. *Nature Communications*, 8. <https://doi.org/10.1038/s41467-017-00914-9>

- 592 Pawlowski, J., Apothéloz-Perret-Gentil, L., & Altermatt, F. (2020). Environmental DNA: What's behind
593 the term? Clarifying the terminology and recommendations for its future use in biomonitoring.
594 *Molecular ecology*, 29(22), 4258-4264. <https://doi.org/10.1111/mec.15643>
- 595 Polling, M., Buij, R., Laros, I., & de Groot, G. A. (2024). Continuous daily sampling of airborne eDNA
596 detects all vertebrate species identified by camera traps. *Environmental DNA*, 6(4).
597 <https://doi.org/10.1002/edn3.591>
- 598 Rodriguez-Ezpeleta, N., Morissette, O., Bean, C. W., Manu, S., Banerjee, P., Lacoursière-Roussel, A.,
599 Beng, K. C., Alter, S. E., Roger, F., Holman, L. E., Stewart, K. A., Monaghan, M. T.,
600 Mauvisseau, Q., Mirimin, L., Wangenstein, O. S., Antognazza, C. M., Helyar, S. J., Boer, H.,
601 Monchamp, M. E.,...Deiner, K. (2021). Trade-offs between reducing complex terminology and
602 producing accurate interpretations from environmental DNA: Comment on “Environmental
603 DNA: What's behind the term?” by Pawlowski et al., (2020). *Molecular ecology*, 30(19), 4601-
604 4605. <https://doi.org/10.1111/mec.15942>
- 605 Roger, F., Ghanavi, H. R., Danielsson, N., Wahlberg, N., Löndahl, J., Pettersson, L. B., Andersson, G. K.
606 S., Boke Olén, N., & Clough, Y. (2022). Airborne environmental DNA metabarcoding for the
607 monitoring of terrestrial insects—A proof of concept from the field. *Environmental DNA*, 4(4),
608 790-807. <https://doi.org/10.1002/edn3.290>
- 609 Rowney, F. M., Brennan, G. L., Skjøth, C. A., Griffith, G. W., McInnes, R. N., Clewlow, Y., Adams-
610 Groom, B., Barber, A., de Vere, N., Economou, T., Hegarty, M., Hanlon, H. M., Jones, L.,
611 Kurganskiy, A., Petch, G. M., Potter, C., Rafiq, A. M., Warner, A., Wheeler, B.,...Creer, S.
612 (2021). Environmental DNA reveals links between abundance and composition of airborne grass
613 pollen and respiratory health. *Current biology*, 31(9), 1995-2003.e1994.
614 <https://doi.org/10.1016/j.cub.2021.02.019>
- 615 Runnel, K., Lohmus, P., Kuengas, K., Marmor-Ohtla, L., Palo, A., Pütsepp, G., Tamm, H., Tammekänd,
616 I., & Lohmus, A. (2024). Aerial eDNA contributes vital information for fungal biodiversity
617 assessment. *Journal of Applied Ecology*. <https://doi.org/10.1111/1365-2664.14691>
- 618 Sanders, M., Tardani, R., Locher, A., Geller, K., & Partridge, C. G. (2023). Development of Novel Early
619 Detection Technology for Hemlock Woolly Adelgid, *Adelges tsugae* (Hemiptera: Adelgidae).
620 *Journal of economic entomology*, 116(1), 168-180. <https://doi.org/10.1093/jee/toac175>
- 621 Sbrocchi, C. (2015). Building Australia through Citizen Science. *Office of the Chief Scientist Occasional
622 Paper Series*.
- 623 Schlegel, M., Treindl, A. D., Panziera, J., Zengerer, V., Zani, D., Brannhage, J., & Gross, A. (2024). A
624 case study on the application of spore sampling for the monitoring of macrofungi. *Mol Ecol
625 Resour*, 24(4), e13941. <https://doi.org/10.1111/1755-0998.13941>
- 626 Sepulveda, A. J., Hutchins, P. R., Forstchen, M., Mckeefry, M. N., & Swigris, A. M. (2020). The elephant
627 in the lab (and field): Contamination in aquatic environmental DNA studies. *Frontiers in Ecology
628 and Evolution*, 8, 609973.
- 629 Sepulveda, A. J., Nelson, N. M., Jerde, C. L., & Luikart, G. (2020). Are environmental DNA methods
630 ready for aquatic invasive species management? *Trends in ecology & evolution*, 35(8), 668-678.

- 631 Shogren, A. J., Tank, J. L., Andruszkiewicz, E., Olds, B., Mahon, A. R., Jerde, C. L., & Bolster, D.
632 (2017). Controls on eDNA movement in streams: Transport, Retention, and Resuspension.
633 *Scientific Reports*, 7(1), 5065. <https://doi.org/10.1038/s41598-017-05223-1>
- 634 Trujillo-González, A., Thuo, D. N., Divi, U., Sparks, K., Wallenius, T., & Gleeson, D. (2022). Detection
635 of Khapra Beetle Environmental DNA Using Portable Technologies in Australian Biosecurity.
636 *Frontiers in insect science*, 2, 795379-795379. <https://doi.org/10.3389/finsc.2022.795379>
- 637 Whittington, J., Heuer, K., Hunt, B., Hebblewhite, M., & Lukacs, P. M. (2015). Estimating occupancy
638 using spatially and temporally replicated snow surveys. *Animal Conservation*, 18(1), 92-101.
639 <https://doi.org/10.1111/acv.12140>
- 640 Wilcox, P. L., Charity, J. A., Roberts, M. R., Tauwhare, S., Tipene-Matua, B., Kereama-Royal, I., Hunter,
641 R., Kani, H. M., & Moke-Delaneyz, P. (2008). A values-based process for cross-cultural dialogue
642 between scientists and Maori. *Journal of the Royal Society of New Zealand*, 38(3), 215-227.
643 <https://doi.org/10.1080/03014220809510555>
- 644 Xu, C. C. Y., Yen, I. J., Bowman, D., & Turner, C. R. (2015). Spider Web DNA: A New Spin on
645 Noninvasive Genetics of Predator and Prey. *PloS one*, 10(11).
646 <https://doi.org/10.1371/journal.pone.0142503>
- 647