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Review

# Expanding the Horizons of DNA Barcoding: Mini-Barcodes and Alternative Genes in Biodiversity Assessment

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**Abstract:** DNA barcoding has emerged as a transformative tool in the realm of biodiversity assessment, facilitating rapid and precise species identification. This review article delves into the evolving landscape of DNA barcoding, with a particular focus on the emergence of mini-barcodes and alternative genes as innovative approaches. Traditional DNA barcoding, anchored in the COI gene, has significantly advanced our understanding of species diversity; however, inherent challenges persist, especially when dealing with degraded samples or taxonomic groups where COI falls short. The introduction of mini-barcodes, characterized by their reduced sequence length, has revolutionized DNA barcoding by expanding its applicability. We explore the utility of mini-barcodes in various scenarios, ranging from DNA extraction from ancient or fragmented specimens to in-field identification using portable sequencing technologies. Case studies and practical insights into their effectiveness are presented, emphasizing their role in overcoming traditional limitations. Alternative genes, a complementary facet of DNA barcoding, offer a novel avenue for enhancing taxonomic resolution and accuracy. This review showcases instances where researchers have harnessed alternative genes to overcome COI's constraints, particularly in diverse taxonomic groups, such as fungi, plants, and microorganisms. The selection of these genes is discussed, along with their potential to uncover hidden biodiversity and improve species delimitation. Examining the broader implications of mini-barcodes and alternative genes, we unveil their pivotal roles in advancing conservation efforts, forensic science, and citizen science initiatives. The adaptable nature of these approaches empowers a diverse range of stakeholders, from scientists conducting critical research to concerned citizens contributing to our collective understanding of the natural world. Looking ahead, we envision an exciting future for DNA barcoding, as these innovations continue to evolve. Integration with cutting-edge sequencing technologies, data analysis methods, and the harnessing of big data hold immense potential. Nonetheless, challenges related to standardization, scalability, and data sharing persist.

**Keywords:** DNA barcoding; mini-barcodes; alternative genes; biodiversity assessment; taxonomic resolution; conservation genetics; species identification

## 1. Introduction

Biodiversity, the intricate tapestry of life on Earth, is central to our understanding of ecosystems, ecological processes, and the sustainable management of our planet's resources. Yet, uncovering and documenting this vast diversity of species has been a formidable challenge for biologists and ecologists for centuries. In the quest to decipher the identity of species, DNA barcoding has emerged as a transformative tool, akin to a universal translator in the realm of biodiversity assessment. This review article embarks on a journey into the expanding horizons of DNA barcoding, casting light on two groundbreaking innovations: mini-barcodes and alternative genes. The traditional anchor of DNA barcoding has been the mitochondrial cytochrome c oxidase subunit 1 (COI) gene [1]. The COI gene's utility in identifying species has revolutionized the field, enabling researchers to swiftly and accurately identify a vast array of organisms by analyzing a short, standardized DNA sequence [2]. Yet, the relentless pursuit of knowledge often leads us to uncharted territories, revealing challenges that beckon innovation. Dealing with degraded or minute DNA samples is a persistent hurdle in

biodiversity research, often requiring Herculean efforts for successful DNA extraction and sequencing. Mini-barcodes, characterized by their reduced sequence length, have emerged as a beacon of hope in this struggle [3]. These shorter sequences, typically spanning 200-300 base pairs, present a nimble alternative to the traditional COI gene, particularly in scenarios where DNA quality is compromised [4].

In this review, we navigate through the utility of mini-barcodes, showcasing their effectiveness in various contexts. From extracting ancient DNA specimens trapped in time to the in-field utilization of portable sequencing technologies, mini-barcodes have redefined the boundaries of DNA barcoding [5]. Through case studies and practical insights, we explore how these miniature genetic markers conquer the traditional limitations, ushering in an era of enhanced applicability in biodiversity assessment [6]. While the COI gene has been a stalwart companion in DNA barcoding, it is not a universal panacea. Taxonomic groups such as fungi, plants, and microorganisms often elude its grasp, necessitating a broader arsenal of genetic markers. Alternative genes, a complementary facet of DNA barcoding, offer a novel avenue for enhancing taxonomic resolution and accuracy [7]. In this review, we shine a spotlight on the promising world of alternative genes. By delving into instances where researchers have harnessed these genetic markers, we unveil their potential to surmount COI's constraints, particularly in taxonomically diverse groups [8]. The process of selecting these genes, guided by their suitability for specific research objectives, emerges as a pivotal consideration, further enriching our understanding of their role in DNA barcoding. Beyond the laboratory and the taxonomist's desk, the innovations of mini-barcodes and alternative genes carry profound implications for biodiversity conservation, forensic science, and citizen science initiatives [9]. These adaptable approaches empower a diverse range of stakeholders, from scientists conducting critical research to concerned citizens contributing to our collective understanding of the natural world. As we peer into the future, the DNA barcoding landscape appears poised for evolution. Integration with cutting-edge sequencing technologies, data analysis methods, and the harnessing of big data hold immense potential. However, challenges related to

## 2. Literature Review

### 2.1. Unveiling the Power of DNA Barcoding

Biodiversity, the dazzling array of life that populates our planet, is a source of endless fascination and scientific inquiry. From the humblest microbes to the mightiest mammals, every species plays a unique role in the intricate web of life, shaping ecosystems and sustaining our planet's health. Yet, despite centuries of exploration and taxonomic cataloging, we have only scratched the surface of Earth's biological diversity [1].

The task of identifying, cataloging, and understanding the millions of species that inhabit our planet has been a Herculean challenge. Traditional taxonomy, reliant on morphological features, has been invaluable but fraught with limitations, especially in cases of cryptic species or organisms with indistinct characteristics [2]. It was clear that a transformative tool was needed, one capable of rapidly and precisely identifying species across the vast spectrum of life forms.

#### The Quest for Precise Species Identification

In the quest for a universal species identification tool, the concept of DNA barcoding emerged as a beacon of hope. DNA barcoding, fundamentally grounded in molecular genetics, offered the promise of overcoming the taxonomic hurdles that had confounded traditional taxonomy. The essence of DNA barcoding lies in the analysis of short, standardized DNA sequences from specific genetic regions, enabling the identification of species through their unique genetic signatures [3].

This innovative approach heralded a new era in biodiversity assessment, revolutionizing the way we explore, document, and conserve Earth's biological riches. DNA barcoding promised not only to accelerate species identification but also to facilitate the discovery of previously unknown or cryptic species, ultimately enhancing our understanding of the natural world [4].

## COI Gene: The Traditional Anchor

At the heart of DNA barcoding lies the mitochondrial cytochrome c oxidase subunit 1 (COI) gene, affectionately known as the “barcode of life” [5]. The COI gene’s choice as the standard barcode marker was no accident; its characteristics, such as evolutionary conservation across animal taxa and a comparatively high mutation rate, made it an ideal candidate for species discrimination [6].

The COI gene’s utility in species identification has been a hallmark of DNA barcoding, enabling researchers to venture into diverse ecosystems and swiftly identify species without the need for specialized taxonomic expertise [7]. Its standardized nature has facilitated the creation of reference databases, such as the Barcode of Life Data Systems (BOLD), which have grown to become invaluable resources for the global scientific community [8].

However, even as COI became the cornerstone of DNA barcoding, challenges remained. Some taxonomic groups showed resistance to COI-based identification, while the fragmentation and degradation of DNA in environmental samples presented hurdles that needed to be overcome [9]. This led to the emergence of two pioneering innovations: mini-barcodes and alternative genes. These innovations, explored in detail in subsequent sections, expanded the horizons of DNA barcoding, offering novel solutions to address the limitations that COI-based barcoding encountered [10].

As we embark on this journey into the expanding realm of DNA barcoding, we will unravel the potential of mini-barcodes and alternative genes in overcoming these challenges. These innovations have ushered in a new era in biodiversity assessment, propelling us toward a more comprehensive understanding of the intricate tapestry of life on Earth.

## 2.2. Mini-Barcodes: Redefining DNA Barcoding

### Mini-Barcodes: A Glimpse into the Future

In the ever-evolving landscape of DNA barcoding, mini-barcodes have emerged as a revolutionary concept, promising to redefine the field’s possibilities. These truncated genetic markers, often spanning 200-300 base pairs, represent a compact alternative to the traditional, longer COI gene. Mini-barcodes have opened doors to new frontiers in DNA barcoding by addressing fundamental challenges and expanding the applicability of the technique [1].

### Overcoming DNA Extraction Challenges

One of the primary challenges that mini-barcodes successfully address is the extraction of DNA from challenging samples. In biodiversity research, ancient or degraded specimens, as well as those preserved in suboptimal conditions, pose significant hurdles. Mini-barcodes, with their shorter sequences, provide a lifeline for researchers striving to obtain DNA from such samples, where conventional methods often fail [2].

### Portable Sequencing Technologies: In-Field Identification

Advances in sequencing technologies have given rise to portable, hand-held sequencers capable of delivering real-time DNA analysis even in remote field settings. Mini-barcodes, owing to their reduced sequence length, are well-suited for integration with these cutting-edge technologies. This convergence of mini-barcodes and portable sequencing devices has transformed DNA barcoding into a field-friendly tool for in-situ species identification [3].

### Case Studies: Mini-Barcodes in Action

The true power of mini-barcodes becomes evident when we examine their application in real-world scenarios. Through a series of case studies and practical insights, we delve into how mini-barcodes have revolutionized DNA barcoding. From resolving taxonomic uncertainties in cryptic species complexes to identifying organisms in challenging environments, these case studies underscore the versatility and efficacy of mini-barcodes in biodiversity research [4].

As we journey deeper into the realm of mini-barcodes, we unravel the potential they hold in advancing DNA barcoding and the broader field of biological science. Mini-barcodes offer a glimpse into a future where the barriers to DNA extraction and species identification are diminished, enabling researchers to explore previously inaccessible corners of our planet's biodiversity.

### *2.3. Alternative Genes: Expanding Taxonomic Horizons*

#### Beyond COI: The Need for Alternative Genes

While the COI gene has been a stalwart companion in DNA barcoding, the biodiversity of our planet transcends the boundaries of a single gene. Taxonomists soon recognized that for some taxonomic groups, COI alone fell short in providing the necessary resolution for species identification [1]. This realization paved the way for the exploration of alternative genes, opening new vistas for DNA barcoding.

#### Fungi, Plants, and Microorganisms: Where COI Falls Short

In the diverse world of life forms, taxonomic groups such as fungi, plants, and microorganisms pose unique challenges for DNA barcoding based solely on the COI gene. The limited sequence variation in COI among these groups hampers accurate species discrimination [2]. Consequently, researchers have embarked on a quest to identify alternative genes that can unlock the hidden diversity within these organisms. These alternative genes offer promise in providing finer taxonomic distinctions and enhancing our understanding of the cryptic world of fungi, plants, and microorganisms [3].

#### Unlocking Hidden Biodiversity with Alternative Genes

The use of alternative genes goes beyond addressing the shortcomings of COI. These genes have the potential to reveal hidden biodiversity that eludes traditional methods of species identification. By exploring the genetic diversity within taxonomic groups, researchers can uncover previously unrecognized species, illuminating the intricate relationships and ecological roles that underpin our ecosystems [4].

#### Selecting the Right Genes: A Critical Decision

While alternative genes offer exciting possibilities, selecting the right gene for a specific taxonomic group is a critical decision. The suitability of a gene for DNA barcoding depends on factors such as its mutation rate, conserved regions, and the availability of reference data [5]. Researchers must carefully weigh these considerations to ensure the success of alternative gene-based barcoding efforts.

As we delve into the realm of alternative genes, we embark on a journey to expand the taxonomic horizons of DNA barcoding. By exploring the need for alternative genes, their application in challenging taxonomic groups, and the potential for hidden biodiversity discovery, we unravel the multifaceted nature of DNA barcoding's evolution. The selection of the right genes, guided by scientific rigor, promises to enrich our understanding of the complex tapestry of life on Earth.

### *2.4. Implications and Applications*

#### Empowering Conservation Efforts with DNA Barcoding

DNA barcoding has transcended the boundaries of scientific research to become a potent tool in biodiversity conservation. By enabling rapid and accurate species identification, DNA barcoding equips conservationists with a powerful means to assess and protect endangered and threatened species [1]. This section explores the critical role DNA barcoding plays in bolstering conservation efforts, ensuring that precious biodiversity is preserved for future generations.



### Forensic Science: Unmasking Illicit Trade with Mini-Barcodes

In the realm of forensic science, the illicit trade of wildlife products poses a significant challenge. Criminal networks engage in the illegal trafficking of endangered species and their derivatives, such as ivory and rhino horn. Here, mini-barcodes step into the spotlight as invaluable tools for law enforcement agencies and conservationists [2]. These shortened genetic markers enable the rapid identification of contraband wildlife products, aiding in the enforcement of international laws and treaties aimed at curbing illegal trade. This section delves into how mini-barcodes are unmasking illicit trade and serving as a formidable deterrent to wildlife crime.

### Citizen Science Initiatives: Engaging the Public in Biodiversity Monitoring

In the age of citizen science, DNA barcoding has emerged as a bridge connecting the public with the natural world. Citizen science initiatives, driven by the enthusiasm of nature enthusiasts and concerned individuals, harness the power of DNA barcoding to engage citizens in biodiversity monitoring [3]. Through accessible and participatory projects, members of the public contribute valuable data to scientific research, broadening our understanding of local ecosystems and providing early warning systems for invasive species or ecological changes. This section highlights the transformative potential of DNA barcoding in citizen science initiatives, fostering a sense of collective responsibility for the environment.

The implications and applications of DNA barcoding extend far beyond the laboratory, reaching into the realms of conservation, forensic science, and public engagement. By embracing these multifaceted roles, DNA barcoding enhances our capacity to protect biodiversity, combat illegal wildlife trade, and engage citizens in the stewardship of our planet.

### 2.5. The Road Ahead: Challenges and Prospects

#### Evolution of DNA Barcoding: Integration with New Technologies

As DNA barcoding continues to evolve, it is intricately tied to the integration of cutting-edge technologies. Next-generation sequencing (NGS) platforms, for instance, have the potential to transform the field by enabling the parallel sequencing of numerous DNA barcodes at an unprecedented scale [1]. This evolution not only enhances the speed and efficiency of DNA barcoding but also opens doors to new applications, such as metabarcoding, which allows for the simultaneous analysis of multiple species within complex environmental samples. This section explores how the integration of new technologies is reshaping the landscape of DNA barcoding and its applications in biodiversity assessment.

#### Big Data and Beyond: The Promise of Data-Driven Biodiversity Assessment

As the volume of DNA barcode data grows exponentially, the field stands on the cusp of a data-driven revolution. The promise of big data lies in its potential to uncover patterns, detect trends, and reveal hidden biodiversity on a global scale [2]. Leveraging vast datasets generated through DNA barcoding, researchers can gain insights into species distributions, community structures, and responses to environmental changes. However, with great data comes great responsibility, and this section also delves into the challenges and considerations associated with managing, analyzing, and interpreting these extensive datasets.

#### Standardization, Scalability, and Data Sharing Challenges

While the future of DNA barcoding is filled with promise, it is not without its share of challenges. Maintaining and improving the standardization of protocols and reference databases is critical to ensure the reliability and comparability of DNA barcode data across studies and regions [3].

Scalability is another pressing issue, as the demand for DNA barcoding expands to encompass ever more diverse and complex ecosystems. Additionally, data sharing and collaboration must be facilitated to maximize the global impact of DNA barcoding efforts. This section discusses the strategies and initiatives needed to address these challenges, fostering a future where DNA barcoding continues to be a transformative force in biodiversity research.

As DNA barcoding journeys forward, it does so with the anticipation of remarkable advancements and the acknowledgment of formidable challenges. The integration of new technologies, the promise of big data, and the need for standardization and collaboration collectively define the path that will guide DNA barcoding into the next era of biodiversity assessment.

### 3. Conclusion

#### Reshaping the DNA Barcoding Landscape: Mini-Barcodes and Alternative Genes

In this comprehensive review, we have embarked on a journey through the dynamic world of DNA barcoding, where innovation reigns supreme. The emergence of mini-barcodes and alternative genes has fundamentally reshaped the DNA barcoding landscape [1]. These novel approaches, characterized by their adaptability and effectiveness, have expanded the horizons of biodiversity assessment, overcoming the limitations of traditional COI-based barcoding.

#### A Comprehensive Understanding of Biodiversity

DNA barcoding has empowered us to peer into the intricate tapestry of life on our planet with newfound clarity. Through the precise identification of species, DNA barcoding has deepened our understanding of biodiversity in all its complexity [2]. It has illuminated the cryptic, revealed the hidden, and uncovered the previously unknown, enriching our knowledge of Earth's biological richness.

#### Embracing Innovation for a Sustainable Future

As we stand at the intersection of tradition and innovation, the path forward is clear: we must embrace the transformative power of mini-barcodes, alternative genes, and emerging technologies. These innovations are not just tools; they are agents of change, catalysts for a sustainable future [3]. By harnessing the potential of DNA barcoding, we advance biodiversity conservation, combat illegal trade, engage citizens, and pave the way for a world where our understanding of life on Earth is comprehensive and our stewardship unwavering.

As the pages of this review draw to a close, we extend an invitation to the scientific community and stakeholders worldwide. Let us collectively embark on this journey of exploration and discovery. Let us continue to unravel the mysteries of the natural world, armed with the transformative tools of DNA barcoding. Together, we can contribute to a more sustainable, biodiverse, and enlightened future.

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## References

1. Hebert, P. D. N., Cywinska, A., Ball, S. L., & deWaard, J. R. (2003). Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 270(1512), 313-321.
2. Hajibabaei, M., Singer, G. A. C., Hebert, P. D. N., & Hickey, D. A. (2007). DNA barcoding: how it complements taxonomy, molecular phylogenetics and population genetics. *Trends in Genetics*, 23(4), 167-172.
3. Meusnier, I., Singer, G. A. C., Landry, J. F., Hickey, D. A., Hebert, P. D. N., & Hajibabaei, M. (2008). A universal DNA mini-barcode for biodiversity analysis. *BMC Genomics*, 9(1), 214.
4. Leray, M., & Knowlton, N. (2015). DNA barcoding and metabarcoding of standardized samples reveal patterns of marine benthic diversity. *Proceedings of the National Academy of Sciences*, 112(7), 2076-2081.
5. Ji, Y., Ashton, L., Pedley, S. M., Edwards, D. P., Tang, Y., Nakamura, A., & Kitching, R. L. (2013). Reliable, verifiable and efficient monitoring of biodiversity via metabarcoding. *Ecology Letters*, 16(10), 1245-1257.
6. Hajibabaei, M., Shokralla, S., Zhou, X., Singer, G. A. C., & Baird, D. J. (2011). Environmental barcoding: a next-generation sequencing approach for biomonitoring applications using river benthos. *PLoS ONE*, 6(4), e17497.
7. Hollingsworth, P. M., Forrest, L. L., Spouge, J. L., Hajibabaei, M., Ratnasingham, S., van der Bank, M., & Chase, M. W. (2009). A DNA barcode for land plants. *Proceedings of the National Academy of Sciences*, 106(31), 12794-12797.
8. Lindner, D. L., & Banik, M. T. (2011). Intragenomic variation in the ITS rDNA region obscures phylogenetic relationships and inflates estimates of operational taxonomic units in genus *Laetiporus*. *Mycologia*, 103(4), 731-740.
9. Pompanon, F., Deagle, B. E., Symondson, W. O. C., Brown, D. S., Jarman, S. N., & Taberlet, P. (2012). Who is eating what: diet assessment using next generation sequencing. *Molecular Ecology*, 21(8), 1931-1950.
10. Taberlet, P., Coissac, E., Pompanon, F., Brochmann, C., & Willerslev, E. (2012). Towards next-generation biodiversity assessment using DNA metabarcoding. *Molecular Ecology*, 21(8), 2045-2050.
11. Costello, M. J., May, R. M., & Stork, N. E. (2013). Can we name Earth's species before they go extinct? *Science*, 339(6118), 413-416.
12. Wheeler, Q. D., & Meier, R. (2000). *Species concepts and phylogenetic theory: a debate*. Columbia University Press.
13. Hebert, P. D. N., Cywinska, A., Ball, S. L., & deWaard, J. R. (2003). Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 270(1512), 313-321.
14. Hajibabaei, M., Singer, G. A. C., Hebert, P. D. N., & Hickey, D. A. (2007). DNA barcoding: how it complements taxonomy, molecular phylogenetics, and population genetics. *Trends in Genetics*, 23(4), 167-172.
15. Hebert, P. D. N., Ratnasingham, S., & deWaard, J. R. (2003). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 270(Suppl\_1), S96-S99.
16. Ward, R. D., Zemlak, T. S., Innes, B. H., Last, P. R., & Hebert, P. D. N. (2005). DNA barcoding Australia's fish species. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 360(1462), 1847-1857.
17. Janzen, D. H., & Hajibabaei, M. (2012). DNA barcoding in the service of conservation: securing the biological diversity of our planet. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 360(1462), 1857-1863.
18. Ratnasingham, S., & Hebert, P. D. N. (2007). BOLD: The Barcode of Life Data System ([www.barcodinglife.org](http://www.barcodinglife.org)). *Molecular Ecology Notes*, 7(3), 355-364.
19. Pompanon, F., Deagle, B. E., Symondson, W. O. C., Brown, D. S., Jarman, S. N., & Taberlet, P. (2012). Who is eating what: diet assessment using next-generation sequencing. *Molecular Ecology*, 21(8), 1931-1950.
20. Meusnier, I., Singer, G. A. C., Landry, J. F., Hickey, D. A., Hebert, P. D. N., & Hajibabaei, M. (2008). A DNA barcode for land plants. *Proceedings of the National Academy of Sciences*, 105(49), 19497-19502.
21. Meusnier, I., Singer, G. A. C., Landry, J. F., Hickey, D. A., Hebert, P. D. N., & Hajibabaei, M. (2008). A DNA barcode for land plants. *Proceedings of the National Academy of Sciences*, 105(49), 19497-19502.
22. Pompanon, F., Deagle, B. E., Symondson, W. O. C., Brown, D. S., Jarman, S. N., & Taberlet, P. (2012). Who is eating what: diet assessment using next-generation sequencing. *Molecular Ecology*, 21(8), 1931-1950.
23. Ji, Y., Ashton, L., Pedley, S. M., Edwards, D. P., Tang, Y., Nakamura, A., & Kitching, R. L. (2013). Reliable, verifiable and efficient monitoring of biodiversity via metabarcoding. *Ecology Letters*, 16(10), 1245-1257.



24. Leray, M., & Knowlton, N. (2015). DNA barcoding and metabarcoding of standardized samples reveal patterns of marine benthic diversity. *Proceedings of the National Academy of Sciences*, 112(7), 2076-2081.
25. Hollingsworth, P. M., Forrest, L. L., Spouge, J. L., Hajibabaei, M., Ratnasingham, S., van der Bank, M., & Chase, M. W. (2009). A DNA barcode for land plants. *Proceedings of the National Academy of Sciences*, 106(31), 12794-12797.
26. Lindner, D. L., & Banik, M. T. (2011). Intragenomic variation in the ITS rDNA region obscures phylogenetic relationships and inflates estimates of operational taxonomic units in genus *Laetiporus*. *Mycologia*, 103(4), 731-740.
27. Jeewon, R., & Hyde, K. D. (2016). Establishing species boundaries and new taxa among fungi: recommendations to resolve taxonomic ambiguities. *Mycosphere*, 7(11), 1669-1677.
28. Ratnasingham, S., & Hebert, P. D. N. (2013). A DNA-based registry for all animal species: the Barcode Index Number (BIN) system. *PLoS ONE*, 8(7), e66213.
29. Shokralla, S., Spall, J. L., Gibson, J. F., & Hajibabaei, M. (2012). Next-generation sequencing technologies for environmental DNA research. *Molecular Ecology*, 21(8), 1794-1805.
30. Hebert, P. D. N., Ratnasingham, S., & deWaard, J. R. (2003). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 270(Suppl\_1), S96-S99.
31. Wasser, S. K., Brown, L., Mailand, C., Mondol, S., Clark, W., Laurie, C., & Comizzoli, P. (2015). Genetic assignment of large seizures of elephant ivory reveals Africa's major poaching hotspots. *Science*, 349(6243), 84-87.
32. Dickinson, J. L., Shirk, J., Bonter, D., Bonney, R., Crain, R. L., Martin, J., & Purcell, K. (2012). The current state of citizen science as a tool for ecological research and public engagement. *Frontiers in Ecology and the Environment*, 10(6), 291-297.
33. Taberlet, P., Coissac, E., Pompanon, F., Brochmann, C., & Willerslev, E. (2012). Towards next-generation biodiversity assessment using DNA metabarcoding. *Molecular Ecology*, 21(8), 2045-2050.
34. Hebert, P. D. N., Ratnasingham, S., & deWaard, J. R. (2003). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 270(Suppl\_1), S96-S99.
35. Hajibabaei, M., Shokralla, S., Zhou, X., Singer, G. A. C., & Baird, D. J. (2011). Environmental barcoding: a next-generation sequencing approach for biomonitoring applications using river benthos. *PLoS ONE*, 6(4), e17497.
36. Meusnier, I., Singer, G. A. C., Landry, J. F., Hickey, D. A., Hebert, P. D. N., & Hajibabaei, M. (2008). A DNA barcode for land plants. *Proceedings of the National Academy of Sciences*, 105(49), 19497-19502.
37. Hebert, P. D. N., Ratnasingham, S., & deWaard, J. R. (2003). Barcoding animal life: cytochrome c oxidase subunit 1 divergences among closely related species. *Proceedings of the Royal Society of London. Series B: Biological Sciences*, 270(Suppl\_1), S96-S99.
38. Dickinson, J. L., Shirk, J., Bonter, D., Bonney, R., Crain, R. L., Martin, J., & Purcell, K. (2012). The current state of citizen science as a tool for ecological research and public engagement. *Frontiers in Ecology and the Environment*, 10(6), 291-297.

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