





# Hybrids Along a Natural-Anthropogenic Gradient: Improving Policy and Management Across All Levels of Biodiversity

<sup>1</sup>Centre for Research and Conservation, Royal Zoological Society of Antwerp, Antwerp, Belgium | <sup>2</sup>Department of Biology, University of Copenhagen, Copenhagen, Denmark | <sup>3</sup>National Centre for Biological Society of Scotland, Conservation and Science Programmes, Edinburgh, UK | <sup>5</sup>Department of Agriculture, Landscape, and Environment and Gund Institute for the Environment, University of Vermont, Burlington, Vermont, USA | <sup>6</sup>School of Bioscience, Cardiff University, Cardiff, UK | <sup>7</sup>Center for Tree Science, Morton Arboretum, Lisle, Illinois, USA | <sup>8</sup>European Association of Zoos and Aquaria (EAZA), Population Management Centre, Amsterdam, The Netherlands | <sup>9</sup>MIT Media Lab, Massachusetts Institute of Technology, Cambridge, Massachusetts, USA | <sup>10</sup>Department of Wildlife Ecology and Management, University Freiburg, Freiburg, Germany | <sup>11</sup>Institute of Ecology and Evolution, University of Oregon, Eugene, Oregon, USA | <sup>12</sup>Department of Fish and Wildlife Sciences, University of Idaho, Moscow, Idaho, USA | <sup>13</sup>Biotechnical Faculty, University of Ljubljana, Ljubljana, Slovenia | <sup>14</sup>Department of Chemistry and Bioscience, Aalborg University, Aalborg, Denmark | <sup>15</sup>DivjaLabs Ltd, Ljubljana, Slovenia | <sup>16</sup>Norwegian Institute for Nature Research, Terrestrial Ecology, Trondheim, Norway

Correspondence: Peter Galbusera (peter.galbusera@kmda.org)

Received: 22 November 2024 | Revised: 18 September 2025 | Accepted: 30 September 2025

Keywords: biodiversity | genetic diversity | hybrids | management | monitoring | policy | population viability | resilience

## **ABSTRACT**

Hybridization has long been a central topic in evolution and conservation. Recent developments in genomics have increased the ability to detect hybridization, defined here as breeding between species, subspecies or distinct populations, and assess levels of introgression between taxa. For decades, hybrids directly or indirectly created and/or spread by humans have typically been considered as threats to conservation, reflected by current regional and national environmental policies that focus largely on potential negative effects. In the context of the latest global conservation policy goals, and increasing evidence of historic natural hybridization events, we call for science-based, reflective and context-dependent management of hybrids, applying a framework that shifts focus towards measuring the impact of hybrids, and assessing potential risks and benefits. Alongside demographic and ecological information, it is crucial for impact assessments to consider genetic information, and conservation management of hybrids needs to be more case-specific.

Peter Galbusera, Laura D. Bertola, Eric Bishop von Wettberg, Michael W. Bruford, Sean Hoban, Isa-Rita M. Russo, Gernot Segelbacher, Nelson Ting, Lisette P. Waits, Astrid Vik Stronen, and Alexander Kopatz are members of the IUCN SSC Conservation Genetics Specialist Group.

†Deceased 13 April 2023

This is an open access article under the terms of the Creative Commons Attribution License, which permits use, distribution and reproduction in any medium, provided the original work is properly cited.

© 2025 The Author(s). Conservation Letters published by Wiley Periodicals LLC.

1 of 10

## 1 | The Ambiguity of Hybrids

Hybrids are the result of mating between organisms of different species, subspecies and genetically distinct populations (Rhymer and Simberloff 1996), leading to the (genetic) admixture of these (hereafter called) taxa. Introgression occurs when hybrids breed (or backcross) with individuals from the parental groups. Natural, non-anthropogenic, hybridization is an important evolutionary process that can lead to new species as well as reverse speciation (e.g., Kearns et al. 2018). Hybridization can also occur in situ during domestication, stockbreeding, conservation management, or following the introduction of species that become invasive (e.g., Blackwell et al. 2021). In addition, humans may produce hybrids ex situ and release them into the wild, deliberately or unintentionally (e.g., Pogorevc et al. 2024). Whereas natural hybrids that occur without human influence have long been recognized for their important role in evolution (Allendorf et al. 2001), range expansion in wild species following human-induced environmental changes can lead to hybridization with both wild and domestic species that raises complex management challenges (e.g., Trouwborst et al. 2015). Because these human-induced changes are often indirect, there is not always a clear line between hybrids of natural and human-induced origin (Donfrancesco and Luque-Lora 2022; Figure 1). We acknowledge that hybridization can be problematic, and in many cases the costs will exceed any benefits. Nevertheless, our aim with this paper is to present a nuanced approach to encourage case-by-case management. One difficulty is finding the framework and language to effectively address this case-specificity in hybrid policy and management. and we seek to address these obstacles in a constructive and balanced manner.

Recent genomic and analytical methods have broadened our knowledge on hybridization and improved the detection of hybrids (Wang 2024; see Supplementary Information, SI1). Studies revealed both higher numbers of hybrid individuals, and hybrids occurring between a greater number of taxa, than previously thought (Taylor and Larson 2019; Brown et al. 2024). Additional undetected cases may also be discovered in the future, raising new conservation questions. Though likely representing only a small proportion of the population in most cases, hybrids were found in about 23% of all carnivore species (Tensen and Fischer 2024). Populations in areas altered by ever-growing global trade and international travel (Ottenburghs 2021), or at range edges affected by anthropogenic changes (Lobo et al. 2023), might in the future experience increased rates of hybridization. Hence, environmental policy makers and natural resource managers are increasingly challenged to handle and manage hybrids (Grobler et al. 2018) influenced to various extents by human activities, either directly (e.g., release of nonnative species) or indirectly, linked to climate or habitat changes (Allendorf et al. 2001; Figure 1).

In early conservation literature, hybrids between native and nonnative taxa were primarily considered a threat (e.g., Simberloff 1996). Such hybrids could lead to loss of biodiversity by replacing resident taxa through introgression and genetic swamping (Todesco et al. 2016; Figure 1, Examples 11–15). Genetic swamping is the extensive displacement of alleles in a taxon by those from another taxon via hybridization (Figure 2, Examples 5 and 6). In other cases, native taxa may decline and disappear due to hybrid offspring being unviable ("demographic swamping", e.g., Mikkelsen and Irwin 2021; Figure 2, Examples 1 and 2) or sterile. Beyond overall loss of biodiversity, specific alleles that underlie local adaptation may disappear (Olden et al. 2004), or hybrids may introduce maladaptive alleles given local climates or pathogens (Banes et al. 2016), potentially reducing adaptation and viability (Stockwell et al. 2003). Hybrids can also reduce fitness (Todesco et al. 2016) via reduced fertility and outbreeding depression when the parent taxa are strongly differentiated (e.g., large geographic, phylogenetic and/or environmental distance) (Frankham et al. 2017). At the species level, few extinctions caused by hybrids have been documented (Draper et al. 2021; Tensen and Fischer 2024) but see Rhymer and Simberloff 1996. However, negative fitness consequences sometimes only become apparent after two or three generations (Bell et al. 2019). Importantly, the effect of heterosis, the enhanced fitness sometimes observed in hybrid offspring, is often only temporary (Bell et al. 2019).

Recent studies have shown that hybrids are omnipresent and can, at times, play a key role in evolutionary processes (vonHoldt et al. 2018; Runemark et al. 2019; Hirashiki et al. 2021; Ottenburghs 2021). Some potentially positive impacts of hybridization that have been highlighted, despite a degree of human influence, are:

- For taxa at the brink of extinction and displaying negative growth rates, mixing of different gene pools can improve and restore genetic variation (Lucena-Perez et al. 2024), often to the benefit of those taxa (e.g., through heterosis ("hybrid vigor"); Jackiw et al. 2015; Frankham et al. 2017; Ralls et al. 2018; Rodger et al. 2024).
- 2. Hybrids may provide important genetic diversity to certain taxa that otherwise would not survive new challenges. As climate change causes spatial shifts in the suitable habitat or niche of taxa, introgression could allow them to more rapidly adapt to changing conditions (Bell et al. 2019; de Jong et al. 2023; Taylor and Larson 2019). For example, recent genomic evidence in snow sheep showed that past hybridization with Dall and Argali sheep has contributed to adaptation to snow conditions (Figure 1, Example 5/SI2). In forestry, hybrids may help numerous tree species currently suffering from introduced pests and diseases (e.g., butternut case in SI3). Also, in crop species, novel traits introduced from wild relatives provide critical agronomic characteristics or human-valued attributes (e.g., SI4).
- 3. Hybrids might harbor genetic diversity of species that are extinct, extirpated, or at risk, as exemplified in Galapagos tortoises (Quinzin et al. 2019). The alleles from the lost or at-risk species might also be "revived" through controlled breeding (e.g., Lawson et al. 2024), genetic rescue or reintroduction efforts (e.g., Quinzin et al. 2019).
- 4. Hybrids may also fulfill an important role in an ecosystem, maintaining certain processes (e.g., predator–prey relationships, Stronen and Paquet 2013). Hybrid salt marsh grasses play a crucial role in ecosystem functioning. They help stabilize coastal environments, prevent erosion, and enhance biodiversity (Rezek et al. 2017). Potentially important functional variation needs to be investigated in the future (vonHoldt et al. 2022).

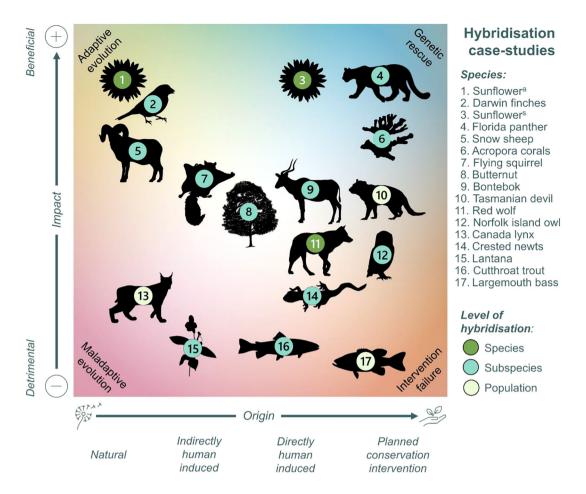


FIGURE 1 | Selection of 17 case-studies and examples of beneficial or detrimental (known or suspected) impacts (on an approximate gradient on the *y*-axis) from hybridization at the species, subspecies or population level. Intermixing by natural and artificial, human (intentional and unintentional) interference is placed approximately along a stylized gradient of natural-anthropogenic origin (*x*-axis). Detrimental impacts are those that are considered to have likely negative consequences for the taxa, i.e., lower fitness, depressed survival or reproduction, loss of unique gene variants, whereas (potential) beneficial impacts are considered to promote survival capabilities and restore genetic diversity. The sunflower examples (1 and 3) contain ancient<sup>a</sup> and human-mediated<sup>s</sup> hybridization. Every case of hybridization should be examined within its specific context (see Table S1 in S12 for more details).

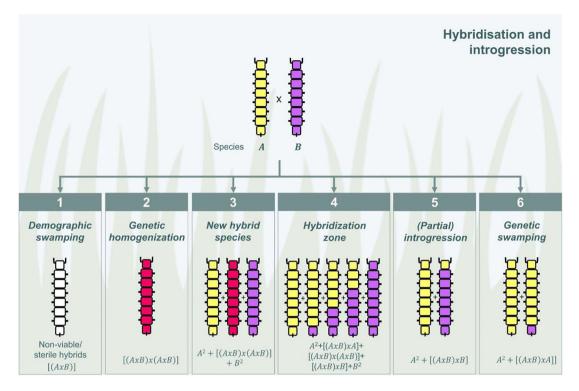
More data will likely emerge on negative consequences of hybridization for wild taxa, including risks to survival and long-term conservation. If none have been reported to date for a specific taxon, this can also reflect limited research efforts on hybrid organisms, which are often difficult to study. One recent example is wolf-dog hybridization, where new findings indicate behavioral differences between wolves and admixed individuals, with potential long-term implications for evolution and conservation (Amici et al. 2024). More research is thus essential to help quantify the ecological and evolutionary consequences of hybridization. Knowledge gaps and examples of taxa where these issues have been investigated or where further research has been identified as a priority, are listed in SI4.

# 2 | The Challenge of Managing Hybrids in the Wild

The International Union for Conservation of Nature (IUCN) Red Listing process generally considers hybrids as a threat to biodiversity conservation (IUCN 2021). Additionally, hybrids often lack

legal status and are disregarded during conservation planning and actions, for example, with a goal to maintain the current status of a species gene pool (O'Brien et al. 2022). However, disregarding the potential of hybrids may, at times, impede conservation, for example, by limiting genetic diversity (Lucena-Perez et al. 2024). Reduced genetic diversity results in lower ecosystem resilience and impedes long-term survival (Frankham 2005; Figure 4; Kettenring et al. 2014). High genetic diversity often correlates with higher fitness. For example, Holzmann et al. (2023) found that montane lizard populations that survived climate changes had higher levels of genomic diversity than extinct populations. Conservation policy and nature management have therefore been encouraged to focus on maintaining genetic diversity for the future, as recently agreed at the 15th meeting of the Conference of Parties to the United Nations Convention on Biological Diversity (Kunming-Montreal GBF 2022). Although detrimental effects of human-induced hybridization need continued attention, further recognition of scenarios where hybrids might help maintain, restore, or enhance adaptive genetic variation can support effective conservation legislation and actions. A major challenge is to integrate traditional, species-focused conservation approaches with the current understanding of hybrids (but see also SI4

Conservation Letters, 2025 3 of 10



**FIGURE 2** Six possible (multi-generational) outcomes, on genetic composition, of hybridization (1–4) and introgression (4–6) between hypothetical, simplified arthropod species A (yellow) and B (purple). Hybrid zones, outcome 4, occur when these events are spatially restricted. Colors represent the (proportion of) species-specific genetic characteristics (after figure 1 in Runemark et al. 2019) and formulas represent the parental composition(s) of the outcomes (parental A or B, and/or hybrid  $(A \times B)$ ).

and Table S2) in conservation policy and management (see e.g., Quilodrán et al. 2020).

Intentional anthropogenic hybridization of a wild population is, at times, a tool in conservation management, in the form of genetic rescue and/or demographic rescue, or to improve adaptive diversity (but for further discussion on these topics, see e.g., DeMay et al. 2017; Van Oppen et al. 2015). In addition, unintentional anthropogenic hybridization (Ottenburghs 2021) can occur because of the inadvertent introduction of an invasive or domesticated species and may result in hybrids that are eligible for protection, if this can improve the conservation of a parent species at risk (Stoskopf et al. 2005 and SI3.B). Building on earlier frameworks for hybrid assessment (e.g., Allendorf et al. 2001; Jackiw et al. 2015; Wayne and Schaffer 2016; Ottenburghs 2021; Tensen and Fischer 2024), we propose a tailored approach to deal with hybrids on a case by case basis. We reconsider existing policy and management in light of ongoing challenges in biodiversity conservation, of new scientific developments and the increased recognition of the importance of genetic diversity (Hoban et al. 2021; Tensen and Fischer 2024; Norderhaug et al. 2024).

Because most assessments have previously centered on risks, we also address possible benefits that hybrids might yield in specific conservation cases. Importantly, these points should not be seen as promoting anthropogenic hybrids or ignoring their known or potential conservation impacts. Instead, we seek to discuss how to promote much-needed international coordination (e.g., Salvatori et al. 2020) while still permitting flexible, context-dependent decision-making. We outline recommendations to policy makers

and managers with examples across taxa in various contexts. We reflect on the distinction between natural and human-induced hybridization, and advocate that policy makers and managers need to consider the origin of hybrids, their role in the ecosystem and their (observed or expected) impact (Quilodrán et al. 2020) on the fitness and gene pool of the taxa in question. The decision of whether to remove or accept hybrids or to prioritize certain populations, ultimately depends on (i) the conservation status of taxa involved, (ii) the level of anthropogenic influence, (iii) the impact on the taxa of interest (see Figure 3), (iv) political will and (v) the relevant spatiotemporal scale. As such, we recommend careful case-by-case assessments, analyzing possible positive and negative outcomes (in terms of ecological, demographic, and genetic parameters). We advocate for policies that strive for nuanced conservation management with the possibility of including hybrid organisms, if beneficial, and provide practical guidelines for (individual) management (in Section 5).

# 3 | Current Policies, Legislations, Regulations, and Practice

Hybrid management in practice can take on many forms, but often it is a question of whether to ignore or remove hybrids (e.g., see bontebok case study in SI3). However, removal of hybrids may, at times, undermine long-term restoration efforts, especially for taxa that naturally experience a high frequency of hybridization (vonHoldt et al. 2018). At the global scale, hybrids (and backcrosses up to the fourth generation) are protected by CITES and the EU Wildlife Trade Regulations when at least one

of the two "parents" is (CITES) listed in Appendix I or II (Fossati 2024). Other international legal instruments (i.e., the Habitats Directive and the Bern Convention) also allow for the protection or removal of hybrids. However, this approach is currently not followed by the IUCN. As such, the IUCN, with the exception of apomictic hybrid plants, excludes interspecific hybrids from the Red List of Threatened Species (IUCN 2021), which limits the ability to evaluate the status of hybrids (Bauer et al. 2021).

Moreover, there is a discrepancy between international policy and agreements versus national rules or laws and their application. In general, there is a lack of formal policies on the status or value of hybrids for the agencies responsible for managing endangered taxa (Rees 2002), although hybrids have been discussed extensively in the United States and Canada (USFWS 1996; Allendorf et al. 2001; Haig and Allendorf 2006, Jackiw et al. 2015, Wayne and Schaffer 2016, COSEWIC 2018, Hirashiki et al. 2021). To our knowledge, evidence-based legislation regarding hybrids is lacking in many countries, often resulting in ad hoc decision-making. Although some guidance to control hybrids is provided, its implementation in management is not guaranteed. For example, wolf-dog hybrids have been reported in all nine extant European wolf populations (Salvatori et al. 2020). In the absence of international policies on hybrid management, national interpretations of standing guidelines could lead to conflicting strategies even in neighboring countries (Salvatori et al. 2020), highlighting the need for clearer policies and more international coordination, including standardized genetic methods for the detection of hybrids. Trouwborst (2014) previously recommended for the Standing Committee of the Bern Convention and the European Commission to adopt a common and scientificallybased understanding of what hybrids are and to promote a uniform application of the legal instruments concerning hybrids.

However, we recognize the challenge in achieving a balance between international harmonization and flexibility. Hence, in the next section we propose a common framework to advance evidence-based decision-making.

# 4 | Framework for Future Conservation Policy and Management Including Hybrids

We present a process-based framework (Figure 3) that can help national and subnational entities to build legal schemes for evidence-based decision-making regarding hybrids. This framework includes elements of the IUCN-SSC's "Assess-Plan-Act" framework in the IUCN Species Strategic Plan for 2021–2025. Our framework does not consider hybrids to be a threat or benefit a priori, but states that hybrids should not by default be excluded from protection, as avoiding hybrids can result in the loss of genetic diversity and adaptive potential (see e.g. Coleman et al. 2013).

It focuses on measuring the impact of hybrids and introgression, before considering management actions, and takes into account the specific context (e.g., natural vs. human-induced hybrids).

## 4.1 | Analyze

Here, we focus on gathering knowledge regarding all three levels of biodiversity (ecosystem, species and genetic diversity) with specific focus on the available genetic/genomic information (The IUCN SSC Conservation Genetics Specialist Group, CGSG focus), as genetic diversity is the basis for future selection and adaptation (Powell 2023). Hence, a first step in this framework is to obtain,

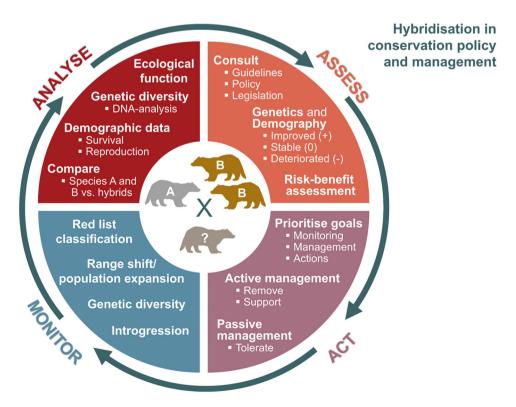


FIGURE 3 | Proposed framework for guidance in evidence-based management and decision-making of hybrids with parental taxa (A and B).

Conservation Letters, 2025 5 of 10

analyze and compare genetic, demographic and ecological data of the hybrid and the parental taxa. Managers and scientists need to address questions such as: How long have the taxa been separated (naturally or by e.g., domestication)? Is the hybridization of anthropogenic origin? How many known hybrids and individual parents of each taxon exist in the wild, and how are they distributed over populations and the landscape? Do the parental taxa and hybrids have different traits and/or preferences in terms of habitat, species (predator–prey) interactions? What are the levels of genetic diversity? Are there indications of inbreeding and/or outbreeding depression?

## 4.2 | Assess

Risk assessments looking at both negative and positive effects on long-term survival have been put forward as an appropriate tool. Management decisions and actions to either remove or protect hybrids need to be based on these assessments, considering other guidelines (e.g., see Section 5), available time, expertise, budgets, and legislation. A review indicated that such overarching risk assessments increase the probability of the recommendation of mixing gene pools (Liddell et al. 2021). Managers, in collaboration with scientists, need to address questions such as: If hybridization increased, how will genetic and demographic parameters change? What impacts will this have on other taxa and the ecosystem (e.g., change in diet)? These can be categorized into (likely) positive and negative impacts by consulting a range of experts and knowledge holders, and by carefully designed research. Conservation planning could then proceed, resources depending, in either qualitative (scenario planning, in which general possible futures are described in a storytelling fashion) and/or quantitative analyses (modelling, in which simulations are used to predict different outcomes based on certain assumptions).

# 4.3 | Act

If an assessment leads to the insight that some populations are at higher risk for hybridization than others or, to the contrary, that they have minimal nonnative ancestry (Kovach et al. 2025), those could be prioritized for monitoring, management and possible action. Further assessment outcomes include passive management, where hybrids are tolerated and monitored to study long-term impacts, and active management (see also Sections 2 and 3). The latter might consider the removal of hybrids when the relative risks are outweighing the benefits. For example, the Assess stage may show that hybrids pose a serious threat to endemic endangered taxa when simulations suggest that hybrids will continue to displace alleles of these taxa (Tensen and Fischer 2024). On the other hand, simulations may show that hybrids prevent the loss of an endangered taxon while maintaining much of its genetic integrity (Miller et al. 2003; Stoskopf et al. 2005, see red wolf case study SI3.B). Once an overall decision on a specific case is made, managers can decide on the fate of (groups of) individuals (see Section 5).

## 4.4 | Monitor

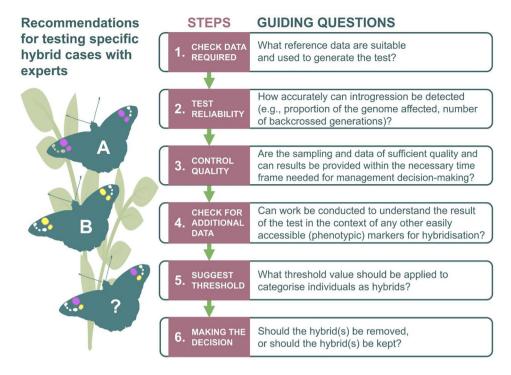
Given that the effects caused by hybridization can span over several generations, it is advised to monitor genetic diversity and introgression across time and space, for example, using genetic indicators (Hoban et al. 2021) and/or changes in Red List classification (but see Norderhaug et al. 2024). In many cases there may be insufficient data to make a well-informed decision. For example, it may be that the relative fitness of hybrids needs to be evaluated in an experiment, or the diet and aggressiveness of hybrids needs to be determined. Here, researchers and managers can benefit from close collaboration in designing research that includes specific, applied conservation questions relative to hybridization.

# 5 | Managing Individual Hybrids in Practice: Setting Thresholds

Practical conservation management at the individual level needs clear definitions to prescribe designated actions (e.g., on livecaptured individuals): Is a potential hybrid to be euthanized, sterilized, or permitted to reproduce? However, proposing an unequivocal, operational definition of hybrids for conservation management is not straight-forward (see SI3), especially when hybridization is followed by introgression (Figure 2). This process leads to a genetic continuum spanning from parental to introgressed individuals. If managers decide to remove hybrids, they must set a threshold of hybrid ancestry somewhere on this continuum (Stoskopf et al. 2005; Senn et al. 2019; Donfrancesco and Luque-Lora 2022; Kovach et al. 2025). Most hybridization management case studies seem to accept 1%-25% introgression (Wayne and Shaffer 2016), depending on available resources (reference data, samples and funds) and the conservation objectives (demographics, genetics and ecology).

In addition, the "introgression-threshold" in the management of hybrids is partially determined by their detection reliability. For instance, it is not practical to recommend the removal of hybrids with very low, undetectable levels of introgression. Developing a reliable hybridization test depends on the availability of good quality samples and reference data for the parental taxa (see SII). Furthermore, the selected genetic markers need to detect hybrids with high accuracy (Miller et al. 2003). However, several questions have to be answered before determining the precise introgression-threshold value (Figure 4). Over time, broader application of these questions across jurisdictions and populations, for example, standardizing markers for hybrid detection, can help balance international harmonization and flexibility.

If hybridization is advanced and the measures taken to eradicate hybrids are stringent (low introgression-threshold value), population numbers could go down severely (Miller et al. 2003). Also, such management decisions could unintentionally reduce historic genetic diversity found in threatened taxa (e.g., Kovach et al. 2025), which will be disadvantageous for their survival on an evolutionary timescale (Hoban et al. 2021; see also bontebok case study in SI3). Conversely, if the measures taken to eliminate hybrids are too weak, and individuals with substantially introgressed genomes are allowed to breed, then even elaborate conservation actions might have little impact. Furthermore, the risk-benefit assessment on whether or not to remove introgressed individuals (and how stringent a threshold to apply) may change with the severity of the conservation crisis (Stoskopf et al. 2005; Senn et al. 2019). Hence, we suggest



**FIGURE 4** Recommended steps with guiding questions for hybrid testing when categorizing individuals for management actions. The answers to these questions can be highly species, habitat, and context specific. Therefore collaboration with species experts and conservation geneticists is required. Managers may commission genetic testing in order to make management decisions on individuals, based on commonly-agreed introgression-threshold value (between taxa A and B).

that introgression-thresholds need to be decided (i) on a case-by-case basis, as part of the "Assess" step (Allendorf et al. 2001), (ii) in discussion with experts and stakeholders (using e.g., Population Viability Analysis simulations), (iii) with a clear understanding of the conservation objectives, and (iv) followed by regular review that allows for nuanced management (e.g., by integrating new information from high-resolution data and evolving taxonomies). Accordingly, it is important that scientists, policy makers and natural resource managers strive toward openness and develop/agree on terminology, avoiding loaded labels such as "pure" which can be misleading or even misused for a political agenda, when describing individuals or taxa (see e.g., Donfrancesco and Luque-Lora 2022; Hirashiki et al. 2021).

## 6 | Conclusions

Hybrids require and deserve more attention. Because genomics is a rapidly evolving field and management of wild hybrids is relatively new, further efforts are needed to improve conservation management and develop policy and legislation for hybrids influenced to various extents by human activities. So far, hybrids have been largely ignored in conservation management planning because of their complexity, variable impact, the science-policy gap and the fact that they often lack legal status. Here, we recommend carefully evaluating hybrids with focus on the evolutionary consequences, including overall genetic diversity, adaptive variants, and ecological function, on a case-by-case basis.

#### **Author Contributions**

Conceptualization: All authors. Investigation: All authors. Visualization: PG, LDB, AS, AK. Project administration: PG, AK. Writing—original draft: PG, MWB, AK, EvW, LDB, IMR, AVS. Writing—review and editing: All authors

### Acknowledgments

This article was initiated under the impulse of the IUCN SSC Conservation Genetics Specialist Group (CGSG). It is partially based upon work from COST Action G-BiKE, CA 18134, and GENOA, CA23121, supported by COST (European Cooperation in Science and Technology). Michael Bruford was involved since the conceptualization of this manuscript but sadly passed away before its completion. We acknowledge stimulating discussions with G-BiKE members, and Helen Senn, Jeremie Fant, Paul Sunnucks, and Robin Waples at the initial stages of the manuscript. Silhouettes of the species, backgrounds in the figures were taken from PhyloPic.org and Flaticon.com.

### **Funding**

PG acknowledges the structural support of the Flemish government. LPW acknowledges support from NSF-Idaho-EPSCoR OIA-1757324. AVS was supported by the Research Program P1-0184 funded by ARIS, and the European Commission through LIFE WOLFALPS EU (LIFE18 NAT/IT/000972), LIFE WILD WOLF (101074417), and GA N°101052342 co-funding for the Biodiversa+ project Wolfness (in Slovenia, the Ministry of Higher Education, Science and Innovation), under the 2021–2022 BiodivProject joint call. AK was supported by the NINA basic funding, financed by The Research Council of Norway, project no. 160022/F40. SH was supported by The Walder Foundation, the US Forest Service, the Northern States Research Cooperative, and IMLS grant MG-251613-OMS-22.

### **Conflicts of Interest**

The authors declare no conflicts of interest.

Conservation Letters, 2025 7 of 10

## **Data Availability Statement**

Data sharing is not applicable to this article as no new data were created or analyzed in this study.

#### References

Allendorf, F. W., R. F. Leary, P. Spruell, and J. K. Wenburg. 2001. "The Problems With Hybrids: Setting Conservation Guidelines." *Trends in Ecology & Evolution* 16, no. 11: 613–622. https://doi.org/10.1016/S0169-5347(01)02290-X.

Amici, F., S. Meacci, E. Caray, L. Oña, K. Liebal, and P. Ciucci. 2024. "A First Exploratory Comparison of the Behaviour of Wolves (*Canis lupus*) and Wolf-Dog Hybrids in Captivity." *Animal Cognition* 27, no. 1: 9. https://doi.org/10.1007/s10071-024-01849-7.

Banes, G. L., B. M. F. Galdikass, and L. Vigilant. 2016. "Reintroduction of Confiscated and Displaced Mammals Risks Outbreeding and Introgression in Natural Populations, as Evidenced by Orangutans of Divergent Subspecies." *Scientific Reports* 6, no. 1: 22026. https://doi.org/10.1038/srep22026.

Bauer, H., A. C. Tehou, M. Gueye, et al. 2021. "Ignoring Species Hybrids in the IUCN Red List Assessments for African Elephants May Bias Conservation Policy." *Nature Ecology & Evolution* 5, no. 8: 1050–1051. https://doi.org/10.1038/s41559-021-01491-3.

Bell, D. A., Z. L. Robinson, W. C. Funk, et al. 2019. "The Exciting Potential and Remaining Uncertainties of Genetic Rescue." *Trends in Ecology & Evolution* 34, no. 12: 1070–1079. https://doi.org/10.1016/j.tree.2019.06.006.

Blackwell, T., A. G. P. Ford, A. G. Ciezarek, et al. 2021. "Newly Discovered Cichlid Fish Biodiversity Threatened by Hybridization With Non-Native Species." *Molecular Ecology* 30: 895–911. https://doi.org/10.1111/mec.15638.

Brown, M. R., R. J. Abbott, and A. D. Twyford. 2024. "The Emerging Importance of Cross-Ploidy Hybridisation and Introgression." *Molecular Ecology* 33, no. 8: e17315. https://doi.org/10.1111/mec.17315.

Coleman, R. A., A. R. Weeks, and A. A. Hoffmann. 2013. "Balancing Genetic Uniqueness and Genetic Variation in Determining Conservation and Translocation Strategies: A Comprehensive Case Study of Threatened Dwarf Galaxias, *Galaxiella Pusilla* (Mack) (Pisces: Galaxiidae)." *Molecular Ecology* 22: 1820–1835.

COSEWIC. 2018. COSEWIC Guidelines on Manipulated Wildlife Species. https://cosewic.ca/index.php/en/reports/preparing-status-reports/guidelines-manipulated-wildlife-species.html#:~:text= COSEWIC%20will%20generally%201%20not,geographically%20or% 20genetically%20distinct%20from.

de Jong, M., A. J. van Rensburg, S. Whiteford, et al. 2023. "Rapid Evolution of Novel Biotic Interactions in the UK Brown Argus Butterfly Uses Genomic Variation From Across Its Geographical Range." *Molecular Ecology* 32, no. 21: 5742–5756. https://doi.org/10.1111/mec.17138.

DeMay, S. M., P. A. Becker, J. L. Rachlow, and L. P. Waits. 2017. "Genetic Monitoring of an Endangered Species Recovery: Demographic and Genetic Trends for Reintroduced Pygmy Rabbits (*Brachylagus idahoensis*)." *Journal of Mammalogy* 98, no. 2: 350–364. https://doi.org/10.1093/jmammal/gyw197.

Donfrancesco, V., and R. Luque-Lora. 2022. "Managing Hybridization Beyond the Natural-Anthropogenic Dichotomy." *Conservation Biology* 36, no. 2: e13816. https://doi.org/10.1111/cobi.13816.

Draper, D., E. Laguna, and I. Marques. 2021. "Demystifying Negative Connotations of Hybridization for Less Biased Conservation Policies." *Frontiers in Ecology and Evolution* 9: 637100. https://doi.org/10.3389/fevo. 2021.637100.

Fossati, P. 2024. "Wildlife Hybrids: Insights Into the European Approach." *Sustainable Futures* 8: 100350. https://doi.org/10.1016/j.sftr.2024.100350.

Frankham, R. 2005. "Genetics and Extinction." *Biological Conservation* 126, no. 2: 131–140. https://doi.org/10.1016/j.biocon.2005.05.002.

Frankham, R., J. D. Ballou, K. Ralls, et al. 2017. *Genetic Management of Fragmented Animal and Plant Populations*. Oxford University Press.

Grobler, P., A. M. van Wyk, D. L. Dalton, B. J. van Vuuren, and A. Kotzé. 2018. "Assessing Introgressive Hybridization Between Blue Wildebeest (*Connochaetes taurinus*) and Black Wildebeest (*Connochaetes gnou*) From South Africa." *Conservation Genetics* 19, no. 4: 981–993. https://doi.org/10.1007/s10592-018-1071-x.

Haig, S. M., and F. W. Allendorf. 2006. "Hybrids and policy." In *The Endangered Species Act at Thirty, Volume 2: Conserving Biodiversity in Human-Dominated Landscapes*, edited by J. M. Scott, D. D. Goble, and F. W. Davis, 150–163. Island Press.

Hirashiki, C., P. Kareiva, and M. Marvier. 2021. "Concern Over Hybridization Risks Should Not Preclude Conservation Interventions." *Conservation Science and Practice* 3, no. 4: e424. https://doi.org/10.1111/csp2.424.

Hoban, S., M. W. Bruford, W. C. Funk, et al. 2021. "Global Commitments to Conserving and Monitoring Genetic Diversity Are Now Necessary and Feasible." *Bioscience* 71, no. 9: 964–976. https://doi.org/10.1093/biosci/biab054.

Holzmann, K. L., R. L. Walls, and J. J. Wiens. 2023. "Accelerating Local Extinction Associated With Very Recent Climate Change." *Ecology Letters* 26, no. 11: 1877–1886. https://doi.org/10.1111/ele.14303.

IUCN. 2021. The IUCN Red List of Threatened Species. Version 2021–3. https://www.iucnredlist.org/resources/redlistguidelines. Downloaded on December 14.

Jackiw, R. N., G. Mandil, and H. A. Hager. 2015. "A Framework to Guide the Conservation of Species Hybrids Based on Ethical and Ecological Considerations." *Conservation Biology* 29, no. 4: 1040–1051. https://doi.org/10.1111/cobi.12526.

Kearns, A. M., M. Restani, I. Szabo, et al. 2018. "Genomic Evidence of Speciation Reversal in Ravens." *Nature Communications* 9, no. 1: 906. https://doi.org/10.1038/s41467-018-03294-w.

Kettenring, K. M., K. L. Mercer, C. Reinhardt Adams, and J. Hines. 2014. "Application of Genetic Diversity-ecosystem Function Research to Ecological Restoration." *Journal of Applied Ecology* 51, no. 2: 339–348. https://doi.org/10.1111/1365-2664.12202.

Kovach, R. D. Bell, S. Amish, et al. 2025. "Defining Hybridization Thresholds for Native Species Conservation in the Genomic Era." *Fisheries* 50, no. 10: 438–450. https://doi.org/10.1093/fshmag/vuaf023.

Kunming-Montreal Global Biodiversity Framework. 2022. https://www.cbd.int/conferences/2021-2022/cop-15/documents.

Lawson, D. J., J. Howard-McCombe, M. Beaumont, and H. Senn. 2024. "How Admixed Captive Breeding Populations Could Be Rescued Using Local Ancestry Information." *Molecular Ecology* 00: e17349. https://doi.org/10.1111/mec.17349.

Liddell, E., P. Sunnucks, and C. N. Cook. 2021. "To Mix or Not to Mix Gene Pools for Threatened Species Management? Few Studies Use Genetic Data to Examine the Risks of Both Actions, but Failing to Do so Leads Disproportionately to Recommendations for Separate Management." *Biological Conservation* 256: 109072. https://doi.org/10.1016/j.biocon.2021. 109072.

Lobo, D., J. V. López-Bao, and R. Godinho. 2023. "The Population Bottleneck of the Iberian Wolf Impacted Genetic Diversity but Not Admixture With Domestic Dogs: A Temporal Genomic Approach." *Molecular Ecology* 32, no. 22: 5986–5999. https://doi.org/10.1111/mec.17171.

Lucena-Perez, M., J. L. A. Paijmans, F. Nocete, et al. 2024. "Recent Increase in Species-wide Diversity After Interspecies Introgression in the Highly Endangered Iberian Lynx." *Nature Ecology & Evolution* 8, no. 2: 282–292. https://doi.org/10.1038/s41559-023-02267-7.

Mikkelsen, E. K., and D. Irwin. 2021. "Ongoing Production of Low-Fitness Hybrids Limits Range Overlap Between Divergent Cryptic Species." *Molecular Ecology* 30, no. 16: 4090–4102. https://doi.org/10.1111/mec. 16015

Miller, C. R., J. R. Adams, and L. P. Waits. 2003. "Pedigree-Based Assignment Tests for Reversing Coyote (*Canis latrans*) Introgression Into the Wild Red Wolf (*Canis rufus*) Population." *Molecular Ecology* 12, no. 12: 3287–3301. https://doi.org/10.1046/j.1365-294X.2003.02003.x.

Norderhaug, K. M., H. Knutsen, K. Filbee-Dexter, et al. 2024. "The International Union for Conservation of Nature Red List Does Not Account for Intraspecific Diversity." *ICES Journal of Marine Science* 81, no. 5: 815–822. https://doi.org/10.1093/icesjms/fsae039.

O'Brien, D., L. Laikre, S. Hoban, et al. 2022. "Bringing Together Approaches to Reporting on Within Species Genetic Diversity." *Journal of Applied Ecology* 59, no. 9: 2227–2233. https://doi.org/10.1111/1365-2664. 14225.

Olden, J. D., N. LeRoy Poff, M. R. Douglas, M. E. Douglas, and K. D. Fausch. 2004. "Ecological and Evolutionary Consequences of Biotic Homogenization." *Trends in Ecology & Evolution* 19, no. 1: 18–24. https://doi.org/10.1016/j.tree.2003.09.010.

Ottenburghs, J. 2021. "The Genic View of Hybridization in the Anthropocene." *Evolutionary Applications* 14, no. 10: 2342–2360. https://doi.org/10.1111/eva.13223.

Pogorevc, N., A. Dotsev, M. Upadhyay, et al. 2024. "Whole-genome SNP Genotyping Unveils Ancestral and Recent Introgression in Wild and Domestic Goats." *Molecular Ecology* 33, no. 1: e17190. https://doi.org/10.1111/mec.17190

Powell, D. M. 2023. "Losing the Forest for the Tree? On the Wisdom of Subpopulation Management." *Zoo Biology* 42, no. 5: 591–604. https://doi.org/10.1002/zoo.21776.

Quilodrán, C. S., J. I. Montoya-Burgos, and M. Currat. 2020. "Harmonizing Hybridization Dissonance in Conservation." *Communications Biology* 3: 391. https://doi.org/10.1038/s42003-020-1116-9.

Quinzin, M. C., J. Sandoval-Castillo, J. M. Miller, et al. 2019. "Genetically Informed Captive Breeding of Hybrids of an Extinct Species of Galapagos Tortoise." *Conservation Biology* 33, no. 6: 1404–1414. https://doi.org/10.1111/cobi.13319.

Ralls, K., J. D. Ballou, M. R. Dudash, et al. 2018. "Call for a Paradigm Shift in the Genetic Management of Fragmented Populations: Genetic Management." *Conservation Letters* 11, no. 2: e12412. https://doi.org/10.1111/conl.12412

Rees, P. A. 2002. "European and International Wildlife Law." In *Urban Environments and Wildlife Law*, edited by P. A. Rees, (255–307. John Wiley & Sons, Ltd. https://doi.org/10.1002/9780470758519.ch7.

Rezek, R. J., B. Lebreton, B. Sterba-Boatwright, and J. Beseres Pollack. 2017. "Ecological Structure and Function in a Restored Versus Natural Salt Marsh." *PLoS ONE* 12, no. 12: e0189871. https://doi.org/10.1371/journal.pone.0189871.

Rhymer, J. M., and D. Simberloff. 1996. "Extinction by Hybridization and Introgression." *Annual Review of Ecology and Systematics* 27, no. 1: 83–109. https://doi.org/10.1146/annurev.ecolsys.27.1.83.

Rodger, Y. S., R. Dillon, K. Monro, et al. 2024. "Benefits of Outcrossing and Their Implications for Genetic Management of an Endangered Species With Mixed-Mating System." *Restoration Ecology* 32, no. 1: e14057. https://doi.org/10.1111/rec.14057.

Runemark, A., M. Vallejo-Marin, and J. I. Meier. 2019. "Eukaryote Hybrid Genomes." *PLOS Genetics* 15, no. 11: e1008404. https://doi.org/10.1371/journal.pgen.1008404.

Salvatori, V., V. Donfrancesco, A. Trouwborst, et al. 2020. "European Agreements for Nature Conservation Need to Explicitly Address Wolf-Dog Hybridisation." *Biological Conservation* 248: 108525. https://doi.org/10.1016/j.biocon.2020.108525.

Senn, H. V., M. Ghazali, J. Kaden, et al. 2019. "Distinguishing the Victim From the Threat: SNP-Based Methods Reveal the Extent of Introgressive Hybridization Between Wildcats and Domestic Cats in Scotland and Inform Future In Situ and Ex Situ Management Options for Species

Restoration." *Evolutionary Applications* 12, no. 3: 399–414. https://doi.org/10.1111/eva.12720.

Simberloff, D. 1996. "Hybridization Between Native and Introduced Wildlife Species: Importance for Conservation." *Wildlife Biology* 2, no. 3: 143–150. https://doi.org/10.2981/wlb.1996.012.

Stockwell, C. A., A. P. Hendry, and M. T. Kinnison. 2003. "Contemporary Evolution Meets Conservation Biology." *Trends in Ecology & Evolution* 18, no. 2: 94–101. https://doi.org/10.1016/S0169-5347(02)00044-7.

Stoskopf, M. K., K. Beck, B. B. Fazio, et al. 2005. "From the Field: Implementing Recovery of the Red Wolf—Integrating Research Scientists and Managers." *Wildlife Society Bulletin* 33, no. 3: 1145–1152. https://doi.org/10.2193/0091-7648(2005)33%5B1145:FTFIRO%5D2.0.CO;2.

Stronen, A. V., and P. C. Paquet. 2013. "Perspectives on the Conservation of Wild Hybrids." *Biological Conservation* 167: 390–395. https://doi.org/10.1016/j.biocon.2013.09.004.

Taylor, S. A., and E. L. Larson. 2019. "Insights From Genomes Into the Evolutionary Importance and Prevalence of Hybridization in Nature." *Nature Ecology & Evolution* 3, no. 2: 170–177. https://doi.org/10.1038/s41559-018-0777-y.

Tensen, L., and K. Fischer. 2024. "Evaluating Hybrid Speciation and Swamping in Wild Carnivores With a Decision-Tree Approach." *Conservation Biology* 38, no. 1: e14197. https://doi.org/10.1111/cobi.14197.

Todesco, M., M. A. Pascual, G. L. Owens, et al. 2016. "Hybridization and Extinction." *Evolutionary Applications* 9, no. 7: 892–908. https://doi.org/10.1111/evs.12367

Trouwborst, A. 2014. "Exploring the Legal Status of Wolf-Dog Hybrids and Other Dubious Animals: International and EU Law and the Wildlife Conservation Problem of Hybridization With Domestic and Alien Species." *Review of European, Comparative & International Environmental Law* 23, no. 1: 111–124. https://doi.org/10.1111/reel.12052.

Trouwborst, A., M. Krofel, and J. D. C. Linnell. 2015. "Legal Implications of Range Expansions in a Terrestrial Carnivore: The Case of the Golden Jackal (*Canis aureus*) in Europe." *Biodiversity and Conservation* 24: 2593–2610. https://doi.org/10.1007/s10531-015-0948-y.

USFWS. 1996. "Endangered and Threatened Wildlife and Plants; Proposed Policy and Proposed Rule on the Treatment of Intercrosses and Intercross Progeny (the Issue of 'Hybridization'); Request for Public Comment." *Federal Register* 61, no. 26: 4710–4713.

Van Oppen, M. J. H., J. K. Oliver, H. M. Putnam, and R. D. Gates. 2015. "Building Coral Reef Resilience Through Assisted Evolution." *Proceedings of the National Academy of Sciences* 112, no. 8: 2307–2313. https://doi.org/10.1073/pnas.1422301112.

vonHoldt, B. M., J. W. Hinton, A. C. Shutt, et al. 2022. "Reviving Ghost Alleles: Genetically Admixed Coyotes Along the American Gulf Coast Are Critical for Saving the Endangered Red Wolf." *Science Advances* 8, no. 26: eabn7731. https://doi.org/10.1126/sciadv.abn7731.

vonHoldt, B. M., K. E. Brzeski, D. S. Wilcove, and L. Y. Rutledge. 2018. "Redefining the Role of Admixture and Genomics in Species Conservation." *Conservation Letters*, 11: e12371. https://doi.org/10.1111/conl.12371

Wang, S. 2024. "Divergent Island Hybrids Mixed Waves of Ancient Gene Flow." *Molecular Ecology* 33, no. 5: e17279. https://doi.org/10.1111/mec. 17279.

Wayne, R. K., and H. B. Shaffer. 2016. "Hybridization and Endangered Species Protection in the Molecular Era." *Molecular Ecology* 25, no. 11: 2680–2689. https://doi.org/10.1111/mec.13642.

## **Supporting Information**

Additional supporting information can be found online in the Supporting Information section.

Supplementary Material: conl13158-sup-0001-SuppMat.docx

Conservation Letters, 2025 9 of 10