

Review

Scientists' warning on genetic pollution

Anagnostis Theodoropoulos^{1,2} · Kathryn A. Stewart³ · Ben Wielstra^{1,2}

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© The Author(s) 2025 **OPEN****Abstract**

Genetic pollution (i.e. anthropogenic hybridization) is insidious; it is a worryingly common problem that should be taken more seriously. Advances in DNA sequencing technologies make it possible to obtain the information to make management decisions. Yet, policy uptake is urgently needed.

1 Main text

Our world is bleeding biodiversity, from the genes that make up species to the ecosystems that they inhabit [1]. Drivers are multifaceted, with invasive species being major contributors. Invasive species are known to prey on, compete with, and transmit diseases to native species [2–5]. However, a less known – and more insidious – threat is anthropogenic hybridization [6–12]. This may occur when native species are reproductively compatible with introduced species, including non-native species, domesticated species, and genetically modified organisms (Fig. 1). Furthermore, human disturbance, via habitat modification and climate change, may intensify hybridisation in natural hybrid zones [13–15].

Similar to natural hybridization, the extent of gene flow during anthropogenic hybridization depends on the fitness of the hybrid offspring [12, 16–18]. If hybrids are sterile, gene flow between species is absent. However, if hybrids are fertile, the issue becomes more complicated. Backcrossing with one of their parent species facilitates the seeping of alleles that evolved in one species into the gene pool of another species – a process called introgression [19]. If introgression runs from the introduced into the native species, the arguably loaded term that can be used to refer to such anthropogenic introgression is 'genetic pollution' [8, 20, 21]. Various other terms such as 'swamping', 'infection', 'deterioration', 'assimilation' or 'mixing' have been used before, but, in our opinion, 'pollution' conveys the seriousness of the issue and emphasizes its human-induced nature. The term genetic pollution also applies below the species level (e.g. subspecies or populations) [8].

How does genetic pollution unfold? If an introduced species expands at the expense of the native species and the two hybridize in the process, then genetic pollution is typically restricted to the area directly surrounding the introduced species ('edge' in Fig. 1). Such a pattern has been documented in crested newts across Europe, where the Italian crested newt has been introduced within the range of the northern crested newt, resulting in genetic pollution [10, 22–25]. However, if an introduced allele has a fitness benefit, it will be 'dragged' into the native gene pool by natural selection, far beyond the area in which the introduced species is genetically dominant ('outside' in Fig. 1). For example, in *Helicoverpa* moths in Brazil, a native species has become more resistant to insecticides because of

✉ Ben Wielstra, b.m.wielstra@biology.leidenuniv.nl | ¹Institute of Biology Leiden, Leiden University, 2300 RA Leiden, The Netherlands. ²Naturalis Biodiversity Center, 2300 RA Leiden, The Netherlands. ³Institute of Environmental Sciences, Leiden University, Leiden, Netherlands.



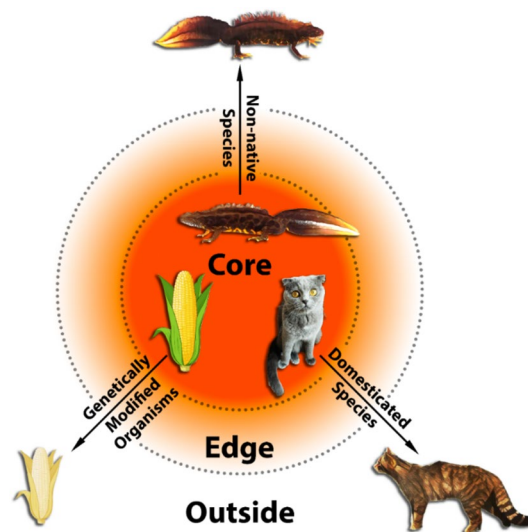


Fig. 1 Impact of genetic pollution following an invasion. The 'core' region represents the area where the genetic material of non-native species, domesticated species or genetically modified organisms is introduced and dominant. The 'edge' region reflects the surrounding areas where the native gene pool is infiltrated by non-native genetic material. The 'outside' region indicates the portion of the native gene pool that remains unaffected by this intrusion. The presented species pairs are the Italian crested newt (*Triturus cristatus*) and the Northern crested newt (*T. cristatus*), the domestic house cat (*Felis catus*) and the European wildcat (*F. silvestris*) and genetically modified and non-GMO corn (*Zea mays*)

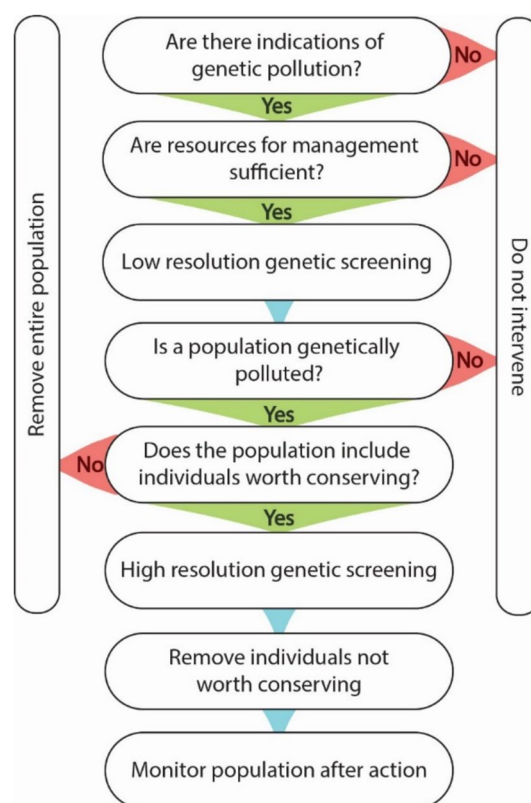
introgression of an allele 'donated' by an invasive moth species [26]. Similarly, weedy rice in the southern US has gained herbicide resistance through introgressive hybridization with cultivated rice varieties [27].

Many examples of genetic pollution have accumulated. For instance, genes have transferred from introduced mallards into New Zealand grey ducks and Hawaiian ducks [28, 29] and white-headed ducks in Europe are considered at risk from genetic pollution by ruddy ducks introduced from North America [30]. Transmarine dispersal has led to introgression from the invasive turnstone *Ciconia robusta*, originally from the Northeast Pacific, into its congeners, *C. intestinalis* and *C. roulei*, native to the Northeast Atlantic [31, 32]. The genetic integrity of wildcats [33–35] and wolves [35–38] is compromised by ongoing hybridization with their domestic (and sometimes feral) counterparts. Transgenes have 'escaped' from multiple genetically modified organisms, such as salmon, rapeseed, rice and sunflowers, into wild populations [27, 39–44]. Given that 10% of animal species and 25% of plant species are capable of hybridization [19, 45], it is not surprising that anthropogenic hybridization occurs regularly and documented cases may only represent the tip of the iceberg [46].

Why should we be concerned about genetic pollution? Put bluntly, genetic pollution equals biodiversity loss by extinction at the genetic level [9, 47]. It adds an additional layer of complications to an already difficult conservation problem. In addition to native species being directly outcompeted by introduced species, native alleles can also be replaced by introduced alleles via introgression. The net result is even greater biodiversity loss. Moreover, admixed hybrids may influence the local ecosystems differently compared to native or introduced species. For instance, in California, tiger salamander hybrids remain in their larval stage longer than the native species, which leads to more intensive predation on tadpoles of other amphibian species [48].

Despite being highlighted for decades, genetic pollution is not universally acknowledged as a conservation problem [49–52], but see a rare example of recent progress [53]. Although there are strict rules to prevent genetic pollution by genetically modified organisms, this is not the case for domesticated and non-native species [49]. Beyond minimal policy-uptake or recognition of genetic pollution over the last 25 years (188 policy documents out of 18 million globally; see Appendix), a legislative grey area exists because anthropogenic hybrids do not have a clear legal status. In the US, efforts have been made to establish legislation regarding genetic pollution, but currently no strategy has been formalized and the situation remains in limbo [49]. The largest obstacle is that a one-size-fits-all solution does not apply [52]. When hybrids have genetic ancestry of both introduced and endangered species, this begs the question: should these hybrids be subject to legal removal or legal protection? For example, if the native species is rare and most individuals possess at least some introduced alleles, their removal might not be the optimal

Fig. 2 Genetic pollution management decision tree. We summarize the key questions and actions that policy makers and management authorities need to consider. Low resolution genetic screening would, for example, be the use of mitochondrial DNA barcoding, while high resolution genetic screening would encompass a panel of nuclear DNA markers to establish the degree of genetic admixture



management strategy [54–57]. Furthermore, the controlled introduction of introduced alleles might actually be used in the context of ‘genetic rescue’ to counteract inbreeding depression [58–61].

What is required to tackle genetic pollution? Incontrovertibly: avoid introducing non-native species in the first place because prevention is better than a cure. And if non-native species are introduced, act as soon as possible because invasion is an exponential problem [4, 5, 50, 62]. Compared to a ‘regular’ introduction, however, genetic pollution brings another layer of complexity to the table. Distinguishing closely related species – let alone their genetically admixed progeny – from appearance alone is a major challenge [10, 54]. The solution lies in genome-wide data [11, 12, 63–66]. Advances in availability and affordability of DNA sequencing technologies promise that such data could be generated efficiently for many individuals [13]. For example, population-level genetic data could potentially be collected without the need to sample individual organisms from environmental DNA (eDNA) [67, 68]. Mapping how genes spread from introduced species into native populations provides the input required to make more effective and informed management decisions [12, 35, 49, 54, 69].

While genetic pollution may seem like an esoteric problem, we call for vigilance against this increasing yet often underappreciated (or legislated) biodiversity-eroding force. By improving awareness of genetic pollution we hope to foster public support for conservation actions and promote uptake into policy decision making [70–76]. We provide a decision tree to support policy makers in drafting legislation and management authorities in the planning of conservation actions (Fig. 2).

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Data availability Data files can be found on Figshare (<https://doi.org/10.6084/m9.figshare.28240736>).

Declarations

Competing Interests The authors declare no competing interests.

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Appendix

Genetic pollution/hybridization search results in overton

Searching through Overton.io (search date 20/01/2025), a policy document database of over 18 million documents globally, we collected sources (originating from government or governmental agencies) referencing genetic pollution as it pertains to hybridization/hybridisation using the Boolean search terms “genetic pollution” and “hybrid*”. We recovered a total of 188 policy documents referring to these terms, with a total of 718 mentions of these terms within document texts. Globally, documents referring to genetic pollution remained low, averaging 9 documents per year since 1999 but steadily increasing over time. Of all policy documents referencing genetic pollution, these documents originated mostly from OECD members (n = 220), G20 (n = 192), Europe (n = 117) and G7 countries (n = 114) (among others). Data files can be found on Figshare (<https://doi.org/10.6084/m9.figshare.28240736>).

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