

ADAPTATION TO BIOINVASIONS: WHEN DOES IT OCCUR?

Journal:	Global Change Biology
Manuscript ID	GCB-23-2702
Wiley - Manuscript type:	Review
Date Submitted by the Author:	08-Nov-2023
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Keywords:	alien species, non-indigenous species, invasive species, alien species adaptation, genetic paradox of invasions, adaptation, adaptation in invasions
Abstract:	The presence of alien species represents a major cause of habitat degradation and biodiversity loss worldwide, constituting a critical environmental challenge of our time. Despite sometimes experiencing reduced propagule pressure, leading to a reduced genetic diversity and an increased chance of inbreeding depression, alien invaders are often able to thrive in the habitats of introduction, giving rise to the so-called "genetic paradox" of biological invasions. The adaptation of alien species to the new habitats is therefore a complex aspect of biological invasions, encompassing genetic, epigenetic, and ecological processes. Albeit numerous studies and reviews investigated the mechanistic foundation of the invaders' success and aimed to solve the genetic paradox, still remains a notable oversight regarding the temporal context in which adaptation takes place. Given the profound knowledge and management implications, this neglected aspect of invasion biology should receive more attention when examining invaders' ability to thrive in the habitats. Here, we discuss the adaptation mechanisms exhibited by alien species with the purpose of highlighting the timing of their occurrence during the invasion process. We analyse each stage of the invasion separately, providing evidence that adaptation mechanisms play a role in all of them. However, these mechanisms vary across the different stages of invasion, and are also influenced by other factors, such as the transport speed, the reproduction type of the invader, and the presence of human interventions. Finally, we provide insights into the implications for management and identify knowledge gaps, suggesting avenues for future research that can shed light on species adaptability. This, in turn, will contribute to a more comprehensive understanding of biological invasions.

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- 1 Title: ADAPTATION TO BIOINVASIONS: WHEN DOES IT OCCUR?
- 2 Running Head: Alien species' adaptation along invasion

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ABSTRACT

The presence of alien species represents a major cause of habitat degradation and biodiversity loss worldwide, constituting a critical environmental challenge of our time. Despite sometimes experiencing reduced propagule pressure, leading to a reduced genetic diversity and an increased chance of inbreeding depression, alien invaders are often able to thrive in the habitats of introduction, giving rise to the so-called "genetic paradox" of biological invasions. The adaptation of alien species to the new habitats is therefore a complex aspect of biological invasions, encompassing genetic, epigenetic, and ecological processes. Albeit numerous studies and reviews investigated the mechanistic foundation of the invaders' success and aimed to solve the genetic paradox, still remains a notable oversight regarding the temporal context in which adaptation takes place. Given the profound knowledge and management implications, this neglected aspect of invasion biology should receive more attention when examining invaders' ability to thrive in the habitats. Here, we discuss the adaptation mechanisms exhibited by alien species with the purpose of highlighting the timing of their occurrence during the invasion process. We analyse each stage of the invasion separately, providing evidence that adaptation mechanisms play a role in all of them. However, these mechanisms vary across the different stages of invasion, and are also influenced by other factors, such as the transport speed, the reproduction type of the invader, and the presence of human interventions. Finally, we provide insights into the implications for management and identify knowledge gaps, suggesting avenues for future research that can shed light on species adaptability. This, in turn, will contribute to a more comprehensive understanding of biological invasions.

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1. INTRODUCTION

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53 Biological invasions are one of the main drivers of global change and pose significant threats to biodiversity, ecosystems, and human well-being (Bellard et al., 2016; Shackleton et al., 2019; Pyšek 54 et al., 2020). Besides, the magnitude of alien species introduction continues to increase (Seebens et 55 al., 2017), and the negative effects they bring are expected to exacerbate further (Hulme et al., 56 2014; Juliano & Lounibos, 2005; Haubrock et al., 2021; Fantle-Lepczyk et al., 2022). 57 However, despite their concerning impact on global biodiversity, biological invasions also offer a 58 unique opportunity to investigate population evolution within a timescale compatible with human 59 life. Indeed, the intentional or unintentional introduction of species into new habitats serves as a 60 61 recurring and unique experiment involving many different taxa. These experiments shed light on the adaptation mechanisms of invaders, which play a role in their ability to survive, establish and 62 spread into new areas with different biotic and abiotic components (e.g. Estoup et al., 2016; Marin 63 et al., 2019). These mechanisms are particularly intriguing when the introduced population is built 64 up and becomes invasive starting from just a few initial founders. 65 Allendorf and Lundquist (2003) used the concept of "genetic paradox" to describe the contradiction 66 arising from the ability of some species to establish invasive populations starting from small 67 propagules, despite having reduced genetic variation due to demographic bottlenecks and genetic 68 69 drift. This reduced variation is indeed expected to lead to inbreeding depression, thus hindering the ability of the introduced population to persist and evolve in the new environment (Allendorf & 70 Lundquist, 2003). While many possible explanations have been proposed to unravel the genetic 71 paradox underlying biological invasions (Estoup et al., 2016; Marin et al., 2019; Stapley et al., 72 2015; Hawes et al., 2016), the chronological order in which adaptation events occur still remains a 73 74 crucial knowledge gap. 75 Understanding when and under which evolutionary processes adaptation is mostly like to develop is critical to thoroughly comprehend the invasion process. Furthermore, this understanding holds 76

significant implications for management, as it can help design strategies to effectively counter the 77 invasion process. 78 In this review, we used as reference the framework proposed by Blackburn et al. (2011), which 79 80 breaks down the invasion process into stages. These stages include the movement from the native range towards new areas, the release or escape from confinement, the establishment of populations 81 and their subsequent spread. Each stage is characterised by a specific barrier that individuals must 82 overcome to progress to the next step. 83 While it may be intuitive to assume that the adaptation process primarily takes place in the new 84 range (as introduced organisms do not face the new habitat before), existing literature demonstrates 85 that adaptation can occur in each stage of the invasion process. Besides, adaptation in the different 86 stages is not mutually exclusive. Our purpose is to illustrate how adaptation mechanisms helping 87 invaders in overcoming their barriers can evolve during each phase of the invasion process 88 described by Blackburn et al. (2011), and even earlier in the native range of the invader. Moreover, 89 90 we aim to highlight the management and research implications resulting from a full understanding 91 of the adaptation timeframe. In this review, we firstly explain the main adaptation mechanisms occurring during invasions, 92 subdivided into three main phases of the invasion process. First, the (future) invader is in its native 93 geographic range, where it naturally lives. Second, the transport: the invading organisms leave their 94 native range, transit across geographical barriers and reach a non-native environment; this stage also 95 includes the captivity and/or cultivation phases in the new range. Third, the establishment and 96 spread of the introduced population in the new area. Then we analyse how adaptation can develop 97 within each specific stage, providing concrete examples and insights into the implications for 98 effective management. Finally, we discuss how future research efforts should attempt to disentangle 99 the role of each stage in the adaptation of invaders. 100

A comprehensive awareness of these invasion dynamics can significantly enhance our ability to 101 effectively address the challenges posed by invasive alien and protect biodiversity and ecosystems. 102 103 2. PRE-ADAPTATION IN BIOLOGICAL INVASIONS 104 The definition of "pre-adaptation" here adopted is "adaptation to an environmental circumstance of 105 106 the new range which evolved in the native range and which, thus, both the introduced and nativesource populations are able to display". 107 Pre-adaptation is a prevalent feature in biological invasions, and it can be driven by a variety of 108 109 mechanisms. First, introduced organisms tend to derive from populations living in native environments that resemble the recipient ones (Peterson, 2003; Dlugosch & Parker, 2007; Cope et 110 al., 2019). When the ecological characteristics of the donor and recipient areas sufficiently match, 111 invading organisms do not face an adaptive challenge, as their success in the novel habitat does not 112 require further adaptations (Estoup et al., 2016), and their ability to establish, thus, mainly hinges on 113 114 their dispersal abilities. However, if native and recipient environments significantly differ for one or more variables, various other pre-adaptation mechanisms can intervene to help the invaders 115 overcome the constraints of the new environmental conditions. 116 2.1 Phenotypic plasticity 117 The most investigated pre-adaptation mechanism is **phenotypic plasticity**, both in animals (e.g. 118 Kistner et al., 2012; Lucek et al., 2014) and plants (e.g. Lamarque et al., 2013; Colomer-Ventura et 119 al., 2015; Elst et al., 2016). Despite not consistently being adaptive (Ghalambor et al., 2007; Lande, 120

of invasion success (Geng et al., 2016; Hahn et al., 2012; Liao et al., 2019). Although the term

"plasticity" is typically used to describe morpho-physiological characteristics, it also encompasses

2009; Davidson et al., 2011), phenotypic plasticity can facilitate invasion by allowing the

introduced organisms to adjust towards the new optimal phenotype in the first phases of invasion

(Ghalambor et al., 2007; Lande, 2009). In fact, many authors propose plasticity as a possible driver

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behavioral traits. In the context of biological invasions, this aspect is particularly significant for mammals (Gil-Fernández et al., 2020; Chow et al., 2021; Kowalczyk & Zalewski, 2009; Zalewski & Bartoszewicz, 2012, but see also Sol et al., 2002). An example of behavioral plasticity can be observed in the shelter preferences exhibited by invasive raccoon dogs (*Nyctereutes procyonoides*) in Poland (Kowalczyk & Zalewski, 2009). This species responds to predation risk and harsh climatic conditions by changing its preferential use of different shelter types during the year. winter, raccoon dogs prefer burrows and hollow trees, as they offer less visibility from predators and thermoregulation advantages. However, during reproduction and pups-rearing season, they prefer hollow trees and dense vegetation, as burrows contemplate a major contact risk with the host, pups-predator, species (i.e. badger, Kowalczyk & Zalewski, 2009). Phenotypic plasticity is a product of the evolutionary history of the species, and environmental fluctuations are known to facilitate its evolution (Meyers et al., 2005; Lee & Gelembiuk, 2008; Kristensen et al., 2018); it would thus be spontaneous to think of it as a common, equal feature of the invading and the native-source populations, as it turned out to be for many alien species (Colomer-Ventura et al., 2015; Palacio-Lopez & Gianoli, 2011). Nevertheless, it must be emphasized that plasticity can also increase after the colonization event as the result of the invasion process (Liao et al., 2019; Davidson et al., 2011; Mounger et al., 2021). An explanation for this apparent contradiction has been proposed by Lande (2009): following a sudden environmental change, selection will shape individuals' phenotypes towards a new optimal state, and this can result in an increase in plasticity. Afterwards, genetic assimilation of the new optimal phenotype will scale back the phenotypic plasticity by replacing it (Lande, 2009; Lande, 2015). A temporary increase in plasticity during the invasion has been observed bserved, for example, in the fungal pathogen Seiridium cardinale (Garbelotto et al., 2015). A fluctuation in the behavioral plasticity pattern may also occur within a single generation through individual learning (Wright et al., 2010). The new environment will thus induce plastic (and sometimes adaptive) responses in the invaders through a series of mechanisms, such as epigenetic modifications, which we discuss later in this review. If

plasticity evolves in the new environment to approach the new optimal phenotype, it should not be considered a pre-adapted trait.

2.2 Anthropogenically Induced Adaptation to Invade (AIAI)

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Pre-adaptation can result from anthropization and human activities. Hufbauer et al. (2011) introduced the model of Anthropogenically Induced Adaptation to Invade (AIAI). According to the authors, human-altered habitats within the native range can make the (future) invader adapt to a set of characteristics typical of anthropogenically-altered habitats, which the species could find again in the introduction range. Furthermore, the presence of organisms in anthropogenic areas increases the likelihood of their transportation to new geographical regions, thereby increasing the probability of their settlement there. Therefore, the already-adapted invaders do not need to face a significant adaptive challenge to succeed in the anthropized introduction area. Once introduced, they can even expand and adapt to natural habitats (Hufbauer et al., 2011). The AIAI model probably fits the invasion of the gram-negative phytopathogen *Xylella fastidiosa* in Europe. This bacterium is native to America, where the introduction of coffee cultivation (i.e. anthropogenic disturbance) allowed it to infect coffee plants (Marcelletti & Scortichini, 2016). Subsequently, the trade of coffee plants transported the bacterium to European countries, where – presumably after being initially adapted to coffee plants – it turned to other host species, such as *Olea europaea* (Marcelletti & Scortichini, 2016). The AIAI model could probably also describe the invasion of many marine, hull-fouling, alien species. In fact, harbours, marinas and their artificial substrates can host many biofouling organisms, which can colonize boat hulls and be transported to other marinas around the world (Ulman et al., 2017; Ferrario et al., 2017). However, it is worth emphasizing that the AIAI scenario is not easy to document, as it requires demonstrating (i) the adaptation of a population to human-altered habitats within its native range, and evidence that (ii) the introduced population originates from the native human-altered habitat and (iii) such population is more

adaptable compared to populations living in natural areas in the native range (Hufbauer et al., 2011).

2.3 Resistance characteristics and life-history traits

Pre-adaptation can also result from the **innate characteristics of resistance** to environmental constrain or the invaders' **life-history traits**. These general "predictors of invasion success" are several and diverse, and they have been investigated across a wide range of organisms. These traits encompass factors such as heat (Bates et al., 2013) and salinity tolerance (Piscart et al., 2011), immune response (Møller & Cassey, 2004), germination speed (Schlaepfer et al., 2009), time until reproduction (Schlaepfer et al., 2009), fecundity and reproductive rate (Jenkins & Keller, 2011; Epifanio, 2013; Cappellini et al. 2015; Cardeccia et al., 2018). A noteworthy example within this conceptual framework is the pre-adapted trait of tolerance to inbreeding depression, which has been observed in the invasive ant *Brachyponera chinensis*. Native populations of this species already exhibit a sib-mating behaviour, which may have helped them to purge deleterious alleles over generations, thus predisposing this species to invade (Eyer et al., 2018).

2.4 Exaptation

A further form of pre-adaptation could be the so-called "exaptation". Exapted traits are features that did not originally evolve for their current role but were coopted afterwards (Gould & Vrba, 1982). In the context of biological invasions, the evolution of traits that will assume a new adaptive function in the introduction range (i.e. exaptation) has been proposed (Hufbauer et al., 2011). However, despite being theoretically possible, this mechanism has to date no evidence. In addition, it would be challenging to demonstrate that a particular structure/gene plays two different roles in the native and introduction range.

Finally, it is important to emphasize that current literature does not always report a causal explanation for the observed presence of pre-adapted traits in invaders (e.g. Everatt et al., 2012). More research is required to elucidate the factors driving the ability of some organisms to thrive in sometimes very different environments although their evolutionary history has – at least apparently – not posed selective pressures in that direction.

3. ADAPTATION DURING TRANSPORT

Once taken from their range, organisms can be transported to other areas through many vectors, including ships, trains, and aircrafts (Hulme et al., 2008). After arriving in a non-native range, however, invaders may face a captivity or cultivation phase before being escaping or being released (Blackburn et al., 2011). In both transport and captivity/cultivation phases, organisms can face admixture and bottlenecks that shape their genetic pool, potentially increasing their fitness and making them adapted to the future environmental conditions they will encounter in the introduction range.

3.1 Genetic admixture during transport

During invasions (and, at least potentially, during both the captivity and cultivation phases), **genetic admixture** between genetically-differentiated individuals of the same species can increase the genetic diversity of a potential invader (Rius & Darling, 2014). However, admixture and the resulting increase in genetic diversity do not always lead to higher fitness of the invaders or, in general, to an increased invasiveness of the introduced population (Chapple et al., 2012; Irimia et al., 2021). This could have different explanations, including the presence of Dobzhansky-Muller incompatibilities (Dobzhansky, 1936; Muller, 1942). To understand such incompatibilities, consider two allopatric populations with identical genotypes at two loci (AABB). One population evolves the allele *A'*, which over generations goes to fixation (A'A'BB); the other evolves the allele *B'*, which goes to fixation as well (AAB'B'). Both populations are viable and fertile, but when they come into

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contact and mix, two alleles that do not share a common evolutionary history (A' and B') can become present in the same heterozygote genotypes (AA'BB'), potentially leading to the production of non-viable or sterile individuals. Still, in some cases, genetic admixture between individuals with different genetic backgrounds has proved to be advantageous for invaders. This can happen because of increased levels of adaptive potential (Facon et al., 2011b; Rius & Darling, 2014; Kleunen et al., 2015; Calfee et al., 2020), or even because of a reduction of Allee effects when mating availability is limited (Mesgaran et al., 2016). The outcome of a crossing between different populations (whether positive, negative or neutral) might vary even within a single species, as demonstrated with the invasive forb Centaurea solstitialis (Irimia et al., 2021), making the role of admixture in invasion biology very elusive. Nevertheless, it must be emphasized that current literature is primarily focused on demonstrating admixture between already-introduced organisms (as discussed in section 4.2), overlooking its potential role in captivity/cultivation phases. Admixture can even occur between different species, usually congeneric (Ainouche et al., 2009; Kovach et al., 2015; but see also Haynes et al., 2011). This seems to be important in plants, where hybrids are usually invasive (Ainouche et al., 2009; Pandit et al., 2006). Albeit it might not always be clear whether hybridization occurred during the cultivation phase or in the new environment, some evidences suggest a possible role of cultivation in this regard. For example, the Oxford ragwort Senecio squalidus has a hybrid origin, resulting from a cross between S. aethnensis and S. chrysanthemifolius, two Italian species. Senecio squalidus is believed to have arisen through hybridization in the gardens of Badminton (UK), where both S. aethnensis and S. chrysanthemifolius were cultivated at the end of the 17th century. After escaping cultivation, the species then rapidly spread throughout the UK (Nevado et al., 2020). Despite other species (or populations of a species) might share similar evolutionary histories, demonstrating the occurrence of hybridization events giving rise to ecologically-dominant invaders is rather challenging, as it would require at least a partial a priori knowledge of the invasion history of the species.

Nevertheless, whether hybridization in captivity/cultivation might promote invasions should be properly assessed.

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3.2 Founder events and genetic bottlenecks

The collection, transport, and captivity/cultivation of organisms can also expose populations to founder effects and genetic bottlenecks that will shape their genetic pools. In fact, both domestic animals and cultivated plants often have a reduced genetic diversity due to bottlenecks that occurred at the time of the founders collection and genetic drift occurring during the initial period of domestication when the population sizes are typically small (Makino et al., 2018; Tamburino et al., 2020). These genetic bottlenecks may act as a brake for invaders expansion, as they are well known to originate populations with reduced genetic variability, increased inbreeding depression and subsequent reduced ability to adapt (Hoelzel et al., 2008; Thévenon et al., 2002). However, despite being generally negative for populations, bottlenecks have occasionally proved to promote biological invasions. Genetic bottlenecks can, for example, lead to a decrease in intraspecific competition. An example of increased ability to invade is given by Tsutsui et al. (2000), who demonstrated that introduced populations of the invasive Argentine ant (*Linepithema humile*) in California showed less intraspecific aggression compared to native ones ones, and highlighted a negative correlation between genetic similarity and the levels of aggression between colonies, in both native and introduction areas. Thus, they suggested that a reduction of genetic diversity of the introduced populations, resulting from bottleneck events during introduction led to a reduction of the intraspecific aggression among those populations. The decrease in intraspecific aggression leads to lower territoriality costs and thus allows the formation of increased colony size, making these colonies interspecifically-dominant (Tsutsui et al., 2000). In fact, loss of intraspecific aggression is expected to allow a growth in colonies size and the formation of super-colonies (i.e. colonies made up of several interconnected nests), thus enhancing ants interspecific competitive ability (Suarez et al., 2008).

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Moreover, inbreeding depression aroused by genetic bottlenecks can lead to purging of genetic load, in particular reducing highly recessive alleles (Wang et al., 1999; Grossen et al., 2020). However, it is not always clear in which phase the purging of deleterious alleles can occur (Barringer et al., 2012), and in the context of biological invasions, to date, there is no evidence of a pre-introduction bottleneck leading to this purging process.

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3.3 Selection and physiological adaptive responses

Albeit the evolution of invading propagules during transport is commonly attributed to stochastic events (i.e. genetic bottlenecks), a recent review (Briski et al., 2018) emphasized the role that **selection** may play between the collection of organisms and their introduction elsewhere. The authors highlighted that specific selective pressures acting on transported individuals can promote the development of resistance traits. For example, the exposure of the travelling propagule to elevated temperatures, food scarcity or ultraviolet light, could lead to populations that are more prone to survive these stressors upon introduction (Briski et al., 2018). It is important to underlie that the different conditions experienced during transport can also influence the invasion success by enabling physiological (and/or epigenetic) adaptive responses in the invading organisms, rather than merely genetic changes at the population level. For example, slow moving vessels are often expected to let hull-fouling species gradually adapt to changing water temperature and salinity; these conditions of absence of sharp disturbance might also allow the formation of larger colonies (Campbell & Hewitt, 2015). In such scenarios, disentangling the role of physiological adaptations, genetic changes, and epigenetic changes is not easy, and it is highly likely that all these factors contribute to the development of resistance characteristics during the slow transportation process. Hence, the transport process can be a key step for some biological invasions, as it might both sharply alter the genetic pool of the transferred organisms and make them physiologically adapted to succeed in the invasion process.

4. ADAPTATION IN THE NEW HABITAT

In the new range introduced organisms can undergo adaptation, as the new environmental conditions can favour genetic and non-genetic modifications, and human actions (e.g. multiple introductions, habitat alteration, climate change) can favor the process of adaptation itself (Raitsos et al., 2010; Fukasawa et al., 2013; Rius et al., 2014; Negi et al., 2016; Marin et al., 2018). This dynamic interaction between invasive species and their changing environments can lead to the development of new traits that enhance their survival and competitiveness in the invaded ecosystem.

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4.1 Epigenetics and Transposable Elements (TEs)

In this phase of the invasion process, the role of **transposable elements** (TEs) activity and epigenetic modifications can be crucial. Both TEs activity and epigenetic modifications are, in fact, known to be stimulated by novel or stressful environments, and these two mechanisms can act independently or together, since both are sensible to environmental changes. Moreover, epigenetic changes can alter TEs mobility and expression, as to contrast the potentially deleterious consequences of TEs activity, the genome has evolved many epigenetic mechanisms aimed at reducing their activity (Marin et al., 2019; Slotkin & Martienssen, 2007). On the other side, TEs activity may mediate epigenetic regulation as well (Negi et al., 2016). Thus, TEs activity and epigenetic modifications may contribute to the success of invasions by facilitating both adaptive evolution and phenotypic plasticity (Marin et al., 2019). TEs are mobile repeated DNA segments that can move in the genome and induce mutations, thereby altering gene regulation. Despite their possible negative consequences on individuals (as their increase is generally negatively correlated with the individual fitness), TEs can also produce new genetic and phenotypic variation on which selection can act (Slotkin & Martienssen, 2007; Negi et al., 2016). In fact, in native populations, TEs are expected to constitute a great but hidden variation, as their activity is well regulated by a complex epigenetic system (Slotkin & Martienssen,

2007; Marin et al., 2019). However, when organisms face a new environment and experience new 330 stressors, this hidden genetic variation is released. This happens because stress can directly trigger 331 TEs activity and reduce TEs epigenetic silencing mechanisms, indirectly triggering TEs activity. 332 The increase of TEs activity is expected to add to the population new variability on which selection 333 can act, thus favouring long term adaptive responses (Slotkin & Martienssen, 2007; Negi et al., 334 2016; Lanciano & Mirouze, 2018). This pattern has been shown, for example, in invasive 335 populations of the ant Cardiocondyla obscurior (Errbii et al., 2021). The role of TEs in biological 336 invasions has been reviewed by Stapley et al. (2015) and Marin et al. (2019); however, to date, 337 there is no evidence of a direct causal correlation between increase in TEs activity due to new 338 339 habitat-related stress and the success of an invasion. As for epigenetics, although the ability of populations to evolve is generally considered limited by 340 the existing genetic variation, environmental changes and stress can generate epigenetic 341 342 modifications, which can, in turn, alter gene expression to trigger adaptive responses to the new conditions. This happens in a wide range of organisms, including animals and plants (Marin et al., 343 2019; Hawes et al., 2018; Mounger et al., 2021). 344 In fact, phenotypic modifications following environmental changes have often been attributed to 345 changes in gene expression consequent to an alteration of the epigenetic patterns (e.g. Gao et al., 346 347 2010). For example, epigenetic modifications following a stress phase can make plants resistant to the same stress: if the stress recurs in the future, the plant is able to give a more effective response 348 to contrast it. These epigenetic changes are rapid, reversible and can even be inheritable across 349 350 generations (Mauch-Mani et al., 2017; Gao et al., 2010). Furthermore, epigenetic modifications may be able to enhance phenotypic plasticity and generate heritable variation on a shorter timescale than 351 mutations in DNA nucleotide sequences (Hawes et al., 2018; Mounger et al., 2021). A common 352 approach to study the role of epigenetic mechanisms in the success of biological invasions involves 353 comparing methylation patterns of different populations of the same species from different 354 colonized geographical areas. Although this method does not directly examine the relationship 355

between epigenetic modifications and traits variation, it allows to explore how environmental cues shape methylation patterns (Marin et al., 2019). For example, in China, DNA differential methylation patterns are thought to be responsible for the invasion success of the plant *Chenopodium ambrosioides* in metal-contamined sites (Zhang et al., 2022). However, it is worth emphasizing that the correlation between epigenetic variation and the occupied environment is not universal, as epigenetic markings do not always converge in populations occupying similar environments (Marin et al., 2019). Besides, the molecular mechanisms underlying epigenetically-induced adaptation are still not clear, and further research investigating the effects of epigenetic changes on plasticity genes would be required to fulfill this knowledge gap (Mounger et al., 2021).

4.2 Admixture in the new range

Albeit genetic admixture between genetically-differentiated individuals of the same species can occur in cultivation/captivity phases (as explained in section 3.1), its role in invasion biology has mainly been explored when it takes place between wild populations in the introduction range (Kolbe et al., 2008; Chun et al. 2009; Rius & Darling, 2014; Calfee et al., 2020), where it can give the invaders levels of diversity higher than the ones in the native populations.. As previously explained, this process does not always increase the success of invaders (Chapple et al., 2012; Irimia et al., 2021). Nonetheless, a growing body of literature suggests a possible adaptive role of genetic admixture between genetically-differentiated populations occurring in the new ranges (Facon et al., 2011b; Rius et al., 2014; Kleunen et al. 2015; Calfee et al., 2020).

Even in the wild introduction range, admixture can occur between the invading species and a native counterpart (Ainouche et al., 2009; Kovach et al., 2015), or even with another established alien (Haynes et al., 2011). This process becomes particularly critical when it occurs between wild populations, as it can lead to rapid displacement of native species due to the spread of exotic genotypes (Huxel, 1999), posing a major risk in conservation biology. Similarly to admixture between populations of the same species, even hybridization is usually counter selected (Kovach et

al., 2015). However, in certain instances, this process might favor the invader (San Jose et al., 382 2023), probably because it provides alleles that are already adapted to the local environment. 383 384 4.3 Habitat alteration in the new range 385 Lastly, in the introduction range, human alteration of natural habitats can often increase the 386 likelihood of invasion, enhancing the fitness of invaders and reducing the native species' (Fukasawa 387 et al., 2013). These human-induced alterations can encompass changes in both communities 388 composition and abiotic factors. 389 For example, the prevalence of the alien squirrel Sciurus carolinensis over the native S. griseus in 390 391 California has been attributed to the better adaptation of the former to fragmented hardwood forests (Jessen et al., 2018). On a broader scale, seawater warming due to climate change has been 392 observed to facilitate the spread of alien invaders, for example, in the Mediterranean Sea (Raitsos et 393 al., 2010). 394 395 396 5. ADAPTATION ALONG THE INVASION PROCESS AND IMPLICATIONS 397 Mechanisms of adaptation during invasions numerous and multifaced, encompassing genetic, 398 399 epigenetic, and ecological processes (Estoup et al., 2016). Literature investigating adaptation during invasions has traditionally focused on finding mechanistic solutions to the genetic paradox of 400 invasions (Stapley et al., 2015; Estoup et al., 2016; Hawes et al., 2016; Marin et al., 2019). 401 402 However, there has been a general lack of interest in determining the timeframe during which adaptation is most likely to occur. 403 404 Some mechanisms of adaptation can't be avoided, as they arise from natural and innate instances of 405 the species, while others might involve, at least in part human intervention. 406

In Figure 1 we provide an overview of the primary adaptation mechanisms that occur during invasions, categorized within the invasion framework proposed by Blackburn et al. (2011), with the addition of a native range stage. However, it should be emphasized that these mechanisms, albeit typically treated as separated, are often interconnected and reliant on one another. For example, TEs activity and epigenetic modifications can mutually influence each other (Slotkin & Martienssen, 2007; Negi et al., 2016; Marin et al., 2019), and epigenetic modifications can be the basis for the development of phenotypic plasticity and resistance characteristics (Hawes et al., 2018; Mounger et al., 2021).

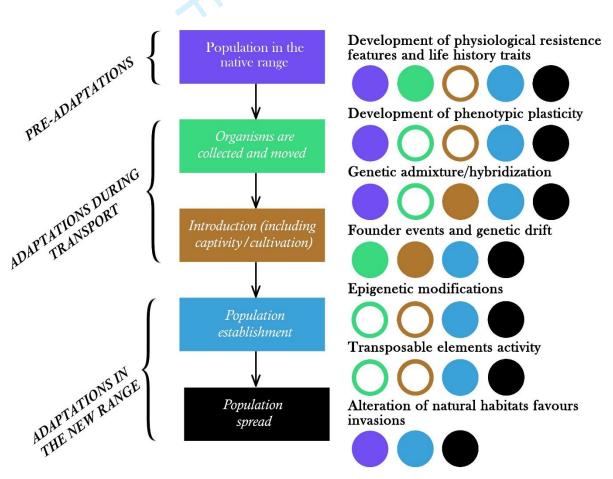


Figure 1. The invasion process is divided into the invasion stages proposed by Blackburn et al. (2011), with the addition of a native range stage. For each stage, circles on the right indicate the mechanisms of adaptation that may play a role. Full circles indicate literature supporting the mechanism occurrence whereas empty circles indicate a potential role in the stage, but absence of supporting literature. Examples are provided within the text where available (full circles).

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Albeit it is theoretically possible that epigenetic changes arisen in the native range may facilitate a future invasion, due to their responsive and reversible nature, their importance primarily stems from their ability to provide rapid adaptive responses to the changing environmental conditions (Hawes et al., 2018). Since their formation is elicited by the new environmental stress (Hawes et al., 2018; Marin et al., 2018), it is most likely to take place between stage 1 and stage 5 (Fig. 1). However, available literature is mainly focused on investigating epigenetic changes that occur in the new range (Hawes et al., 2018), and to the best of our knowledge, there are no studies that have analysed changing epigenetic patterns before organisms are already introduced. Similarly, even TEs activity is induced by environmental stress, and changing frequencies of insertions are usually attributed to the novel environmental conditions of the new range (Marin et al., 2018). Regarding both epigenetic and TEs insertions changes, once organisms are picked up, prevention is no longer possible. To avoid the development of these adaptation mechanisms in invaders, the only possible approach is to prevent the collection and transportation of organisms to other locations. Genetic admixture between genetically differentiated organisms (as well as hybridization) could theoretically occur in each stage of an invasion (Fig. 1). While admixture between alreadyintroduced organisms has often been investigated, literature exploring the role that the process may have before introduction, particularly during cultivation/captivity phases, is still scarce. Besides, some authors proposed that admixture could also occur within the native range (Gillis et al., 2009). We acknowledge that this could be the case of species introduced through hull-fouling or ballast waters. For example, the serpulid *Hydroides elegans* has a cosmopolitan distribution, showing a low genetic differentiation between populations worldwide. The constant genetic flow between populations of the species has been attributed to its biofouling nature, which allows it to be easily transported across the globe (Pettengill et al., 2007). In such cases, it is highly probable that admixture between individuals in the native range may occur even before introduction. Understanding when admixture occurs along the invasion process can have significant management implications, as different stages of the process may require distinct approaches to control this

phenomenon. For instance, in ongoing invasion processes where admixture between new individuals and established invaders can generate heterosis in the introduced population (e.g. Facon et al., 2011; Kleunen et al., 2015), it is crucial for authorities to focus on preventing or managing introductions of individuals from additional native-source populations.

It may be the case, for example, of the ladybug *Harmonia axyridis*, for which it has been proposed that the invasiveness may be enhanced through hybridization between invading individuals and pest-control ones occurring in the introduction range (Facon et al., 2011b). Understanding the phase and mechanisms of adaptation that underpin the success of an invader could, in such cases, lead to significant implications for the management and trade of the species. Thus, we believe that future research should attempt to fulfill the knowledge gaps regarding the time admixture (as well as hybridization) takes place. This knowledge can be invaluable for informed decision-making and management strategies in the context of invasive species.

Alteration of natural habitats, both in the native and the introduction range, can favor invasions. In the native range, this process can lead to the AIAI (Hufbauer et al., 2011; see section 2.2), while in the invaded range it can favor the spread of alien opportunistic species (Jessen et al., 2018).

Albeit some factors of environmental change (such as the presence of urban centers or global climatic changes) may be challenging to control, this underscores that human actions and projects should be opportunely conceived to impede the spread of alien species. For example, the introduction of artificial substrates and the destruction of naturally occurring ones in coastal and estuarine habitats might enhance alien species' advantage over native counterparts (Tyrrel & Byers, 2007). This highlights the need for careful design and planning of underwater facilities to mitigate the impact on native ecosystems. In fact, if properly designed, human-made structures could serve as a barrier to the expansion of invaders, impairing their ability to adapt upon arrival in the new range. For instance, to prevent alien flora colonisation, it has been proposed that road construction and management in natural reserves should consider the following factors (Tyser & Worley, 1992):

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-utilizing original topsoil for filling in the roadside ditches;

-avoid considering the project complete until native vegetation is fully established on the roadside;

-monitoring the presence of alien species on the roadside;

-using seeds of native species to re-establish native flora on the roadside.

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Similar planning and administrative implications have the potential to prevent the establishment of invaders in various other types of infrastructures (e.g. parks, seaports, railways). Therefore, research efforts should aim to uncover and understand these critical management aspects.

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6. CONCLUSION

Here we established a coherent sequence in which adaptation of invading species can occur in the 484 different stages of the invasion process. By structuring these stages logically, we provide 485 486 valuable insights into effective management strategies and highlight the importance of research efforts that incorporate temporal considerations into the study of biological invasions. 487 We believe that this neglected aspect of invasions deserves thorough consideration, as it could carry 488 significant implications for the management of alien invaders. Neglecting the temporal aspects 489 could, indeed, hinder a comprehensive understanding of invasion dynamics: the 490 491 study of explanations underlying the genetic paradox (Estoup et al., 2016) may be pointless if we do not account the temporal scale at which adaptation takes place. On the other hand, when studying 492 adaptation of invaders, focusing only on a few phases of the invasion process could lead to an 493 underestimation of the actual invasion risk. Therefore, we propose that future research should delve 494 into this overlooked aspect of invasion biology, trying not only to elucidate potential solutions to 495 the genetic paradox, but also discern the phases of the invasion process in which adaptation occurs. 496 This comprehensive approach will allow a deeper understanding of invasive species' population 497 dynamics, and contribute to their effective management. 498

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500	AUTHOR CONTRIBUTIONS
501	Alessandro Nota: Conceptualization; investigation; project administration; supervision;
502	visualization; writing – original draft. Sandro Bertolino : Investigation; validation; writing – review
503	& editing. Francesco Tiralongo: Validation; writing – review & editing. Alfredo Santovito:
504	Conceptualization; writing – review & editing.
505	
506	CONFLICT OF INTEREST STATEMENT
507	The authors declare that they have no conflict of interest.
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