Trends in Ecology & Evolution

Review

Adaptive Genetic Exchange: A Tangled History of Admixture and Evolutionary Innovation

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Genetic exchange between divergent evolutionary lineages, from introgressive hybridization between locally adapted populations to insertion of retroviral sequences into eukaryotic genomes, has now been documented. The detection of frequent divergence-with-gene-flow contrasts the neo-Darwinian paradigm of largely allopatric diversification. Nevertheless, of even greater significance is the growing wealth of data suggesting that the recipients of the transferred genomic material gain adaptive phenotypes from the donor lineages. This adaptive enrichment is reflected by changes in pathogenicity in viruses and bacteria, the transformation of ecological amplitude in eukaryotes, and adaptive radiations in extremely diverse lineages. Although genetic exchange may produce maladaptive consequences, most of the recently reported examples suggest increases in fitness, and many such adaptive trait transfers have been identified in our own species.

Genetic Exchange Affects Adaptive Evolution: It Is Time to Move On

When Edgar Anderson stated 'The more imperceptible introgression becomes, the greater its biological significance', and 'the wide dispersal of introgressive genes (perceptible only to the most exquisitely precise techniques) would be a phenomenon of fundamental importance' [1], he was not only predicting the evolutionary significance of genetic exchange but also the type of methodologies that would be needed to demonstrate this significance. Anderson and colleagues such as Ledyard Stebbins predicted a significant contribution of introgressive hybridization [2] to adaptive evolution and biodiversification. In the past decade this prediction has been amply validated with extensive genomic datasets and diverse adaptations in all known microbial and metazoan lineages [3–5]. The long-controversial 'divergence-with-gene-flow' [6] has also been demonstrated in many organisms. Furthermore, genetic exchange between all manner of organisms, reflecting an abundance of avenues such as sexual reproduction, parasitism, viral reassortment, and transduction is now known to have contributed to the evolution of genomes, adaptations, and entire organismic clades [7]. Thus, the field of evolutionary biology can now move past the question of whether or not evolutionary lineages can originate and diverge while undergoing genetic exchange with closely or distantly related organisms. Instead, we should consider the questions (i) how does genetic exchange affect fitness in recipient population(s) [7], and (ii) what roles do the genetic architectures of adaptation, linkage, and selection play in the short- and long-term evolutionary dynamics of introgressed genetic and phenotypic elements (Box 1)? This shift in focus requires a much more dynamic and complex model of evolutionary change, one that includes a central role for 'standing genetic variation' arising from admixture between divergent lineages [8].

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Although the exchange of genetic material between lineages as diverse as viruses and mammals has been recognized for decades, particularly through the analysis of genomic datasets, it has remained an active debate as to whether such exchanges can lead to adaptive evolution.

Recently, the growing wealth of examples of genetic transfer involving organisms from all domains of life has provided the means to test the hypothesis of adaptive genetic exchange. The repeated testing of this hypothesis has revealed not only adaptive effects among viral and prokaryotic lineages but also for plants, animals, and fungi. Indeed, the data now available indicate how profoundly important ancient and more recent gene exchange has been in the evolution of even humans.

Adaptive evolutionary diversification can now be seen as being often facilitated by the addition of standing genetic variation from one divergent lineage to another.

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Box 1. Recombination, Selection, and the Success and Persistence of Adaptive Introgressions

It may be argued that the success of introgressed adaptive traits (including genes and alleles) and the persistence of maladaptive traits depend on the specific trait, ecological parameters, and the strength of selection. Although this may be true (Tables S1 and S2 in the supplemental information online), in evolutionary terms this boils down to four parameters: (i) the rate of hybridization and/or introgression [56,57], (ii) the rate of recombination [58,59], (iii) the nature of genetic dominance [60,61], and (iv) the strength of selection [58]. A high rate of hybridization and little opportunity for recombination and selection may lead to flooding of the recipient genome with maladaptive traits. By contrast, a low rate of hybridization, coupled with an opportunity for recombination and selection, will lead to subsequent incorporation of adaptive traits while purging maladaptive traits in the recipient populations and genomes (following the mechanism of Kondrashov's hatchet [62]). An excellent example of both adaptive and non-adaptive outcomes is the Soay sheep [28]. In this case, the adaptive light coat color was introgressed from domesticated varieties recently introduced to the island habitat. At the same time, maladaptive coat patterning associated with lowered survivorship was also introgressed, but its frequency decreased over a few dozen generations. Thus, maladaptive introgression was purged over time while retaining adaptive introgression, aided by recombination and selection. This is not possible if introgression is continuous or frequent, recombination is rare, and selection is relatively weak.

If recombination and selection lead to retention of only adaptive introgressed traits, our ability to detect maladaptive introgression will deteriorate with time. At shorter time-intervals, it may appear that maladaptive introgression is rampant while adaptive introgression is rare, as judged from many recent cases of introgression between invasive and native species, or between domesticated and wild species or varieties [53,54,63]. However, over longer time-periods, as a result of recombination and selection (or extinction), only adaptive introgression will remain evident. Indeed, most instances of genetic exchange – whether ancient, recent, or current – show adaptive outcomes, but the maladaptive genetic exchanges are almost exclusively attributable to recent genetic exchange. Thus, a challenge for future studies will be to document the relative proportions, actions, and evolutionary trajectories of adaptive and maladaptive traits introgressed as a result of recent bouts of hybridization, where it is possible to study early stages of introgression, recombination, and selection. This field is ripe for theoretical development but so far has been poorly explored. The cheap and now widely accessible genomic technologies should make it possible to simultaneously test these ideas in myriad empirical systems.

We summarize below our current understanding of adaptive genetic exchange with a selection of prominent recent examples. Although Tables S1 and S2 in the supplemental material online provide a wide array of studies reporting consequences from genetic exchange, because of limited space we have essentially provided only a fraction of the examples of adaptive evolution involving prokaryotic, viral, and eukaryote-to-eukaryote horizontal genetic transfers. We will consider some of these examples in detail to illustrate (i) the diversity of phenotypic changes, (ii) the similarity of the effects detected, (iii) the inference that genetic exchange not only contributes to increased fitness but may also result in maladaptation, and (iv) the types of future studies that will clarify the role of genetic exchange in adaptive evolutionary processes.

Genomic Admixture and Reticulate Evolution Are Rampant

The Adaptive Genesis of Influenza Pandemics

Notwithstanding their mechanism of transmission, genomic constitution (i.e., 'DNA' or 'RNA' viruses), and the degree to which mortality accompanies infection, the majority of viral pathogens of humans are good examples of reticulate evolution. A novel methodology for inferring evolutionary history revealed that whereas dengue and West Nile virus isolates show limited and no indication of genetic exchange, respectively, HIV, influenza, and hepatitis C were marked by extensive reticulation [9]. Such genetic exchange is directly involved in the ability of pathogens to adapt to the immune systems of hosts. An excellent example is the ability of influenza viral pathogens of humans to evolve rapidly and thus' . . . evade immunity and reinfect previously infected individuals' [10]. The rapidity of this viral evolution within and across 'flu seasons' reflects the origin of new mutations within genes and the subsequent production of novel combinations of the genes through viral reassortment [11]. Figure 1 illustrates the role of repeated bouts of reassortment between divergent influenza genomes in the derivation of a highly virulent form. The transition from an influenza virus with low pathogenicity in avian hosts to a virulent human pathogen with 30% host mortality was also accompanied by resistance to

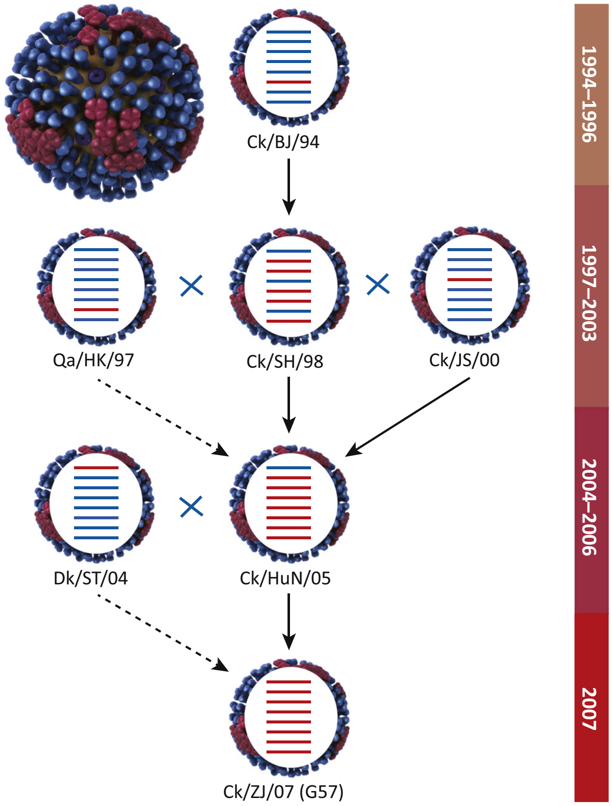

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Figure 1. The Admixed History of a Virulent Influenza. The progenitor lineage (i.e., 'G57′) of the human pathogenic influenza, H7N9, evolved through reassortment events. The horizontal bars within each viral isolate represent the eight influenza genes: PB2, PB1, PA, HA, NP, NA, M, and NS (top to bottom). Red and blue segments derive from G57 and other influenza lineages, respectively. The arrows with broken tails indicate interspecific (i.e., host) gene transmission. The years of occurrence of the various influenza types involved in the evolution of G57 are indicated along the right side of the figure. The following acronyms are used in the delineation of each viral subtype: BJ, Beijing; Ck, chicken; Dk, duck; HK, Hong Kong; HuN, Hunan; JS, Jiangsu; Qa, quail; SH, Shanghai; ST, Shantou; ZJ, Zhejiang. The two-digit number following the acronyms for the host and place of origin indicates the year of appearance of the various influenza lineages [12]. Redrawn from [12]; the image of the generic ultrastructure of the influenza virion was prepared by Dan Higgins, made available in public domain under a copyright-free arrangement [Public Health Image Library (PHIL) of the Centers for Disease Control and Prevention, Atlanta, GA, USA; https://phil.cdc.gov/phil/details.asp?pid=11823].

immunization [12]. This adaptive evolutionary transition required two coordinated processes of antigenic evolution [mostly involving the hemagglutinin (HA) glycoprotein gene] and repeated reassortment, thus unleashing viral evolution that, unfortunately for human hosts, resulted in' . . . novel reassortants with pandemic potential' [12]. Further examples in Table S1 highlight the fact that genetic exchanges and reticulate evolution are now known to be crucial for adaptations in a broad range of organisms. Moreover, these examples highlight the fact that adaptive genetic exchanges can take place in the absence of sexual reproduction not only in prokaryotes but also via horizontal transfers even in more derived eukaryotes, for example, through infections.

Genetic Exchanges Take Complex Forms and Produce Unexpected Adaptive Outcomes

CRISPR Loci and Bacterial/Archaeal Immunity

Science magazine proclaimed CRISPR genome-editing technology its 2015 'Breakthrough of the Year' [13]. This pronouncement reflected the promise and ethical dilemma presented by this molecular tool as evidenced, for example, by the modification of DNA from human embryos [14]. Nonetheless, as powerful as CRISPR will likely be for human-mediated genomic modification, its natural setting and function within the cells of bacteria and archaea reflect a pervasive impact for the biosphere as a whole.

The role played in nature by the 'CRISPR/Cas systems' – so named because of the often adjacent locations of CRISPR sequence arrays and *cas* genes – is the provision of adaptive immunity to bacteria and archaea species against viral infection [15]. When viral DNA invades a bacterial or archaeal cell that contains the CRISPR/Cas system, the following cascade of processes occurs: (i) the viral DNA molecule is fragmented; (ii) a portion of the fragmented DNA is inserted as a 'spacer' into the CRISPR locus; (iii) the CRISPR locus, with new viral DNA spacer, is transcribed and processed, resulting in mature crRNAs; (iv) the mature crRNAs form a complex with Cas proteins; (v) the crRNA/Cas protein complex is compared with invading viral DNA molecules to identify homology; and (vi) following recognition of complementarity with invading viruses, the infecting DNA is degraded by nucleases produced by *cas* loci [15]. The mechanism of genetic exchange in this adaptive process is both complex and ironic: complexity is reflected by the utilization of gene products and DNA sequences from both the host and pathogen to fight the infection; the irony is that the genome of the viral invader is incorporated into that of the host and then used in return by the hosts to identify and destroy further viral infections [15].

Genetic exchanges may take complex forms not only in host–pathogen dynamics (e.g., [16,17]) but also in symbiotic relationships (e.g., [18–20]), and facilitate protection from predators, parasites, and parasitoids (e.g., [21,22]) (Table S2). They may also produce unexpected adaptive outcomes from niche partitioning (e.g., [23,24]) to metabolic innovations (e.g., [19,25–27]), domestication (e.g., [28,29]), and sexual selection (e.g., [30–32]) (Table S2). Thus, genetic exchanges have tremendously impacted on the complexity of evolution and diversification of life on Earth, and they continue to play unexpected roles in natural species interactions and in modern human survival and health.

Genetic Exchanges Contribute to Evolutionary Innovations and Adaptive Radiations

Horizontal Transfer of Bacterial *Tal* Genes and the Evolution of Vascular Plants

The evolutionary innovations necessary for the origin and radiation of land plants from aquatic progenitors included the ability to transport materials such as nutrients and water over long distances within an organism. A key step in the evolution of vasculature of terrestrial plants was the receipt, via an ancient horizontal gene transfer event, of transaldolase (*Tal*) genes from Actinobacteria [33]. These genes, which affect the number and distribution of vascular bundles, occur only in terrestrial plants and bacteria [33]. Furthermore, genomic analyses demonstrated that the *Tal* genes underwent purifying selection following their transfer into terrestrial plants [33]. Taken together, these findings suggest that the horizontal transfer of bacterial *Tal* loci into early plants provided key genetic elements leading to the immense diversification of land plants.

Introgression and the Adaptive Evolution of Flower Color

Floral trait evolution within the *Mimulus aurantiacus* complex provides an excellent illustration of how introgressive hybridization can drive adaptive diversification. Two subspecies of *M. aurantiacus* (the yellow-flowered subspecies *australis*, and the red-flowered subspecies *puniceus*) are partially reproductively isolated owing to differences in pollinator preferences associated with flower color [34]. Genomic and phylogenetic analyses demonstrated that (i) the red-flowered phenotype is caused by *cis*-regulatory mutations in the *MaMyb2* gene, (ii) *MaMyb2* haplotypes in red-flowered but otherwise highly divergent subspecies are extremely similar, suggesting a single evolutionary origin of red coloration, and (iii) there was discordance

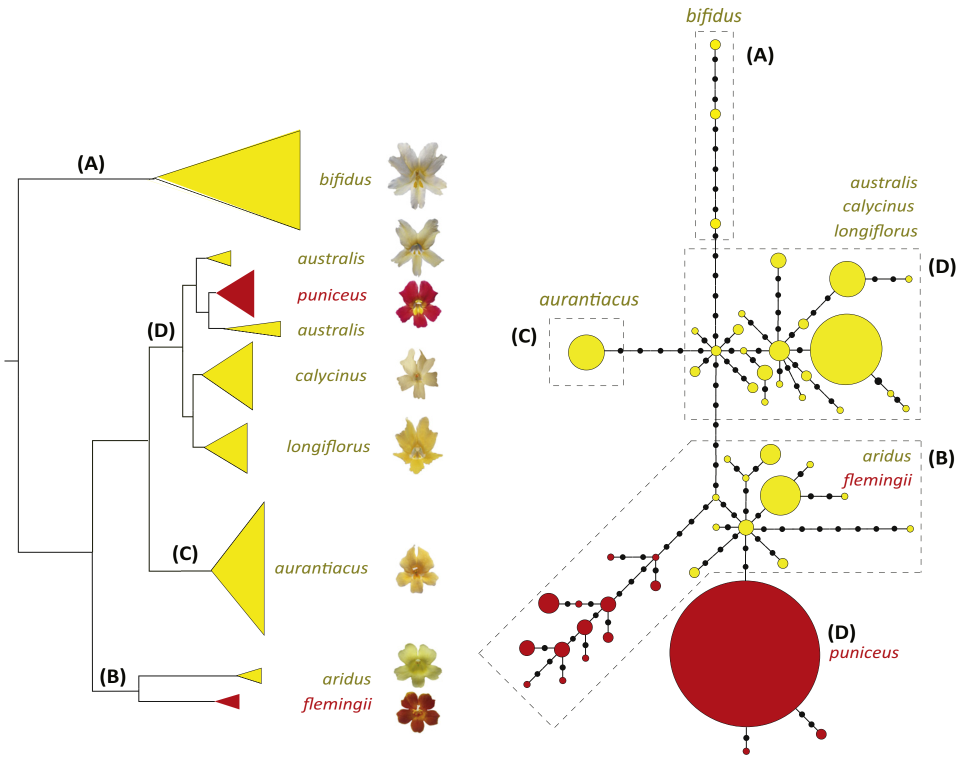

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Figure 2. The Results of Introgressive Hybridization in Transferring Red Flower Color Alleles Between *Mimulus* Clades. The introgression into *M. puniceus* is reflected in the discordance between the 'subspecies phylogeny' (left) and the haplotype network (right), made up of 53 unique *MaMyb2* haplotypes from 76 individuals representing eight subspecies. Circles reflect individual haplotypes, with the size being proportional to the observed frequency. The colors of the haplotype circles relate to flower color and indicate either the presence or absence of anthocyanins, in other words red or yellow coloration, respectively. The black circles indicate the number of mutational differences between the haplotypes. The broken lines delineate haplotypes representing each of four major subspecies clades [34]. Image courtesy of Matt Streisfeld [34], reproduced with permission..

between the taxonomy (i.e., 'subspecies phylogeny') and the haplotype network recovered from eight subspecies [34] (Figure 2). This is a classic signature of an adaptive phenotype–genotype spreading from a single origin into divergent lineages as a result of introgressive hybridization.

Introgression, Beak Shape, and Adaptive Evolution in Darwin's Finches

Although genomic data abundantly reveal adaptive trait transfer in all major organismic clades (Table S1), few studies have tested this inference using cross-generational ecological data. One remarkable exception is the 40 year research endeavor by Peter and Rosemary Grant and their colleagues on Darwin's finches of the Galápagos archipelago and Cocos Island. Aside from testing a wide array of evolutionary and ecological hypotheses, this work has provided arguably the clearest example of genetic exchange-mediated adaptive evolution [35].

The morphological traits most often described in studies of the Darwin's finch species are beak shape and size [35], which prominently affect fitness through foraging efficiency [36]. Introgressive hybridization throughout multiple bouts of climatic perturbations has increased foraging-related standing genetic variation and provided the basis for adaptation of beak morphology in Darwin's finches [36] (Figure 3). The transcription factor gene *ALX1* controls craniofacial development and differentiation, and is a key developmental genetic regulator of beak diversity within and between

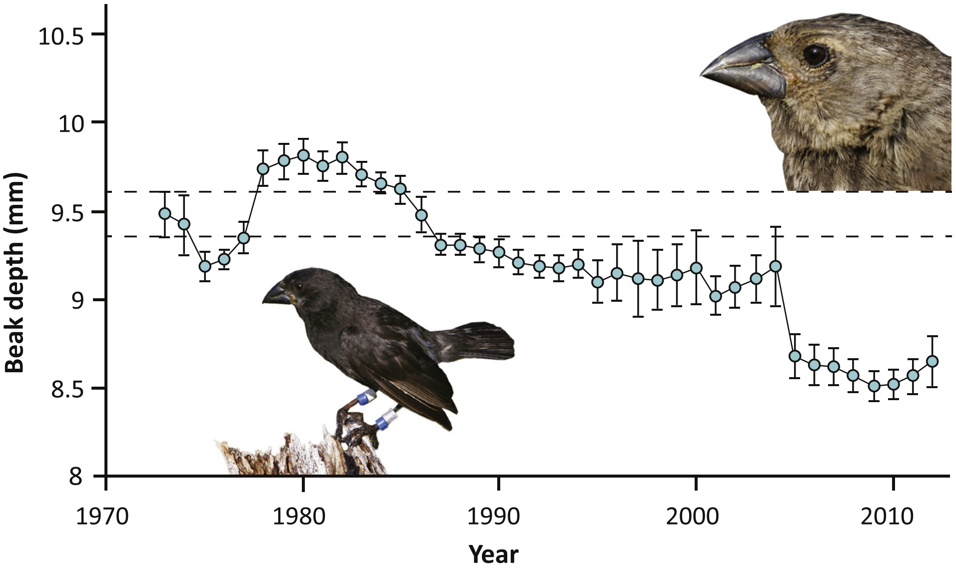

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Figure 3. The Evolution of Beak Morphology and Foraging Efficiency of Darwin's Finches Is Mediated Through Climatic Perturbations, Followed by Introgressive Hybridization and Natural Selection. A male medium ground finch (*Geospiza fortis*) living on Daphne Major Island, Galápagos, is illustrated below, and the beak morphology of the female is illustrated in the top right corner. The data illustrate the evolution of *G. fortis* beak size over a 40 year study. The mean values, together with the 95% confidence limits, reflect the entire population of *G. fortis* in each year, and the parallel horizontal lines indicate the 95% confidence limits on the mean value from the 1973 population [36]. The beak size fluctuated in response to food availability related to climatic perturbations, through which fitness was maintained with the aid of repeated adaptive hybrid introgressions of the transcription factor gene *ALX1*. This gene controls beak development and differentiation, influencing diversification of beaks among Darwin's finches and hence their expanded utilization of food resources [37]. Image courtesy of Peter Grant, reproduced with permission.

finch species [37]. The adaptive craniofacial features of the finches and the introgression of *ALX1* across populations and species suggested that 'Natural selection and introgression affecting this locus have contributed to the diversification of beak shapes among Darwin's finches and hence to their expanded utilization of food resources . . . ' [37].

These three examples (also Table S1b) highlight the fact that genetic exchange involving key genetic elements and eco-morphological innovations can be a frequent driver of adaptive radiations in prominent organismal groups.

Genetic Exchange, Mammalian Evolution, and Human Adaptations

Endogenous Retroviruses and the Evolution of Mammals

Genetic exchange has strongly influenced the evolution and biology of mammals. An important example entails the envelope protein genes, known as syncytins, which perform an essential role in placentation and which were acquired from retroviruses early in the radiation of marsupial and eutherian clades [38]. Retroviral insertions into mammalian genomes have conferred other crucial adaptations. Recent genomic and functional analyses have documented effects from retroviral insertions on the regulation of innate immunity in a diverse array of mammals, including humans [16]. These retroviral sequences have been inserted into binding sites associated with the proinflammatory cytokine interferon-γ (IFNG) [16]. Interferon molecules contribute to innate immunity by controlling the transcription of a network of genes [16]. The evolution of IFNG regulation, and thus a key component of innate immunity across mammalian lineages, involved independent infection and cooption of the gammaretrovirus, MER41 [16]. This virus-to-mammal

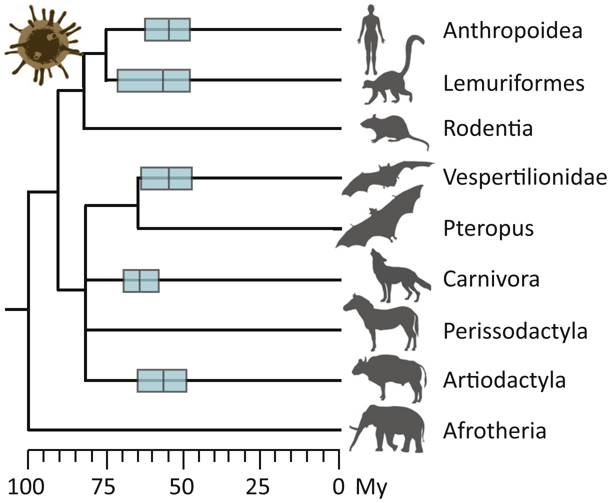

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Figure 4. The Taxonomic Distribution and Estimated Age of Cooption of the Endogenized Gammaretrovirus MER41 into Various Mammalian Genomes [16]. These retroviral sequences were incorporated through multiple, independent infections in the binding sites associated with proinflammatory cytokine interferon-γ (IFNG) [16], which have conferred innate immunity to their mammalian recipients. This is a surprising example of how incorporation of genes from an originally foreign entity in what are normally antagonistic associations could increase the fitness of the recipient genomes. Redrawn from [16].

genetic exchange apparently provided' . . . a dynamic reservoir of IFN-inducible enhancers fueling genetic innovation in mammalian immune defenses' [16] (Figure 4).

Homo sapiens as a Receptacle of Archaic Adaptations

Garrigan and Kingan [39] hypothesized, given introgression from now-extinct species of *Homo* into *Homo sapiens*, that 'the expanding anatomically modern human population [may have] acquired locally adapted genetic variants from endemic archaic populations.' Their hypothesis of adaptive trait transfer has now been repeatedly substantiated by whole-genome data from extinct *Homo* species and population genomics data from *H. sapiens* [40–48]. Some of the introgressed regions appear to be associated with maladaptive phenotypes in modern *H. sapiens*, especially with regard to associations with diseases (e.g., prostate cancer and type 2 diabetes) [47,48]. However, a portion of the allelic variation received by humans from their congeners appears to provide locally adaptive phenotypes, such as innate immunity, response to UV radiation, response to limited oxygen, spermatogenesis, and skin/hair characteristics [40–48].

An example of adaptive trait introgression into humans from Denisovans involved the response to hypoxic environments in extreme altitudes. Resequencing of the genomic interval containing the hypoxia pathway gene, *EPAS1*, in 40 Tibetan and 40 Han Chinese individuals, as well as comparison of genomic variation at this locus in global samples of humans, revealed positive selection providing adaptations to high altitudes in Tibetan populations [46]. Significantly, the pattern of variation at this locus indicated that the novel genomic characteristics resulted from the introgression of *EPAS1* alleles from the Denisovan lineage into humans [46]. As predicted by Garrigan and Kingan [39], the signature of strong, positive selection for the alleles in Tibetan populations suggested 'that admixture with other hominin species . . . provided genetic variation that helped humans to adapt to new environments' [46]. The introgressed Denisovan 'core haplotype' that provides Tibetans with adaptations to hypoxic environments also occurs in humans living above 2000 m in the Himalaya, but is absent in lowland populations [49].

Have Genetic Exchanges Sometimes Been Maladaptive?

A Historical Perspective

A common assumption emerged during the Modern Synthesis (ca 1930–1950) that genetic exchange, in the form of natural hybridization, was almost always maladaptive. This assumption was as much a philosophical as a scientific stance, reflecting the viewpoint of 'species' as sacrosanct units that kept their 'purity' or genetic integrity by avoiding reproduction with other divergent forms [7]. Notwithstanding the non-scientific essence of this assumption, one may characterize some genetic exchanges as potentially contributing to reduced fitness. To underscore this point, Table S1 includes examples of maladaptive consequences for individuals, populations, and species. Specifically, although extensive horizontal transfer of mitochondrial sequences among species from the Saccharomycetaceae has been detected, signatures of selective constraints suggest the removal of deleterious, chimeric haplotypes [50]. In humans and koalas, the insertion of sequences from infectious retroviruses has catastrophic consequences on their immune systems, thus leading to vastly reduced fitness in affected individuals [51,52]. Introgression from archaic species of *Homo* into modern humans may also have resulted in maladaptation for humans, as shown by the presence of some archaic alleles that are associated with disease risk [47,48]. It is possible to find many more examples of maladaptive introgression in contemporary populations of animals and plants, and this has special relevance with respect to invasive species, genetic assimilation, and survival or persistence of native biodiversity [7,53–55]. Thus, the traditional assumption that hybridization leads to maladaptive introgression has some merit. However, the ample evidence for adaptive genetic exchanges presented so far (also Table S1) argues for carefully assessing short- versus long-term evolutionary dynamics of introgression of adaptive and maladaptive genotypes and phenotypes (Box 1).

Separating Milk from Water: Adaptive or Maladaptive Introgression?

While we believe that the 'maladaptive' genetic exchanges listed in Table S1 indeed reflect the introgression of maladaptive genetic variations, we must point out the likelihood that some of these variations may actually be 'post-reproductive age' effects, for example retrovirus insertions in humans and koalas [51,52]. Furthermore, current deleterious effects from introduced alleles may mask an earlier or cycling adaptive role. For example, the contribution of some introgressed alleles from archaic *Homo* to diseases in *H. sapiens* [47,48] may well reflect the radical lifestyle changes in modern humans (e.g., diet) rather than continuous maladaptive effects from the time of their introduction. Thus, it is essential to properly assess fitness consequences of introgressed phenotypes, considering the natural history of organisms under appropriate ecological conditions, and by taking a longer evolutionary perspective.

Adaptive and Maladaptive Introgression in the Soay Sheep

The Soay sheep of the St. Kilda archipelago of Scotland suitably illustrates the mixed fitness effects of introgressive hybridization, and the importance of studying long-term evolutionary consequences. Though this early sheep breed has been living free for up to 4000 years on islands within this archipelago, and is phenotypically similar to wild species such as the Mouflon (*Ovis aries*), it is not reproductively isolated from recent domesticates [28]. The lack of reproductive isolation led to introgressive hybridization when domesticated sheep were recently introduced to the islands. In particular, the adaptive effects from the introgression of alleles from the introduced Dunface breed into the wild Soay sheep that determine either coat color or the patterning of coat color were inferred by combining a 25 year ecological study with data from a population genomics analysis [28]. The comparison of the ecological and genomic data detected the action of both positive and negative selection on the introgressed alleles in the Soay sheep. The selectively favored coat color phenotype (i.e., 'light') in the Soay sheep resulted from adaptive introgression of Dunface alleles at the *TYRP1* locus [28]. By contrast, the introgressed alleles at the *ASIP* locus that cause a domesticated coat patterning phenotype were associated with lowered survivorship in the Soay sheep, resulting in a decrease over time in the frequency of the domesticated alleles [28]. Overall, this analysis confirmed the expectation that introgression among divergent lineages can give rise to evolutionary novelty, but with a portion of the novelty contributing to a maladaptive phenotype.

Concluding Remarks

The traditional view that introgressive hybridization is either absent or rare, and usually maladaptive, is incompatible with the overwhelming evidence for adaptive genetic exchange mounted in the past two decades in a multitude of organisms showing variable evolutionary divergence. These findings, summarized above and in Tables S1 and S2, show that:

(i) The mechanisms of genetic exchange are diverse, and they may be independent of sexual reproduction, as demonstrated in a wide array of viruses, prokaryotes, and eukaryotes (Tables S1 and S2).

(ii) Genetic exchanges can sometimes lead to phenotypic innovations and evolutionary novelties that may affect diversification and niche evolution in adaptive radiations (Figures 3 and 4).

(iii) Genetic exchanges can take complex forms, which may produce a variety of adaptive and non-adaptive consequences (Tables S1 and S2).

(iv) Simultaneous introgression of both adaptive and maladaptive traits is possible, which should lead to conflicting selection pressures on the introgressed alleles at short timescales. This may be resolved at longer timescales as a result of recombination and selective retention of adaptive traits, whether they involve monogenic or polygenic traits, and/or multiple traits (Box 1).

The well-known mantra for buying and selling real estate is ‘location, location, location’. In that spirit, a chant for the current topic would be ‘fitness estimates, fitness estimates, fitness estimates’. Whether through manipulative ecological analyses or population genetic tests of selection on genomic datasets, it is essential to test fitness effects in mosaic genomes resulting from a variety of genetic exchanges (see Outstanding Questions). Such analyses should now be seen as testing fundamentally important evolutionary hypotheses about the mode and tempo of adaptive genetic exchanges at variable timescales, and their impact on morphological diversification and species radiations. As more and more data appear that reflect adaptive genetic exchanges, we predict that demonstrations of how viral reassortment, horizontal gene transfer, and introgressive hybridization have influenced standing genetic variation, recombinational potential, and the adaptive landscape itself across the web of life will likewise multiply.

Outstanding Questions

It is now well established that transfer of genes between divergent lineages can affect fitness. However, can such fitness perturbations lead to adaptive evolution in every type of organism – or are there limitations on such effects because of the biological attributes of the recipients? For example, is it due to a lack of data testing for lower fitness, or are prokaryotic species more likely to have fitness increases due to genetic exchange?

Although examples of adaptive exchange events have been documented in viruses, prokaryotes, and eukaryotes, what is the proportion of gene transfers that have no effect on fitness (i.e., are neutral), reduce the fitness, or increase the fitness of the recipient?

Is the likelihood of a neutral, maladaptive, or adaptive outcome related in any way to the type of molecular mechanism of exchange (i.e., viral reassociation, horizontal gene transfer, introgressive hybridization)?

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Supplemental Information

Supplemental information associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.tree.2017.05.007.

References

1. Anderson, E. (1949) *Introgressive Hybridization,* John Wiley & Sons
2. Anderson, E. and Stebbins, G.L.J. (1954) Hybridization as an evolutionary stimulus. *Evolution* 8, 378–388
3. Boto, L. (2014) Horizontal gene transfer in the acquisition of novel traits by metazoans. *Proc. R. Soc. B* 281, 20132450
4. Boto, L. (2010) Horizontal gene transfer in evolution: facts and challenges. *Proc. R. Soc. B* 277, 819–827
5. Keeling, P.J. and Palmer, J.D. (2008) Horizontal gene transfer in eukaryotic evolution. *Nat. Rev. Genet.* 9, 605–618
6. Rice, W.R. and Hostert, E.E. (1993) Laboratory experiments on speciation: what have we learned in 40 years? *Evolution* 47, 1637–1653

7. Arnold, M.L. (2015) *Divergence with Genetic Exchange,* Oxford University Press
8. Seehausen, O. (2015) Process and pattern in cichlid radiations – inferences for understanding unusually high rates of evolutionary diversification. *New Phytol.* 207, 304–312
9. Chan, J.M. *et al.* (2013) Topology of viral evolution. *Proc. Natl. Acad. Sci.* 110, 18566–18571
10. Neher, R.A. *et al.* (2016) Prediction, dynamics, and visualization of antigenic phenotypes of seasonal influenza viruses. *Proc. Natl. Acad. Sci.* 113, E1701–E1709
11. Neverov, A.D. *et al.* (2015) Coordinated evolution of influenza A surface proteins. *PLOS Genet.* 11, e1005404
12. Pu, J. *et al.* (2015) Evolution of the H9N2 influenza genotype that facilitated the genesis of the novel H7N9 virus. *Proc. Natl. Acad. Sci.* 112, 548–553
13. Travis, J. (2015) Making the cut. *Science* 350, 1456–1457
14. Liang, P. *et al.* (2015) CRISPR/Cas9-mediated gene editing in human tripronuclear zygotes. *Protein Cell* 6, 363–372
15. Mohanraju, P. *et al.* (2016) Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. *Science* 353, aad5147
16. Chuong, E.B. *et al.* (2016) Regulatory evolution of innate immunity through co-option of endogenous retroviruses. *Science* 351, 1083–1087
17. de Been, M. *et al.* (2014) Dissemination of cephalosporin resistance genes between *Escherichia coli* strains from farm animals and humans by specific plasmid lineages. *PLoS Genet.* 10, e1004776
18. Baumgarten, S. *et al.* (2015) The genome of *Aiptasia*, a sea anemone model for coral symbiosis. *Proc. Natl. Acad. Sci. U. S. A.* 112, 11893–11898
19. Stairs, C.W. *et al.* (2011) Eukaryotic pyruvate formate lyase and its activating enzyme eere acquired laterally from a firmicute. *Mol. Biol. Evol.* 28, 2087–2099
20. Pittis, A.A. and Gabaldón, T. (2016) Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. *Nature* 531, 101–104
21. Pease, J.B. *et al.* (2016) Phylogenomics reveals three sources of adaptive variation during a rapid radiation. *PLOS Biol.* 14, e1002379
22. Nadachowska-Brzyska, K. *et al.* (2012) Interspecific hybridization increases MHC class II diversity in two sister species of newts. *Mol. Ecol.* 21, 887–906
23. De Busschere, C. *et al.* (2015) Inter and intra island introgression in a wolf spider radiation from the Galápagos, and its implications for parallel evolution. *Mol. Phylogenet. Evol.* 84, 73–84
24. Kashtan, N. *et al.* (2014) Single-cell genomics reveals hundreds of coexisting subpopulations in wild *Prochlorococcus*. *Science* 344, 416–420
25. Danchin, E.G.J. *et al.* (2016) Horizontal gene transfer from bacteria has enabled the plant-parasitic nematode *Globodera pallida* to feed on host-derived sucrose. *Mol. Biol. Evol.* 33, 1571–1579
26. Cobbs, C. *et al.* (2013) Carotenoids in unexpected places: gall midges, lateral gene transfer, and carotenoid biosynthesis in animals. *Mol. Phylogenet. Evol.* 68, 221–228
27. Nývltová, E. *et al.* (2015) Lateral gene transfer and gene duplication played a key role in the evolution of *Mastigamoeba balamuthi* hydrogenosomes. *Mol. Biol. Evol.* 32, 1039–1055
28. Feulner, P.G.D. *et al.* (2013) Introgression and the fate of domesticated genes in a wild mammal population. *Mol. Ecol.* 22, 4210–4221
29. Skoglund, P. *et al.* (2015) Ancient wolf genome reveals an early divergence of domestic dog ancestors and admixture into high-latitude breeds. *Curr. Biol.* 25, 1515–1519
30. Baldassarre, D.T. *et al.* (2014) Genomic and morphological analysis of a semipermeable avian hybrid zone suggests asymmetrical introgression of a sexual signal. *Evolution* 68, 2644–2657
31. Sardell, J.M. and Uy, J.A.C. (2016) Hybridization following recent secondary contact results in asymmetric genotypic and phenotypic introgression between island species of *Myzomela* honeyeaters. *Evolution* 70, 257–269
32. Janoušek, V. *et al.* (2015) Functional organization of the genome may shape the species boundary in the house mouse. *Mol. Biol. Evol.* 32, 1208–1220
33. Yang, Z. *et al.* (2015) Ancient horizontal transfer of transaldolase-like protein gene and its role in plant vascular development. *New Phytol.* 206, 807–816
34. Stankowski, S. and Streisfeld, M.A. (2015) Introgressive hybridization facilitates adaptive divergence in a recent radiation of monkeyflowers. *Proc. R. Soc. B* 282, 20151666
35. Grant, P.R. and Grant, B.R. (2014) Synergism of natural selection and introgression in the origin of a new species. *Am. Nat.* 183, 671–681
36. Grant, P.R. and Grant, B.R. (2014) *40 Years of Evolution: Darwin's Finches on Daphne Major Island,* Princeton University Press
37. Lamichhaney, S. *et al.* (2015) Evolution of Darwin's finches and their beaks revealed by genome sequencing. *Nature* 518, 371–375
38. Cornelis, G. *et al.* (2015) Retroviral envelope gene captures and *syncytin* exaptation for placentation in marsupials. *Proc. Natl. Acad. Sci. U. S. A.* 112, E487–E496
39. Garrigan, D. and Kingan, S.B. (2007) Archaic human admixture. *Curr. Anthropol.* 48, 895–902
40. Sudmant, P.H. *et al.* (2015) Global diversity, population stratification, and selection of human copy-number variation. *Science* 349, aab3761
41. Dannemann, M. *et al.* (2016) Introgression of Neandertal- and Denisovan-like haplotypes contributes to adaptive variation in human Toll-like receptors. *Am. J. Hum. Genet.* 98, 22–33
42. Vernot, B. and Akey, J.M. (2014) Resurrecting surviving Neandertal lineages from modern human genomes. *Science* 343, 1017–1021
43. Lin, Y.-L. *et al.* (2015) The evolution and functional impact of human deletion variants shared with archaic hominin genomes. *Mol. Biol. Evol.* 32, 1008–1019
44. Schlebusch, C.M. *et al.* (2012) Genomic variation in seven Khoe-San groups reveals adaptation and complex African history. *Science* 338, 374–379
45. Hu, Y. *et al.* (2015) Reintroduction of a homocysteine level-associated allele into East Asians by Neanderthal introgression. *Mol. Biol. Evol.* 32, 3108–3113
46. Huerta-Sánchez, E. *et al.* (2014) Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. *Nature* 512, 194–197
47. Sankararaman, S. *et al.* (2014) The genomic landscape of Neanderthal ancestry in present-day humans. *Nature* 507, 354–357
48. Simonti, C.N. *et al.* (2016) The phenotypic legacy of admixture between modern humans and Neandertals. *Science* 351, 737–741
49. Hackinger, S. *et al.* (2016) Wide distribution and altitude correlation of an archaic high-altitude-adaptive EPAS1 haplotype in the Himalayas. *Hum. Genet.* 135, 393–402
50. Wu, B. *et al.* (2015) Extensive horizontal transfer and homologous recombination generate highly chimeric mitochondrial genomes in yeast. *Mol. Biol. Evol.* 32, 2559–2570
51. Ishida, Y. *et al.* (2015) Proliferation of endogenous retroviruses in the early stages of a host germ line invasion. *Mol. Biol. Evol.* 32, 109–120
52. Sauter, D. *et al.* (2009) Tetherin-driven adaptation of Vpu and Nef function and the evolution of pandemic and nonpandemic HIV-1 strains. *Cell Host Microbe* 6, 409–421
53. Levin, D.A. *et al.* (1996) Hybridization and the extinction of rare plant species. *Conserv. Biol.* 10, 10–16
54. Ellstrand, N.C. *et al.* (2013) Introgression of crop alleles into wild or weedy populations. *Annu. Rev. Ecol. Evol. Syst.* 44, 325–345
55. Lowe, W.H. *et al.* (2015) Spatial sorting promotes the spread of maladaptive hybridization. *Trends Ecol. Evol.* 30, 456–462
56. Lagator, Mato *et al.* (2014) Role of sex and migration in adaptation to sink environments. *Evolution* 68, 2296–2305
57. Lenormand, T. (2002) Gene flow and the limits to natural selection. *Trends Ecol. Evol.* 17, 183–189

58. Ghalambor, C.K. *et al.* (2003) Multi-trait selection, adaptation, and constraints on the evolution of burst swimming performance. *Integr. Comp. Biol.* 43, 431–438
59. Otto, S.P. and Gerstein, A.C. (2006) Why have sex? The population genetics of sex and recombination. *Biochem. Soc. Trans.* 34, 519–522
60. Akerman, A. and Bürger, R. (2014) The consequences of dominance and gene flow for local adaptation and differentiation at two linked loci. *Theor. Popul. Biol.* 94, 42–62
61. Nuismer, S.L. *et al.* (2012) Crossing the threshold: gene flow, dominance and the critical level of standing genetic variation required for adaptation to novel environments. *J. Evol. Biol.* 25, 2665–2671
62. Kondrashov, A.S. (1988) Deleterious mutations and the evolution of sexual reproduction. *Nature* 336, 435–440
63. Todesco, M. *et al.* (2016) Hybridization and extinction. *Evol. Appl.* 9, 892–908

Supplementary Material

Adaptive genetic exchange: a tangled history of admixture and evolutionary innovation

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Table S1a. Examples of adaptive genetic exchange in viral, prokaryotic and eukaryotic assemblages where the exchange is mediated by non-sexual reproduction (i.e. viral recombination and horizontal gene transfer). (All reference numbers in supplementary tables have a 'S' prefix).

Organism (donor)	Organism (recipient)	Genomic Region Involved	Trait Affected	Effect on Recipient	References
	VIRUS				
Influenza A	Influenza A	Haemagglutinin/Neuraminidase	Resistance to host immunity	Adaptive	[1,2]
Bacteria	*Cafeteria roenbergensis* virus (CroV)	Multiple	Carbohydrate metabolism	Adaptive	[3]
	BACTERIA/ARCHAEA				
Bacteriophage	Archaea/Bacteria	CRISPR loci	Immune system	Adaptive	[4]
Vibrio sp.	*Vibrio parahaemolyticus*	*T3SS2*	Infectivity	Adaptive	[5]
Escherichia coli	*Escherichia coli*	Multiple	Antibiotic resistance	Adaptive	[6]
Prochlorococcus	*Prochlorococcus*	Multiple	Niche partitioning	Adaptive	[7]
Cyanobacteria	Proteobacteria	BchL-N-B protein genes	Photosynthesis	Adaptive	[8]
	PROTO-EUKARYOTE				
Bacteria	Proto-eukaryote	Multiple	Multiple	Adaptive	[9]
Alphaproteobacteria	Proto-eukaryote	Mitochondria	Multiple	Adaptive	[9]
	EUKARYOTE – amoeboids				
Firmicute bacteria	*Mastigamoeba*, etc.*	*Pfl/Pfla*	ATP production	Adaptive	[10]
	EUKARYOTE – fungi				
Bacteria	Microsporidia	*TK* genes	Nucleic acid synthesis/salvage	Adaptive	[11]
T. microellipsoides	*Saccharomyces*	*FOT* genes	Oligopeptide transport	Adaptive	[12]
Saccharomycetaceae	Saccharomycetaceae	Mitochondrial genes	Multiple	Adaptive/maladaptive	[13]

	EUKARYOTE – protist				
Bacteria	*Mastigamoeba*	Multiple	Hydrogenosomal metabolism	Adaptive	[14]
	EUKARYOTE – plant				
Eubacteria	*Galdieria* (red alga)	Multiple	Urea hydrolysis	Adaptive	[15]
DNA virus	*Bigelowiella* (alga)	Multiple	Defense against infection	Adaptive	[16]
Actinobacteria	Land plants	*TAL* genes	Plant vascular development	Adaptive	[17]
Hornworts	Ferns	Neochrome gene	Growth in low light	Adaptive	[18]
	EUKARYOTE – animal				
Bacteria	Animals**	Multiple	Cell-cell signaling	Adaptive	[19]
Bacteria	*Aiptasia* (sea anemone)	Multiple	Multiple	Adaptive	[20]
Bacteria	*Globodera* (nematode)	Glycosyl Hydrolase genes	Parasitism	Adaptive	[21]
Bacteria	*Brugia* (nematode)	*BmFeCH* gene	Heme biosynthesis	Adaptive	[22]
Fungi	Arthropods	Carotenoid biosynthesis genes	Multiple	Adaptive	[23,24]
Bacteria	*Hypothenemus* (beetle)	*HhMAN1*	Polysaccharide hydrolysis	Adaptive	[25]
Polydnaviridae	Parasitoid wasps	Multiple	Ability to parasitize hosts	Adaptive	[26,27]
Microsporidia	Parasitoid wasps	*GH19* chitinase gene	Venom	Adaptive	[11]
HIV-1	Humans	Multiple	Disease Susceptibility	Maladaptive	[28]
Endogenous retrovirus	Mammals	Multiple	Innate Immunity	Adaptive	[29]
Koala Retrovirus	Koala	Multiple	Disease Susceptibility	Maladaptive	[30]

*Transfers detected in a number of anaerobic eukaryotes

**Transfers detected in numerous animal clades including invertebrates and vertebrates

Table S1b. Examples of adaptive genetic exchange in eukaryotic assemblages where the exchange is mediated by sexual reproduction (i.e. "introgressive hybridization" or "introgression" [23]).

Organism (donor)	Organism (recipient)	Genomic Region Involved	Trait Affected	Effect on Recipient	References
	FUNGI				
Saccharomyces	*Saccharomyces*	*MEP2* gene	Ammonium permease	Adaptive	[31]
	PLANT				
Arabidopsis	*Arabidopsis*	Multiple	Growth on serpentine soils	Adaptive	[32]
Helianthus	*Helianthus*	Multiple	Female/Male fitness	Adaptive	[33]
Solanum	*Solanum*	*Cf-4/NL* locus	Pathogen resistance	Adaptive	[34]
Cultivated rice	Wild rice	Multiple	Domestication traits	Adaptive	[35]
Iris fulva	*Iris brevicaulis*	Multiple	Flooding tolerance	Adaptive	[36]
Mimulus	*Mimulus*	*MaMyb2* gene	Flower color	Adaptive	[37]
Senecio	*Senecio*	*RAY* locus	Flower-head development	Adaptive	[38]
Populus	*Populus*	Multiple	Multiple	Adaptive	[39]
Pachycladon	*Pachycladon*	Glucosinolate hydrolysis genes	Herbivore resistance	Adaptive	[40]
	ANIMAL – ADAPTIVE RADIATIONS				
Animals***	Animals***	Multiple	Multiple	Adaptive	[41]
	ANIMAL – MOLLUSCS				
Mytilus	*Mytilus*	Multiple	Multiple	Adaptive	[42,43]
	ANIMAL – INSECTS				
Anopheles	*Anopheles*	2La	Resistance to dry environments	Adaptive	[44]
Drosophila	*Drosophila*	Mitochondrial genome	Elimination of deleterious alleles	Adaptive	[45]

Limenitis	*Limenitis*	Multiple	Batesian mimicry	Adaptive	[46]
Heliconius	*Heliconius*	*dennis* and *ray* loci	Müllerian mimicry	Adaptive	[47]
Papilio	*Papilio*	Multiple	Cold tolerance/mimicry	Adaptive	[48]
Lycaeides	*Lycaeides*	Multiple	High altitude niches	Adaptive	[49]
	ANIMAL – ARACHNIDS				
Hogna	*Hogna*	Multiple	Niche occupied	Adaptive	[50]
	ANIMAL – FISH				
African cichlids	African cichlids	Multiple	Feeding apparatus and others	Adaptive	[51]
Gasterosteus	*Gasterosteus*	Multiple	Anti-predation	Adaptive	[52]
	ANIMAL – AMPHIBIANS				
Ambystoma	*Ambystoma*	Multiple	Survivorship	Adaptive	[53,54]
Lissotriton	*Lissotriton*	*MHC* loci	Immune response	Adaptive	[55]
Spea	*Spea*	Multiple	Female mate choice	Adaptive	[56]
Ranitomeya	*Ranitomeya*	Multiple	Mimetic color	Adaptive	[57]
	ANIMAL – BIRDS				
Zimmerius	*Zimmerius*	Multiple	Plumage coloration	Adaptive	[58]
Malurus	*Malurus*	Multiple	Plumage coloration	Adaptive	[59]
Manacus	*Manacus*	Multiple	Plumage coloration	Adaptive	[60]
Myzomela	*Myzomela*	Multiple	Plumage coloration	Adaptive	[61]
Geospiza	*Geospiza*	*ALX1* gene	Beak shape	Adaptive	[62]
	ANIMAL – MAMMALS				
Mus spretus	*Mus musculus*	*Vkorc1* gene	Rodenticide resistance	Adaptive	[63]
Mus musculus	*Mus musculus*	Y-chromosome	Unknown	Adaptive	[64]
Mus musculus	*Mus musculus*	Multiple	Chemical communication	Adaptive	[65]
Dunface sheep	Soay sheep	*TYRP1* gene	Coat color	Adaptive	[66]

Dunface sheep	Soay sheep	*ASIP* gene	Coat pattern	Maladaptive	[66]
Canis lupus	*Canis familiaris*	Multiple	Survivorship in high latitudes	Adaptive	[67]
Canis familiaris	*Canis lupus*	*Mc1r* gene	Coat color	Adaptive	[68,69]
Canis lupus	*Canis latrans*	Multiple	Increased body size	Adaptive	[70]
Homo sapiens	*Homo sapiens*	*ERCC4* gene	Response to UV light	Adaptive	[71]
Denisovan	*Homo sapiens*	microRNA loci	Unknown	Adaptive	[72]
Denisovan	*Homo sapiens*	Toll-like receptor loci	Innate immunity	Adaptive	[73]
Denisovan	*Homo sapiens*	*EPAS1* gene	Hypoxia pathway	Adaptive	[74,75]
Homo neanderthalensis	*Homo sapiens*	Toll-like receptor loci	Innate immunity	Adaptive	[73]
Homo neanderthalensis	*Homo sapiens*	*SPATA45* and *18* genes	Spermatogenesis	Adaptive	[76,77]
Homo neanderthalensis	*Homo sapiens*	*DPEP1* gene	Metabolism	Adaptive	[78]
Homo neanderthalensis	*Homo sapiens*	Multiple	Skin and hair characteristics	Adaptive	[79]
Denisovan/*H. neanderthalensis*	*Homo sapiens*	*GBP4/GBP7* genes	Innate immunity	Adaptive	[80]
Homo neanderthalensis	*Homo sapiens*	Multiple	Disease risk	Maladaptive	[79,81]

***Introgression contributing to adaptive variation during radiations in fish, birds and butterflies.

Table S2: The mode, timing and adaptive significance of genetic transfers (numbers shown are the number of times a particular kind of genetic exchange has been reported in the reviewed recent literature from Table 1).

Mode of genetic transfer	**Donor**	**Recipient**	**Trait type**	**Adaptive significance**	**Timing of genetic exchange**		**Genetic architecture of traits**[1]	**Adaptive value**		**References**[2]
					Ancient	**Recent**		**Adaptive**	**Maladaptive**	
Non-sexual: (n=29)				**Total**	**26**	**8**	**Pgen.: 27** **Mgen.: 2**	**26**	**3**	
	Micro[3]	**Micro**		**Total**	**5**	**5**	**Pgen.: 5** **Mgen.: 1**	**5**	**0**	
			Ecological	immunity/resistance to host immunity	1	2	Pgen.: 2	2		[1,2,4]
				Infectivity/antibiotic resistance	2	2	Pgen.: 1 Mgen.: 1	2		[5,6]
				Niche partitioning	1	1	Pgen.: 1	1		[7,50]
				Photosynthesis	1		Pgen.: 1	1		[8]
	Micro	**Eukar**		**Total**	**18**	**1**	**Pgen.: 16**	**19**	**0**	
			Cellular processes	Metabolism	12		Pgen.: 12	12		[3,9,10,12,14,15,20–22,26]
			Ecological	Immunity/defense	4	1	Pgen.: 4	4		[16,22,23,29,41]
				Infectivity/parasitism	3		Pgen.: 3	3		[24,26,27]
				Symbiosis	3		Pgen.: 3	3		[9,10,22]
	Eukar	**Eukar**		**Total**	**5**	**0**	**Pgen.: 4** **Mgen.: 1**	**5**	**1**	
			Cellular processes	Metabolism	3		Pgen.: 3	3	1	[13,21,23,24]
				Cellular signaling	1		Pgen.: 1	1		[19]
			Ecological	Growth	1		Mgen.: 1	1		[18]

Sexual (n=51)		**Total**	**39**	**32**	**Pgen.: 40** **Mgen.: 10**	**47**	**3**	
	Ecological	**Total**	**31**	**22**	**Pgen.: 29** **Mgen.: 10**	**36**	**3**	
		Adaptation to habitat/environment	12	8	Pgen.: 13 Mgen.: 2	14	1	[36,39,42,43,48–51,53,54,56,67,71,74,75,79,82]
		Growth	1	3	Pgen.: 2 Mgen.: 1	3		[31,32,70]
		Domestication	3	5	Pgen.: 1 Mgen.: 3	4	1	[35,66–69]
		Parasite/herbivore resistance, immunity	6	3	Pgen.: 6 Mgen.: 2	6	1	[34,55,63,76,79–81]
		Predator escape	5	2	Pgen.: 5	5		[46–48,52,57,83]
		Foraging/metabolism	4	1	Pgen.: 2 Mgen.: 2	4		[51,62,78,82,84]
	Sexual/reproductive/ social	**Total**	**8**	**10**	**Pgen.: 11**	**11**	**0**	
		Fitness	3	4	Pgen.: 5	5		[33,65,76,77,85,86]
		Mate choice	5	6	Pgen.: 6	6		[56,58–61,65]

[1] Pgen=polygenic, Mgen=monogenic

[2] The number of examples does not total up because some examples may be included in more than one category and classifications.

[3] Micro=bacteria, virus and archea, Eukar=eukaryote. Donors and recipients are not mentioned for sexual genetic transfers since all genetic transfers here are between closely related taxa, i.e., populations of a species or among congenerics.

Supplementary references:

1 Neverov, A.D. *et al.* (2015) Coordinated evolution of influenza A surface proteins. *PLOS Genet.* 11, e1005404

2 Pu, J. *et al.* (2015) Evolution of the H9N2 influenza genotype that facilitated the genesis of the novel H7N9 virus. *Proc. Natl. Acad. Sci.* 112, 548–553

3 Fischer, M.G. *et al.* (2010) Giant virus with a remarkable complement of genes infects marine zooplankton. *Proc. Natl. Acad. Sci. USA* 107, 19508–19513

4 Mohanraju, P. *et al.* (2016) Diverse evolutionary roots and mechanistic variations of the CRISPR-Cas systems. *Science* 353, aad5147-aad5147

5 Hubbard, T.P. *et al.* (2016) Genetic analysis of *Vibrio parahaemolyticus* intestinal colonization. *Proc. Natl. Acad. Sci. USA* 113, 6283–6288

6 de Been, M. *et al.* (2014) Dissemination of cephalosporin resistance genes between *Escherichia coli* strains from farm animals and humans by specific plasmid lineages. *PLoS Genet.* 10, e1004776

7 Kashtan, N. *et al.* (2014) Single-cell genomics reveals hundreds of coexisting subpopulations in wild *Prochlorococcus*. *Science* 344, 416–420

8 Gupta, R.S. (2012) Origin and spread of photosynthesis based upon conserved sequence features in key bacteriochlorophyll biosynthesis proteins. *Mol. Biol. Evol.* 29, 3397–3412

9 Pittis, A.A. and Gabaldón, T. (2016) Late acquisition of mitochondria by a host with chimaeric prokaryotic ancestry. *Nature* 531, 101–104

10 Stairs, C.W. *et al.* (2011) Eukaryotic pyruvate formate lyase and its activating enzyme eere acquired laterally from a firmicute. *Mol. Biol. Evol.* 28, 2087–2099

11 Alexander, W.G. *et al.* (2016) Horizontally acquired genes in early-diverging pathogenic fungi enable the use of host nucleosides and nucleotides. *Proc. Natl. Acad. Sci. USA* 113, 4116–4121

12 Marsit, S. *et al.* (2015) Evolutionary advantage conferred by an eukaryote-to-eukaryote gene transfer event in wine yeasts. *Mol. Biol. Evol.* 32, 1695–1707

13 Wu, B. *et al.* (2015) Extensive horizontal transfer and homologous recombination generate highly chimeric mitochondrial genomes in yeast. *Mol. Biol. Evol.* 32, 2559–2570

14 Nývltová, E. *et al.* (2015) Lateral gene transfer and gene duplication played a key role in the evolution of *Mastigamoeba balamuthi* hydrogenosomes. *Mol. Biol. Evol.* 32, 1039–1055

15 Qiu, H. *et al.* (2013) Adaptation through horizontal gene transfer in the cryptoendolithic

red alga *Galdieria phlegrea*. *Curr. Biol.* 23, R865–R866

16 Blanc, G. *et al.* (2015) Provirophages in the *Bigelowiella* genome bear testimony to past encounters with giant viruses. *Proc. Natl. Acad. Sci. USA* 112, E5318–E5326

17 Yang, Z. *et al.* (2015) Ancient horizontal transfer of transaldolase-like protein gene and its role in plant vascular development. *New Phytol.* 206, 807–816

18 Lia, F.-W. *et al.* (2014) Horizontal transfer of an adaptive chimeric photoreceptor from bryophytes to ferns. *Proc. Natl. Acad. Sci. USA* 111, 6672–6677

19 Iyer, L.M. *et al.* (2004) Evolution of cell–cell signaling in animals: did late horizontal gene transfer from bacteria have a role? *Trends Genet.* 20, 292–299

20 Baumgarten, S. *et al.* (2015) The genome of *Aiptasia*, a sea anemone model for coral symbiosis. *Proc. Natl. Acad. Sci. USA* 112, 11893–11898

21 Danchin, E.G.J. *et al.* (2016) Horizontal gene transfer from bacteria has enabled the plant-parasitic nematode *Globodera pallida* to feed on host-derived sucrose. *Mol. Biol. Evol.* 33, 1571–1579

22 Wu, B. *et al.* (2013) Interdomain lateral gene transfer of an essential ferrochelatase gene in human parasitic nematodes. *Proc. Natl. Acad. Sci. USA* 110, 7748–7753

23 Cobbs, C. *et al.* (2013) Carotenoids in unexpected places: gall midges, lateral gene transfer, and carotenoid biosynthesis in animals. *Mol. Phylogenet. Evol.* 68, 221–228

24 Moran, N.A. and Jarvik, T. (2010) Lateral transfer of genes from fungi underlies carotenoid production in aphids. *Science* 328, 624–627

25 Acuña, R. *et al.* (2012) Adaptive horizontal transfer of a bacterial gene to an invasive insect pest of coffee. *Proc. Natl. Acad. Sci. USA* 109, 4197–4202

26 Martinson, E.O. *et al.* (2016) Laterally transferred gene recruited as a venom in parasitoid wasps. *Mol. Biol. Evol.* 33, 1042–1052

27 Burke, G.R. *et al.* (2014) Widespread genome reorganization of an obligate virus mutualist. *PLoS Genet.* 10, e1004660

28 Sauter, D. *et al.* (2009) Tetherin-driven adaptation of Vpu and Nef function and the evolution of pandemic and nonpandemic HIV-1 strains. *Cell Host Microbe* 6, 409–421

29 Chuong, E.B. *et al.* (2016) Regulatory evolution of innate immunity through co-option of endogenous retroviruses. *Science* 351, 1083–1087

30 Ishida, Y. *et al.* (2015) Proliferation of endogenous retroviruses in the early stages of a host germ line invasion. *Mol. Biol. Evol.* 32, 109–120

31 Dunn, B. *et al.* (2013) Recurrent rearrangement during adaptive evolution in an interspecific yeast hybrid suggests a model for rapid introgression. *PLoS Genet.* 9,

e1003366

32 Arnold, B.J. *et al.* (2016) Borrowed alleles and convergence in serpentine adaptation. *Proc. Natl. Acad. Sci. USA* 113, 8320–8325

33 Whitney, K.D. *et al.* (2015) Quantitative trait locus mapping identifies candidate alleles involved in adaptive introgression and range expansion in a wild sunflower. *Mol. Ecol.* 24, 2194–2211

34 Pease, J.B. *et al.* (2016) Phylogenomics reveals three sources of adaptive variation during a rapid radiation. *PLOS Biol.* 14, e1002379

35 Sun, J. *et al.* (2013) Introgression and selection shaping the genome and adaptive loci of weedy rice in northern China. *New Phytol.* 197, 290–299

36 Martin, N.H. *et al.* (2005) Detecting adaptive trait introgression between *Iris fulva* and *I. brevicaulis* in highly selective field conditions. *Genetics* 172, 2481–2489

37 Stankowski, S. and Streisfeld, M.A. (2015) Introgressive hybridization facilitates adaptive divergence in a recent radiation of monkeyflowers. *Proc. R. Soc. B* 282, 20151666

38 Kim, M. *et al.* (2008) Regulatory genes control a key morphological and ecological trait transferred between species. *Science* 322, 1116–1119

39 Suarez-Gonzalez, A. *et al.* (2016) Genomic and functional approaches reveal a case of adaptive introgression from *Populus balsamifera* (balsam poplar) in *P . trichocarpa* (black cottonwood). *Mol. Ecol.* 25, 2427–2442

40 Becker, M. *et al.* (2013) Hybridization may facilitate in situ survival of endemic species through periods of climate change. *Nat. Clim. Chang.* 3, 1039–1043

41 Berner, D. and Salzburger, W. (2015) The genomics of organismal diversification illuminated by adaptive radiations. *Trends Genet.* 31, 491–499

42 Fraïsse, C. *et al.* (2016) Local interspecies introgression is the main cause of extreme levels of intraspecific differentiation in mussels. *Mol. Ecol.* 25, 269–286

43 Fraïsse, C. *et al.* (2014) Gene-Flow in a mosaic hybrid zone: is local introgression adaptive? *Genetics* 197, 939–951

44 Fontaine, M.C. *et al.* (2015) Extensive introgression in a malaria vector species complex revealed by phylogenomics. *Science* 347, 1258524–1258524

45 Llopart, A. *et al.* (2014) Sequential adaptive introgression of the mitochondrial genome in *Drosophila yakuba* and *Drosophila santomea*. *Mol. Ecol.* 23, 1124–1136

46 Savage, W.K. and Mullen, S.P. (2009) A single origin of Batesian mimicry among hybridizing populations of admiral butterflies (*Limenitis arthemis*) rejects an evolutionary reversion to the ancestral phenotype. *Proc. R. Soc. B* 276, 2557–2565

47 Wallbank, R.W.R. *et al.* (2016) Evolutionary novelty in a butterfly wing pattern through enhancer shuffling. *PLoS Biol.* 14, e1002353

48 Kunte, K. *et al.* (2011) Sex chromosome mosaicism and hybrid speciation among tiger swallowtail butterflies. *PLoS Genet.* 7, e1002274

49 Nice, C.C. *et al.* (2013) Hybrid speciation and independent evolution in lineages of alpine butterflies. *Evolution (N. Y).* 67, 1055–1068

50 De Busschere, C. *et al.* (2015) Inter and intra island introgression in a wolf spider radiation from the Galápagos, and its implications for parallel evolution. *Mol. Phylogenet. Evol.* 84, 73–84

51 Keller, I. *et al.* (2013) Population genomic signatures of divergent adaptation, gene flow and hybrid speciation in the rapid radiation of Lake Victoria cichlid fishes. *Mol. Ecol.* 22, 2848–2863

52 Lucek, K. *et al.* (2014) Contemporary ecotypic divergence during a recent range expansion was facilitated by adaptive introgression. *J. Evol. Biol.* 27, 2233–2248

53 Fitzpatrick, B.M. *et al.* (2010) Rapid spread of invasive genes into a threatened native species. *Proc. Natl. Acad. Sci. USA* 107, 3606–3610

54 Fitzpatrick, B.M. and Shaffer, H.B. (2007) Hybrid vigor between native and introduced salamanders raises new challenges for conservation. *Proc. Natl. Acad. Sci. USA* 104, 15793–15798

55 Nadachowska-Brzyska, K. *et al.* (2012) Interspecific hybridization increases MHC class II diversity in two sister species of newts. *Mol. Ecol.* 21, 887–906

56 Pfennig, K.S. (2007) Facultative mate choice drives adaptive hybridization. *Science* 318, 965–967

57 Vestergaard, J.S. *et al.* (2015) Number of genes controlling a quantitative trait in a hybrid zone of the aposematic frog *Ranitomeya imitator*. *Proc. R. Soc. B* 282, 20141950–20141950

58 Rheindt, F.E. *et al.* (2014) Introgression and phenotypic assimilation in Zimmerius flycatchers (Tyrannidae): population genetic and phylogenetic inferences from genomewide SNPs. *Syst. Biol.* 63, 134–152

59 Baldassarre, D.T. *et al.* (2014) Genomic and morphological analysis of a semipermeable avian hybrid zone suggests asymmetrical introgression of a sexual signal. *Evolution (N. Y).* 68, 2644–2657

60 Parchman, T.L. *et al.* (2013) The genomic consequences of adaptive divergence and reproductive isolation between species of manakins. *Mol. Ecol.* 22, 3304–3317

61 Sardell, J.M. and Uy, J.A.C. (2016) Hybridization following recent secondary contact results in asymmetric genotypic and phenotypic introgression between island species of *Myzomela* honeyeaters. *Evolution (N. Y).* 70, 257–269

62 Lamichhaney, S. *et al.* (2015) Evolution of Darwin's finches and their beaks revealed by genome sequencing. *Nature* 518, 371–375

63 Liu, K.J. *et al.* (2015) Interspecific introgressive origin of genomic diversity in the house mouse. *Proc. Natl. Acad. Sci. USA* 112, 196–201

64 Jones, E.P. and Searle, J.B. (2015) Differing Y chromosome versus mitochondrial DNA ancestry, phylogeography, and introgression in the house mouse. *Biol. J. Linn. Soc.* 115, 348–361

65 Janoušek, V. *et al.* (2015) Functional organization of the genome may shape the species boundary in the house mouse. *Mol. Biol. Evol.* 32, 1208–1220

66 Feulner, P.G.D. *et al.* (2013) Introgression and the fate of domesticated genes in a wild mammal population. *Mol. Ecol.* 22, 4210–4221

67 Skoglund, P. *et al.* (2015) Ancient wolf genome reveals an early divergence of domestic dog ancestors and admixture into high-latitude breeds. *Curr. Biol.* 25, 1515–1519

68 Schweizer, R.M. *et al.* (2016) Targeted capture and resequencing of 1040 genes reveal environmentally driven functional variation in grey wolves. *Mol. Ecol.* 25, 357–379

69 Anderson, T.M. *et al.* (2009) Molecular and evolutionary history of melanism in North American gray wolves. *Science* 323, 1339–1343

70 Monzón, J. *et al.* (2014) Assessment of coyote-wolf-dog admixture using ancestry-informative diagnostic SNPs. *Mol. Ecol.* 23, 182–197

71 Schlebusch, C.M. *et al.* (2012) Genomic variation in seven Khoe-San groups reveals adaptation and complex African history. *Science* 338, 374–379

72 Sudmant, P.H. *et al.* (2015) Global diversity, population stratification, and selection of human copy-number variation. *Science* 349, aab3761-aab3761

73 Dannemann, M. *et al.* (2016) Introgression of Neandertal- and Denisovan-like haplotypes contributes to adaptive variation in human Toll-like receptors. *Am. J. Hum. Genet.* 98, 22–33

74 Huerta-Sánchez, E. *et al.* (2014) Altitude adaptation in Tibetans caused by introgression of Denisovan-like DNA. *Nature* 512, 194–197

75 Hackinger, S. *et al.* (2016) Wide distribution and altitude correlation of an archaic high-altitude-adaptive EPAS1 haplotype in the Himalayas. *Hum. Genet.* 135, 393–402

76 Vernot, B. and Akey, J.M. (2014) Resurrecting surviving Neandertal lineages from

modern human genomes. *Science* 343, 1017–1021

77 Lin, Y.-L. *et al.* (2015) The evolution and functional impact of human deletion variants shared with archaic hominin genomes. *Mol. Biol. Evol.* 32, 1008–1019

78 Hu, Y. *et al.* (2015) Reintroduction of a homocysteine level-associated allele into East Asians by Neanderthal introgression. *Mol. Biol. Evol.* 32, 3108–3113

79 Sankararaman, S. *et al.* (2014) The genomic landscape of Neanderthal ancestry in present-day humans. *Nature* 507, 354–357

80 Vernot, B. *et al.* (2016) Excavating Neandertal and Denisovan DNA from the genomes of Melanesian individuals. *Science* 352, 235–239

81 Simonti, C.N. *et al.* (2016) The phenotypic legacy of admixture between modern humans and Neandertals. *Science* 351, 737–741

82 Martin, C.H. *et al.* (2015) Complex histories of repeated gene flow in Cameroon crater lake cichlids cast doubt on one of the clearest examples of sympatric speciation. *Evolution (N. Y).* 69, 1406–1422

83 Gilbert, L.E. (2003) Adaptive novelty through introgression in Heliconius wing patterns: evidence for a shared genetic "Toolbox" from synthetic hybrid zones and a theory of diversification. In *Butterflies: Ecology and Evolution Taking Flight* (Boggs, C. L. et al., eds), pp. 281–318, University of Chicago Press

84 van Rijssel, J.C. *et al.* (2015) Fast adaptive responses in the oral jaw of Lake Victoria cichlids. *Evolution (N. Y).* 69, 179–189

85 Stankowski, S. and Streisfeld, M.A. (2015) Introgressive hybridization facilitates adaptive divergence in a recent radiation of monkeyflowers. *Proc. R. Soc. B* 282, 20151666

86 Kim, M. *et al.* (2008) Regulatory genes control a key morphological and ecological trait transferred between species. *Science* 322, 1116–1119