Opinion

Hybridization and genome evolution II: Mechanisms of species divergence and their effects on evolution in hybrids

Richard I. BAILEY*, Fabrice EROUKHMANOFF, Glenn-PETER SæTRE
Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, University of Oslo, Norway

Abstract Recent genomic studies have highlighted the importance of hybridization and gene exchange in evolution. We ask what factors cause variation in the impact of hybridization, through adaptation in hybrids and the likelihood of hybrid speciation. During speciation, traits that diverge due to both divergent and stabilizing selection can contribute to the build up of reproductive isolation. Divergent directional selection in parent taxa should lead to intermediate phenotypes in hybrids, whereas stabilizing selection can also produce extreme, transgressive phenotypes when hybridization occurs. By examining existing theory and empirical data, we discuss how these effects, combined with differences between modes of divergence in the chromosomal distribution of incompatibilities, affect adaptation and speciation in hybrid populations. The result is a clear and testable set of predictions that can be used to examine hybrid adaptation and speciation. Stabilizing selection in parents increases transgression in hybrids, increasing the possibility for novel adaptation. Divergent directional selection causes intermediate hybrid phenotypes and increases their ability to evolve along the direction of parental differentiation. Stabilizing selection biases incompatibilities towards autosomes, leading to reduced sexual correlations in trait values and reduced pleiotropy in hybrids, and hence increased freedom in the direction of evolution. Directional selection causes a bias towards sex-linked incompatibilities, with the opposite consequences. Divergence by directional selection leads to greater dominance effects than stabilizing selection, with major but variable impacts on hybrid evolution [Current Zoology 59 (5): 675–685, 2013].

Keywords Evolvability, Constraints, Dimensionality, Hybrid, Adaptation

1 Introduction

Understanding how adaptation occurs lies at the core of evolutionary biology. The ability of organisms to adapt to prevailing ecological conditions can be affected by many factors. Where differences between the sexes occur in what constitutes the optimum phenotype, these same factors may alter the possibility for a resolution to this intersexual conflict. The role of hybridization in evolution and adaptation is a matter of current controversy and is a rapidly developing topic of research (Abbott et al., 2013; Butlin and Ritchie, 2013; Sætre, 2013). Hybridization between genetically divergent taxa is common in nature; as many as 25% of plant and 10% of animal species are known to hybridize, while this figure is much higher for recently radiated groups (Mallet, 2007). Hybridization is perhaps the most rapid generator of novelty, known to produce new hybrid species (Abbott et al., 2013; Rieseberg, 1997; Gross and Rieseberg, 2005; Mavárez et al., 2006; Mallet, 2007; Hermansen et al., 2011) in the order of a hundred generations (Buerkle and Rieseberg, 2008) and to increase genetic variation faster than mutation alone (Stebbins, 1969; but see Barton, 2013). Hence understanding the impacts of hybridization on adaptation can provide tremendous insight into the ability of populations to respond to environmental change and to evolve new reproductive barriers. A primary set of impacts of hybridization is that it can alter phenotypic trait values, the amount of additive genetic variation in a trait, and the pattern of genetic correlations between traits (e.g. Guillaume and Whitlock, 2007). For example, it can lead to hybrid trait values that are beyond the range of those of the hybridizing parent taxa (so-called transgressive traits; Rieseberg et al., 1999). It can allow the exchange of universally beneficial alleles between populations (Barton, 2000; Barton, 2013; Barton and Gale, 1993; Heliconius Genome Consortium, 2012) or conversely, introduce incompatibilities (Trier et al., personal data). Given these potential effects, can we predict the impact hybridization will have on the effectiveness of selection in a population?
In this paper we focus on evolution and adaptation in hybrids. There is a strong focus in speciation research on the impacts of reduced fitness in hybrids, for example in studies of ecological speciation (Schluter, 2009) and reinforcement (Sætre et al., 1997; Servedio and Noor, 2003; Hopkins and Rausher, 2012). Reduced hybrid fitness is a requirement for divergence by such mechanisms (but see Nosil et al., 2007; ecological selection may also be against parent taxa in the wrong environment). However there exists a small but growing literature dealing with positive impacts of hybridization in aiding adaptation and producing new hybrid species (e.g. Lewontin and Birch, 1966; Stebbins, 1969; Rieseberg et al., 2003; Mavárez et al., 2006). Hybridization has many different possible outcomes, from coexistence and reinforcement of species differences, to the formation of narrow parapatric hybrid zones, broad mosaic and bimodal hybrid zones, hybrid swarms and independently evolving hybrid populations or species. It is timely therefore to broaden the focus from the influence of hybridization on hybrid- and non-hybrid speciation to a more general appraisal of evolution with hybridization. Therefore, while acknowledging the importance of reduced hybrid fitness in typical non-hybrid ‘bifurcating’ speciation, we focus in on the hybrids themselves. We specifically examine the impacts in hybrids of the evolutionary mechanisms contributing to divergence between the taxa that produce those hybrids. We develop hypotheses for hybrid evolution based on existing theory and data, and argue that parent-taxon divergence mechanisms have key effects on the fitness and adaptive potential of hybrids.

Traits that contribute to divergence between two taxa can differ in several interrelated respects (Fig. 1). They can evolve under directional selection (divergent directional selection is typically assumed in studies of ecological speciation) or stabilizing selection. Genes contributing to the trait can diverge disproportionately more on sex chromosomes or on autosomes (Qvarnström and Bailey, 2009). They can be additive, dominant or recessive. Hybrid trait values can fall solely between those of the parent taxa, or can extend beyond those of either parent. Other factors also exist, such as divergence by drift, and epistatic effects, but for clarity we focus on divergence by natural selection and on non-epistatic effects. We argue that there are predictable differences in the impact on hybrids between traits that diverge by directional selection and those that diverge while under stabilizing selection (Fig. 1).

We predict the following general outcomes. Directional selection: If directional selection contributes to species differences, divergence should be disproportionately sex-linked (Box 1; Fig. 1) and, as a consequence, hybrid populations will evolve less freely and

![Fig. 1 Predicted effects of the mode of divergence between parent taxa on the degree of transgression in hybrids, the chromosomal distribution of incompatibilities, the strength of constraints on the direction of evolution, and the influence of dominance in hybrids](https://academic.oup.com/cz/article-abstract/59/5/675/1793731)
be less able to move towards a fitness optimum. Hybrid trait values should fall between those of the parent taxa and be restricted to evolving in the direction of the differences between those parent taxa, further reducing the potential to evolve novel adaptations. This may facilitate maintenance of two distinct genotypes as it facilitates divergence back towards parental trait values. However, it may also facilitate gene exchange because backcrosses will converge towards parental phenotypes. Directional selection favors dominant new mutations, but their impacts in hybrids are difficult to predict. Stabilizing selection: If there is divergence in genes underlying traits under stabilizing selection, whether or not the trait values themselves diverge, genetic divergence should be disproportionately autosomal (Box 1; Fig. 1). Consequently, hybrids are predicted to be less constrained in their phenotypic evolution and hence freer to evolve towards a variety of different potential fitness optima. Hybrid trait values can extend beyond those of the parents even through purely additive effects, further allowing evolution towards novel fitness optima. Backcross hybrids will not uniformly converge towards parental phenotypes, as a result either reducing the effectiveness of divergent selection during periods of contact and gene exchange, or reducing gene exchange itself (i.e. the opposite effects to those of traits diverging under directional selection). There is no expectation of excessive dominance, but we make no firm predictions in this regard.

2 Mode of Divergence and Constraints on Adaptation in Hybrids

Due to interest in ecological speciation (Schluter, 2009; Rice et al., 2011), in which directional selection towards adaptation to different environments directly leads to reproductive isolation, a strong emphasis has been placed on distinguishing divergent ecological selection from other mechanisms of speciation (Schluter, 2009). However, traits that diverge between taxa are very unlikely to all be under divergent selection. As well as those diverging through drift, traits under stabilizing selection can also contribute to reproductive isolation, even in the absence of any phenotypic divergence. This is due to weakly selected turnover of alleles among loci contributing to the trait, leading to divergence at the genomic level whether or not trait divergence occurs. Morphological traits are thought to often be under stabilizing selection, while life history traits – more closely associated with fitness – may be more often under directional selection (Rice and Emerson, 2006). Among sexually selected traits, adaptive mate choice is thought to cause directional selection on sexual signals, while mate recognition and sensory tuning may be more likely to impose stabilizing selection (Bentsen et al., 2006).

The impact of the different modes of divergence on hybrid evolution has only been examined in any detail in the context of homoploid hybrid speciation (HHS;
Rieseberg et al., 1999), in which a novel reproductively isolated hybrid taxon emerges without a change in number of chromosome sets (Mallet, 2007; Buerkle and Rieseberg, 2008; Abbott et al., 2013). How does the mode of divergence between parent taxa alter divergence at the genomic level, and how does this impact hybrid evolution? We outline several mechanisms and their impacts below, which are also represented in Fig. 1 and explained in Box 1.

2.1 Mode of divergence: Effects on transgression and intermediacy

Transgression or transgressive segregation refers to the formation of hybrid phenotypes that fall outside the range of values encompassed by the two parent taxa (Rieseberg et al., 1999). A number of factors can cause transgression in hybrids (Rieseberg et al., 1999), but here we focus on one primary documented cause, that of additive genetic variation. Rieseberg et al. (1999) spelled out the impacts of drift and of stabilizing and directional selection on trait distributions in hybrids. Genes under divergent directional selection should be fixed for alleles with opposite phenotypic effects in the divergent populations (e.g. all '+' alleles in one population and all '-' alleles in the other). If their effects are purely additive then trait values in hybrids and back-crosses will fall between those of the parent taxa. However, divergence due to drift or to weakly selected turn-over of alleles contributing to polygenic traits under stabilizing selection can lead to the phenomenon of complementary gene action. A simple illustration of complementary gene action is when loci contributing to polygenic traits are fixed for a different allele within each taxon, but within each taxon some loci contribute negatively to trait values while others contribute positively, producing an intermediate trait value. If there has been turnover in which loci contribute positively versus negatively since divergence began, such that certain loci have opposite effects in the two taxa, then recombination in hybrids can potentially produce individuals with all positive- or all negative-effect alleles (Rieseberg et al., 1999). Trait values in these individuals will be transgressive. Transgression leading to novel ecological adaptation and subsequent reproductive isolation has been strongly implicated in HHS in Drosophila (Le- wontin and Birch, 1966) and Helianthus sunflowers (Rieseberg et al., 2003) and is considered to be the most likely and most prevalent mechanism of HHS (Rieseberg et al., 1999). Hence, divergence through stabilizing selection or drift should favor HHS, while directional selection should not (Fig. 1; Rieseberg et al., 1999).

While Rieseberg and colleagues have suggested this relationship previously and pointed to the prevalence of transgression among hybrids, this hypothesis remains untested.

Intermediate hybrid phenotypes are generally expected to be less well adapted to the environment than parental phenotypes, which have already been subject to selection. And while transgression may promote adaptation to a novel environment not accessible to the parent species, it suffers from the same issue in being untested by natural selection. Novel adaptation requires the seemingly odd circumstance of the previously untested hybrid phenotypes being adapted to a novel environment that happens to be in the vicinity. Therefore it seems reasonable to assume that both intermediacy and transgression are likely, in most circumstances, to cause reduced hybrid fitness. The extent to which transgressive adaptation to a novel environment can in fact be considered an odd circumstance is an interesting question in itself (Diitrich-Reed and Fitzpatrick, 2013). Clearly transgressive hybrid adaptation does occur, and may for example be a major cause of the evolution of invasiveness in plants (Ellstrand and Schierenbeck, 2000). Gavrilets (1997a, 2004) has been keen to emphasize how there is always a route to high fitness in high-dimensional genotype space. The importance of the novelty of the environment and of hybrid genotypes has been explored to some extent by Barton (2001), and deserves more attention. A fuller review of this subject is beyond the scope of this paper.

2.2 Mode of divergence: Effects on dimensionality, evolvability and constraints

For a population to undergo evolution by natural selection there must be additive genetic variation in fitness, and the greater this heritable fitness variation, the more rapid the response to selection (Fisher, 1930). This requires not only additive genetic variation in fitness-related traits, but also that this variation is available to selection. The pattern of genetic correlations between traits alters their heritable variation in fitness (Hansen and Houle, 2008; Walsh and Blows, 2009). A simple example is antagonistic pleiotropy, in which the same locus causes variation in two different traits but each allele has a positive fitness effect on one trait and a negative effect on the other. If the strength of opposing selection is symmetrical then there will be no deterministic change in allele frequencies. In other words, there will be no heritable variation in fitness. For this simple case and more complex multivariate phenotypes the impact on adaptive evolution of correlations in the addi-
positive genetic variation affecting each trait – the G matrix – can be quantified by a trait’s ‘evolvability’ (Houle, 1992; Hansen and Houle, 2008). Evolvability is a statistical measure of the expected response to selection given the magnitudes and directions in multivariate phenotype space of available additive genetic variation, relative to the direction of maximum increase in fitness. If evolution is not equally possible in all directions in phenotype space due to genetic correlations between traits, these correlations act as a constraint on the direction of evolution (they also act as a constraint on evolution by genetic drift; Walsh and Blows, 2009). Evolvability quantifies constraints with respect to the fitness optimum, but more generally, constraints caused by genetic correlations can be measured as ‘effective dimensionality’ (Kirkpatrick, 2008). This quantity is a measure of the effective number of different dimensions - represented by a set of ordination axes typically produced using Principal Components analysis - a population can evolve in, up to a maximum of the number of traits being measured. In other words, if the G matrix is broken down into a set of Principal Component axes and the different axes explain unequal amounts of the variation present, effective dimensionality is reduced and evolution is constrained (Hine and Blows, 2006). For an extreme example, if all genetic variation is in a single direction in phenotype space due to genetic correlations preventing evolution in any other direction (for example if one trait gets bigger, all traits get bigger), then effective dimensionality is one and constraints on evolution are strong.

2.2.1 Effects of transgression and intermediacy on dimensionality, evolvability and constraints

How does the mode of divergence between parent taxa affect trait evolvability, dimensionality and constraints in hybrids? First, transgression and intermediacy can be couched in these terms: the additive genetic variation introduced by hybridization may increase the magnitude of genetic variation per se but may constrain hybrids to evolve in very limited directions. For example, whether hybrids are all intermediate or the spread of trait values extends beyond those of parents (transgressive segregation), incompatibilities in hybrids may restrict their evolution following a ridge of high fitness that represents the reconstruction of fit ancestral genotypes (e.g. Gavrilets, 1997b; Eroukhmanoff et al., this issue). Should the direction of evolution towards the fitness optimum fall outside of this ridge, evolvability would be low.

Positive genetic correlations between traits with positively correlated fitness effects increase the effectiveness of selection (e.g. Kirkpatrick and Barton, 2005; Via and West, 2008; Kulathinal et al., 2009; Joron et al., 2011; Yeaman and Whitlock, 2011). At levels of parental divergence in which a broad range of hybrid phenotypes are viable and fertile, dimensionality would be lower when the parents diverged by directional selection, due to the lower amount of transgression. This equates to higher genetic correlations, and enhances evolution along the direction of divergence between the parent taxa. Therefore, if the phenotypic optimum/optima lie at or between the parental values rather than outside, divergent selection in parents should increase evolvability in hybrids, in comparison with transgressive segregation in hybrids produced by stabilizing selection in parents. Consequently, traits under divergent selection in parent taxa should facilitate coexistence and the maintenance of two distinct parental phenotypic clusters when parental phenotypes sit at fitness optima. On the other hand, the same lower dimensionality with divergent selection should also facilitate the reconstruction of fit ancestral genotypes and hence potentially increase gene flow. The reconstruction of fit ancestral genotypes results in local populations of high fitness (e.g. Shuker et al., 2005), whereas if this does not occur then more incompatibilities remain within each population across a hybrid zone, as is typically assumed in tension zones (Barton and Hewitt, 1985, 1989). Therefore, as long as fitness does not dissipate too rapidly in space as individuals disperse between populations, a neutral or beneficial allele can cross a hybrid zone quite unperturbed by reduced hybrid fitness. High gene flow between parent taxa would also have the consequence of aligning the G matrix in the two parent taxa with the direction of divergence between them (Guillaume and Whitlock, 2007), further influencing phenotypic evolution and potentially reducing evolvability. Divergent selection can therefore have two opposing effects on gene exchange between parent taxa and the maintenance of a bimodal distribution of genotypes. Whether the effect of divergent selection in constraining the direction of evolution will in fact lead to increases or to decreases in gene flow is unknown and requires theoretical and empirical testing.

2.2.2 Effects of sex linkage on dimensionality, evolvability and constraints

The mode of divergence between parent taxa affects the chromosomal distribution of divergent loci, and we propose that this in turn influences dimensionality, evolvability and constraints in hybrids (Fig. 1). Under
many circumstances the rate of divergence is expected to differ between sex chromosomes and autosomes (Box 1). Both divergence and reproductive isolation are often stronger on sex chromosomes, though less so in the earliest stages of speciation (Qvarnström and Bailey, 2009). While genes under strong directional selection often accumulate differences on sex chromosomes, genes evolving through turnover of alleles contributing to polygenic traits under stabilizing selection are expected to diverge more rapidly on autosomes (Charlesworth et al., 1987; Box 1).

How does this affect the evolvability of hybrid compared to non-hybrid populations? We propose that the principal effects of bias in divergence between sex chromosomes and autosomes are in altering the chromosomal distribution of additive genetic variation in hybrids and altering genetic correlations. We consider that the ultimate consequence would be changes in the degree of constraints on evolution through alteration of phenotypic correlations between the sexes, linkage disequilibrium, and pleiotropic effects of single loci on multiple traits. We describe the mechanisms below.

During the process of hybrid genome stabilization, incompatibilities are expected to be purged (Buerkle and Rieseberg, 2008). Increased divergence means an increase in the potential for incompatibilities in hybrids. The resulting hybrid evolution may differ between isolated hybrid populations and those that continue to receive immigrants. In a relatively isolated hybrid population or one that covers a large geographic area relative to dispersal rate, leading to reduced introgression from parent taxa, incompatibilities would be expected to be purged (Barton, 2001; Buerkle and Rieseberg, 2008; Gompert and Buerkle, 2011; Trier et al. personal data). This purging may occur less readily in ‘open’ hybrid zones such as tension zones maintained by a balance between dispersal into the zone and selection against hybrids (Barton and Hewitt, 1985, 1989) or populations that continue to receive immigrant parental genotypes, because gene flow into the hybrid zone continually replenishes the stock of unfit hybrids (but see Gavrilets, 1997b; fit ancestral gene combinations can still be reconstructed). However, cline movement can still occur in an open hybrid zone, effectively purging incompatibilities from populations in the wake of the moving cline. Directional selection, differences in parental population sizes or dominance can all cause incompatibility clines to move in space (Barton and Hewitt, 1985, 1989; Gompert and Buerkle, 2011).

This purging of incompatibilities has major consequences for hybrids. Due to the initial presence of large linkage blocks from either parent taxon in the early generations of hybridization and the fact that these take time to break down (Baird, 1995), linkage disequilibria will be strong and their effects will spread across larger blocks of chromosomes than is typical in non-hybrid populations (Buerkle and Rieseberg, 2008). The hitchhiking effect due to rapid purging of incompatibilities should therefore lead to reduced polymorphism over much larger genomic regions than would intraspecific hitchhiking (Buerkle and Rieseberg, 2008). How is this linked to the effects of sex chromosomes and autosomes?

A key consequence is that more divergent chromosomes should evolve towards having more and larger regions of reduced polymorphism in hybrids. Fixed loci do not contribute additive genetic variation to traits, so for example if incompatibilities were mostly sex-linked leading to higher levels of purging and fixation on sex chromosomes, autosomes would then contribute proportionally more to additive genetic trait variation and hence to the nature of genetic constraints.

There are further effects of strong linkage disequilibrium combined with the presence of incompatibilities in evolving hybrids. The hitchhiking effect described above can also interfere with selection at linked loci; this is known as Hill–Robertson interference (Hill and Robertson, 1966). If selection on different linked loci (for example an incompatibility gene and a local adaptation gene) is not positively correlated, then they will each reduce the effectiveness of selection on the other locus. In the extreme case of a perfect negative fitness correlation, selection will have no effect on changes in allele frequencies. This is exactly the same result as the case of antagonistic pleiotropy at a single locus described above. Hence, reduced ‘effective’ recombination rate in a region of the genome under selection decreases the probability that a new beneficial allele will become fixed (Barton, 2010).

Overall, if for example sex chromosomes contain an excess of incompatibilities, they will suffer both (i) reduced polymorphism, reducing their contribution to additive genetic trait variation, and (ii) increased interference during purging and genome stabilization, constraining evolution towards fitness optima (i.e. reducing evolvability). Conversely, we note that there are numerous studies showing that linkage between locally adapted genes and between incompatibilities can enhance the effectiveness of selection on these loci (e.g. Barton, 1983; Kirkpatrick and Barton, 2005; Via and West, 2008; Kulathinal et al., 2009; Joron et al., 2011;
Yeaman and Whitlock, 2011). Hence if the fitness effects of local adaptation and incompatibility loci become correlated (Barton and de Cara, 2009; Abbott et al., 2013; Trier et al., personal data) - such as if a moving tension zone (Barton and Hewitt, 1985, 1989) becomes aligned with a sharp environmental ecotone - evolvability will be increased.

Overall therefore the general expectation for an evolving hybrid population is that directional selection in the parent taxa leads to a greater contribution of additive genetic variation on autosomes in hybrid populations, and stabilizing selection shifts the balance towards a bigger contribution of sex chromosomes. What are the consequences of biasing additive genetic variation towards autosomes or sex chromosomes? Genes with sex-biased expression have been shown to be excessively sex-linked (e.g. Ellegren and Parsch, 2007) and to be more tissue-specific and hence less pleiotropic than genes with more sexually correlated expression levels (Mank et al., 2008). Pleiotropy is an important source of genetic correlations constraining adaptive evolution, and less pleiotropic genes have been shown to evolve more rapidly (Mank et al., 2008; Meisel, 2011). Furthermore, the resolution of sexual conflict through the evolution of sexual dimorphism is expected to be biased towards sex chromosomes (Rice, 1984). Based on these empirical patterns and theoretical expectations we predict therefore that, on average, autosomes should host loci causing more sexually correlated variation and greater pleiotropy than sex chromosomes (Fig. 1). As far as we are aware this has not been tested. Modes of evolution that favor divergence on sex chromosomes (Box 1; Qvarnström and Bailey, 2009) should therefore increase evolutionary constraints in hybrids by increasing the contribution of autosomes towards additive genetic variation available to selection (Fig. 1). In many circumstances strong divergent selection is likely to be one such mode of evolution. Meanwhile, because stabilizing selection favors divergence on autosomes (Box 1; Charlesworth et al., 1987), we expect it to lead to reduced constraints and increased dimensionality and evolvability in hybrids relative to non-hybrid taxa. This is because sex chromosomes make a greater contribution to additive genetic trait variation in this situation, and they are predicted to produce less sexually correlated and less pleiotropic phenotypic variation than autosomes.

2.2.3 Effects of dominance on dimensionality, evolvability and constraints

According to ‘Haldane’s sieve’ (Haldane, 1924; Turner, 1981; Charlesworth, 1992), directional selection favors the fixation of new beneficial mutations if they are dominant. This is due to the extreme rarity of homozygotes for a new mutation. Indeed given the strength of this theoretical expectation, dominance is used to infer the direction of past selection (Falconer and Mackay 1995; Barton 2001). There is no such expectation for the neutral or nearly neutral turnover of loci affecting traits under stabilizing selection. Hence divergent selection in parents should increase the effects of dominance in hybrids (Fig. 1; but see Nuïsmere et al., 2012). The consequences for evolvability in hybrids are complex, often asymmetrical, and vary considerably depending on the history of divergence (Barton, 2001). Hence it is difficult to predict whether dominance enhances or reduces hybrid evolvability. However the effects of dominance can be large and must therefore be considered. One possible impact of dominance is in altering the production of parental-like phenotypes in hybrids, for example a fully dominant trait controlled by a single locus would always be parental-like unless it represented an incompatibility. This may improve hybrid fitness if parental phenotypes are fit relative to others. Another potential consequence may be in aiding gene flow between parent taxa. Some alleles may be fit in both parental genomic backgrounds but suffer reduced fitness in hybrids, reducing the potential for the spread of beneficial alleles. Dominance may ameliorate fitness reduction in hybrid genotypes and therefore increase this rate of introgression.

We note that incompatibilities are reported to be both disproportionately sex-linked and disproportionately recessive in hybrids (e.g. True et al., 1996; Tao et al., 2003; Masly and Pregreaves, 2007). This does not necessarily reflect dominance/recessivity relationships within the parent taxa during allelic replacement, and so does not invalidate Haldane’s sieve. It does mean that incompatibilities will be more effectively purged from sex chromosomes than autosomes because they are always exposed to selection in the heterogametic sex (Box 1; Qvarnström and Bailey, 2009). Overall however we remain agnostic on the expected impacts of dominance, both because its effects are known to be complex and because potential changes in dominance/recessivity when loci find themselves in a hybrid genomic background make the impacts of parental divergence mechanisms difficult to predict.

3 Empirical Tests

A first step in testing the hypotheses and predictions
put forward here would be to identify the mechanisms of divergence between the parent taxa. There are a variety of methods for distinguishing mechanisms of evolution and divergence (Box 2). We follow Rieseberg et al. (1999) in supporting a strong impact of traits diverging under stabilizing selection on homoploid hybrid speciation. This might be examined through identification of genes and traits that contribute to isolation between hybrid species and their parents combined with tests of divergence mechanisms.

We predict that divergent directional selection will lead to stronger constraints and lower evolvability in hybrids because additive genetic variation would be biased towards autosomes (the opposite prediction for divergence under stabilizing selection). Gene expression data would be ideal for testing differences in intersexual correlations and pleiotropy between sex chromosomes and autosomes, and data sets may already be available to do so. Methods of measuring correlations in gene expression are now in common usage (e.g. Innocenti and Chenoweth, 2013). Pleiotropy can be tested where expression data exist for multiple different tissues by using a measure of the degree of tissue specificity (e.g. Mank et al., 2008): higher tissue specificity equates to lower pleiotropy.

We suggest that directional and stabilizing selection have differing impacts on gene exchange between parent taxa and the maintenance of a bimodal distribution of genotypes during periods of contact and gene exchange. Combining tests of the mode of divergence (Box 2) with measures of the degree of bimodality and the extent of gene exchange would be required to examine this prediction.

4 Other Processes to Consider

We focus on the different effects on hybrid evolution of divergence between parent taxa by directional versus stabilizing selection because clear and novel predictions can be made. Detailed discussion of other processes lies beyond the scope of this paper, but we briefly mention some other potentially important factors. Drift may influence adaptation in hybrids in a different manner to both divergent selection and stabilizing selection, and deserves equal attention. With respect to transgression and intermediacy we focus mostly on additive genetic effects. Epistatic interactions in hybrids can alter these relationships (Rieseberg et al., 1999) and may be particularly important in fitness-related traits due to the expectation of epistatic fitness effects in hybrids through Dobzhansky-Muller incompatibilities (e.g. Gavrilets, 2004). We believe this deserves extended discussion in the future.

The time since divergence began for the parent taxa will influence the number and magnitude of incompatibilities, altering constraints to the point that hybrids may have low evolvability in every direction in pheno-

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Box 2  Methods for identifying the mode of evolution within species and divergence between species

| Intraspecific fitness landscapes: | Stabilizing and directional selection can be measured and compared in wild populations through the estimation of fitness correlates such as survival or reproductive output. Typically, linear selection gradients (β) estimate the strength of directional selection whereas quadratic selection gradients (γ) estimate the curvature of the selection function. For instance, stabilizing selection on a trait implies that the quadratic selection gradients are negative, and disruptive selection on a trait implies that the quadratic selection gradients are positive. However, in natural populations, both linear and quadratic selection gradients seem relatively weak in general (Kingsolver et al., 2001), and selection may also to a large extent fluctuate both in space and time (Gosden and Svensson, 2008), which makes these types of direct measures of selection sometimes difficult to interpret or to use to predict the state and past mode of divergence between two species. |
| Gene- or trait-environment correlations: | A direct way to test for ecological divergence at the genomic level is to test for associations between markers and environmental variables across multiple populations (e.g. Coop, 2010). This approach can equally be used on phenotypes to test for divergent natural selection, including when no data on the additive genetic basis of the focal traits are available (e.g. Eroukhmanoff et al., 2013). Translocation experiments and other manipulations of the environment can provide decisive evidence of divergent ecological adaptation between lineages (e.g. Vallin et al., 2013). |
| Genome scans of divergence: | The primary objective of genome scans for divergence is to distinguish divergent directional selection from everything else (for reviews see Pool et al., 2010; Rice et al., 2011). They can identify candidate genes under directional (and also balancing) selection, but cannot distinguish between genes diverging by drift versus stabilizing selection because neither shows a signature of strong selection at individual loci. Outlier analysis is useful because it does not require a fully assembled and mapped genome. However, there are several difficulties with this approach. Hitchhiking mapping (reviewed in Pool et al., 2010), which examines the allele frequency spectrum in a mapped genome in order to identify loci under selection, is much more effective in identifying selection. |
| Phylogenetic tests: | Examination of phenotypic trait variation within and among species along an independently derived (normally molecular) phylogeny can be used to distinguish multiple different modes of evolution, including neutral, diversifying and stabilizing selection (e.g. Eng et al., 2009; Kutsukake and Innan, 2012; Thomas and Freckleton, 2012). These methods come in a variety of forms but typically test for deviations from a simple Brownian motion model of evolution with uniform rates across the phylogeny, and in some cases also use the fit of the data to the Ornstein-Uhlenbeck process to specifically test for stabilizing selection (Martins, 1994; Hansen, 1997; Butler and King, 2004). |
type space with highly divergent parents due to strongly reduced fertility or viability. Studies on a variety of organisms have revealed that transgression in hybrids increases with increasing divergence time between the parent taxa (Stelkens and Seehausen, 2009; Stelkens et al., 2009). The chromosomal distribution of divergence may also change with time; Qvarnström and Bailey (2009) suggested that the influence of sex chromosomes will increase along with the temporally increasing influence of new mutations over standing genetic variation. Some trait values, initially present in only one parent taxon, may be adaptive in both. Universally advantageous traits and alleles should then spread easily through hybridization (Barton, 2013). However, transgression and intermediacy may reduce their fitness in hybrids and retard adaptive introgression because the adaptive parental trait values are lost in hybrids. This is particularly true with intermediacy, as transgressive segregation will lead to a wide variety of phenotypes including the fit parental phenotypes. Traits that remain parental-like in hybrids may be more likely to be universally adaptive and hence spread easily. This will typically be the case when traits are fully dominant or recessive. For relationships between dominance, sex linkage and transgression, see Dittrich-Reed and Fitzpatrick (2013).

5 Summary

Divergence by stabilizing selection in parent taxa should lead to transgressive segregation in hybrids, while divergence by directional selection should lead to intermediate hybrid phenotypes. Novel adaptation facilitated by transgressive hybrid phenotypes appears to be quite common, and is considered to be the most likely cause of HHS. Hence stabilizing selection in parent taxa can promote both novel adaptation and HHS (Fig. 1). Transgression in hybrids increases dimensionality and lowers genetic correlations in the direction of divergence between the parent taxa, reducing the effectiveness of selection in that direction relative to intermediacy. Therefore divergent selection in parent taxa has the potential to facilitate both the maintenance of two distinct phenotypic clusters and gene flow between parent taxa; the latter being more likely when fit ancestral genotypes are reconstructed in hybrids. Maintenance of high gene flow is also likely to reduce the dimensionality of additive genetic variation in phenotype space in the parent taxa, constraining adaptation (Guillaume and Whitlock 2007). Divergent selection in parents favors sex-linked reproductive isolation, increasing the contribution of autosomes to additive genetic variation and hence increasing constraints through both reduced sexual dimorphism and increased pleiotropy. The opposite is expected for divergence through stabilizing selection. Directional selection increases the influence of dominant new mutations during divergence, though it is unclear whether such alleles would remain dominant in a hybrid genomic background.

6 Conclusions

A relatively simple set of predictions, grounded in existing theory and data, result from examination of the different impacts in hybrids of genetic divergence between parent taxa due to directional versus stabilizing selection. We are aware there are likely to be exceptions to the hypotheses and predictions discussed here. Indeed, within each pair of parent taxa, different traits are likely to diverge through different mechanisms, and hence have different effects in hybrids. However we regard these hypotheses and predictions as a clear and well-defined starting point for further investigation into adaptation in hybrids.

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