

ORIGINAL ARTICLE

Empirical study of hybrid zone movement

RJA Buggs

Church Farm, Capel, Tonbridge, Kent, UK

Hybrid zones are 'natural laboratories' for studying the origin, maintenance and demise of species. Theory predicts that hybrid zones can move in space and time, with significant consequences for both evolutionary and conservation biology, though such movement is often perceived as rare. Here, a review of empirical studies of moving hybrid zones in animals and plants shows 23 examples with observational evidence for movement, and a further 16 where patterns of introgression in molecular markers could be interpreted as signatures of movement. The strengths and weaknesses of methods used for detecting hybrid zone movement are discussed, including long-term replicated sampling, historical surveys, museum/herbarium collections, patterns of relictual populations and introgression of genetic markers into an advancing taxon. Factors governing hybrid zone movement are assessed in the

light of the empirical studies, including environmental selection, competition, asymmetric hybridization, dominance drive, hybrid fitness, human activity and climate change. Hybrid zone movement means that untested assumptions of stability in evolutionary studies on hybrid zone can lead to mistaken conclusions. Movement also means that conservation effort aimed at protecting against introgression could unwittingly favour an invading taxon. Moving hybrid zones are of wide interest as examples of evolution in action and possible indicators of environmental change. More long-term experimental studies are needed that incorporate reciprocal transplants, hybridization experiments and surveys of molecular markers and population densities on a range of scales.

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Introduction

Hybrid zones occur when the geographic ranges of closely related taxa meet and cross-fertilize to produce hybrids (Barton and Hewitt, 1985, 1989; Harrison, 1993). Such zones have been found in a wide range of both animal and plant groups, and in terrestrial, marine and freshwater systems. They provide 'natural laboratories' for evolutionary biologists investigating the formation (Hewitt, 1988; Howard, 1993; Moore and Price, 1993; Cain *et al.*, 1999; Marshall *et al.*, 2002; Campbell, 2004) and maintenance (Rieseberg and Buerkle, 2002; Lexer *et al.*, 2004) of species differences. Characterization of their spatio-temporal dynamics is essential to such studies, and the movement of a hybrid zone on an ecological time-scale can radically alter evolutionary outcomes.

Case studies of the geographical movement of hybrid zones also provide empirical evidence for conservation biologists investigating the dynamics of species invasions (Endler, 1977; Ellstrand, 1992; Rhymer and Simberloff, 1996; Wolf *et al.*, 2001). Assessing hypotheses of the causes and consequences of hybrid zone movement is critical if their long-term fate, the extinction of one taxon, is to be averted (Ellstrand, 1992; Rhymer and Simberloff, 1996); many threatened species owe their demise at least in part to hybridization with invading relatives (Levin

et al., 1996; Haig, 1998; Allendorf *et al.*, 2001; Wolf *et al.*, 2001; Allendorf and Lundquist, 2003).

A good understanding of the basis for the spatio-temporal dynamics of hybrid zones has been developed from theoretical principles, informed by a number of empirical studies. This initially took place in the context of two evolutionary hypotheses: stasipatric speciation, in which a new chromosomal rearrangement spreads at the expense of parental forms (Key, 1968; White, 1968, 1978), and phase III of Wright's shifting balance model, in which a new adaptive peak spreads to other populations (Wright, 1977, 1982; Barton, 1992; Kondrashov, 1992). The widespread occurrence of natural hybrid zones, the taxonomic questions they pose and the opportunities they present for investigating processes of species isolation make them a research field in their own right (Barton and Hewitt, 1985).

It is recognized that hybrid zones vary greatly in their structures depending on the degree of genetic and ecological differentiation between the two meeting taxa, their rates of dispersal and the fitness of their hybrid offspring (Harrison, 1993). Conditions for movement depend upon these factors. When hybrids have greater fitness than parental taxa, a hybrid zone will be stable if the hybrid's fitness is bounded. In an 'ecotonal' zone, this is in an environment intermediate to that occupied by the parental taxa (Moore, 1977; Moore and Price, 1993; Good *et al.*, 2000). If not thus bounded, the hybrid may expand its range at the expense of parental ranges. Unidirectional expansion might occur if one parental form is of lower fitness than the other and out-competed. Movement in favour of one parental form might appear to occur if hybridization is asymmetric and repeated backcrossing of hybrids with that parental form leads

Correspondence: Dr RJA Buggs, Department of Botany, University of Florida, 220 Bartram Hall, PO Box 118526, Gainesville, FL 32611 USA, E-mail: buggs@ufl.edu

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to the advance of a hybrid much more closely related to that form. Where hybrids are fitter than their parents, pre-zygotic reproductive isolation is unlikely to evolve, so the only way in which the hybrid zone can cease to exist is by the prevalence of one genotype (Paterson, 1978; Liou and Price, 1994).

When hybrids are of lower fitness than parents, a hybrid zone is usually known as a 'tension zone' (Key, 1968; Barton, 1979; Barton and Hewitt, 1985). The low fitness of hybrids causes spatial mixing of the parental taxa to be minimized, leading to narrow, straight hybrid zones (Key, 1968; Barton, 1979; Barton and Hewitt, 1985). Hewitt (1975) and Endler (1977) suggested, and Barton (1979) showed that tension zones can move due to gradients of population density or asymmetry of hybridization between the parental taxa. Differential adaptation of the parents may also cause movement (Key, 1968; Barton and Hewitt, 1985). However, Barton and Hewitt (1985) argued that tension zones will be stable in troughs of low population density and these would be frequent and deep enough to resist movement due to fitness differences or asymmetry of hybridization. This is one reason for scepticism of models of speciation involving hybrid zone movement (Barton and Hewitt, 1981).

Two further causes of hybrid zone movement can be hypothesized. 'Dominance drive' could occur where a dominant allele displaces a recessive allele (Moran, 1981; Mallet, 1986). Climate change could also play a role as it has been implicated in the movement of species range boundaries generally (Parmesan, 1999; Thomas and Lennon, 1999) and the movement of a (non-hybrid) contact zone between red and arctic foxes (Hersteinsson and MacDonald, 1992).

The considerations above predict that hybrid zones can move under a variety of circumstances. However, such movements may be difficult to find in the present because long-term studies, which might detect gradual movements or rare episodes of rapid movement halted by frequent barriers, are rare (Harrison, 1990; Hairston *et al.*, 1992). In 1985, 14 hybrid zones in the literature could be categorized (five of them tentatively) with respect to their geographical stability and of these, five appeared to be unstable (Barton and Hewitt, 1985). Over the last 20 years, more empirical cases have been observed where a hybrid zone appears to be moving. In addition, development and widespread use of molecular markers in ecological studies has greatly increased our knowledge of genetic patterns at a number of hybrid zones. These patterns are sometimes interpreted in terms of zone movement. Current empirical knowledge of hybrid zone movement is reviewed below with discussion of the strengths and weaknesses of the different lines of evidence. This permits assessment of the factors that are driving movement of hybrid zones in nature.

Identifying hybrid zone movement

Observation over time

Observation of hybrid zones over multiple years is the most reliable method of detecting their movement, and such evidence has been found in several genera of both animals and plants. Twenty-three of the clearest exam-

ples are documented in Table 1. The precise nature of the evidence available in each case differs. The best documented have been subject to long-term studies by single research groups. For example, morphological surveys were carried out twice annually for 18 years over a zone between salamanders *Plethodon glutinosus* and *Plethodon jordani* (Hairston *et al.*, 1992), and annually for 17 years between ticks *Aponomma hydrosauri* and *Aponomma limbatum* (Bull and Burzacott, 2001). Fourteen annual isozyme surveys were conducted on a hybrid zone between crickets *Allonemobius socius* and *Allonemobius fasciatus* (Britch *et al.*, 2001). Such long-term studies are difficult to sustain and in most cases in Table 1 evidence is only available for two or three time points, based on historical evidence.

Information on the position of hybrid zones in the past may be provided by records of an alien introduction (for example, *Solenopsis*, *Orchelimum*, *Orconectes*, *Cervus* and *Pseudorasbora* hybrid zones in Table 1), by historical surveys (for example, *Poecile*, *Hippolais*, *Vermivora*, *Corvus*, *Sceloporus* and *Mercurialis* hybrid zones in Table 1), and by museum or herbarium collections (for example, *Quiscalus* hybrid zone in Table 1). Issues of reliability may accompany such historical evidence and researchers occasionally question the data collected by others (Woodruff, 1981). There is sometimes a lack of precision in details of times and locations, as shown by uncertainties indicated for some of the figures in Table 1. However, there are few reasons to suppose that field naturalists of the past were systematically less reliable than those of today, and there is potential for more widespread use of historical collections in tracing past ecological changes (Sparks, 2007).

Replication in space

Comparative studies in space (as well as time) may be useful in drawing inferences about zone movement. In three of the observed cases of hybrid zone movement in Table 1 (*Plethodon*, *Mercurialis* and *Allonemobius*), researchers have examined more than one replicate area of hybrid zone. In each of these cases, the different areas appear to vary in the speed or direction of putative zone movement, cautioning against the drawing of general conclusions from a single transect. Comparisons of two areas where direction or speed of movement appears to differ may help in the identification of factors governing zone movement; for example, in the case of *Mercurialis annua*, the two hybrid zones differ in the sexual system and population density of the hexaploid plants.

Relictual populations

Current patterns of distribution have sometimes been used to draw inferences of past hybrid zone movement. Where relictual populations of one taxon occur in isolated areas within the range of another, it has been invoked as evidence to assess hybrid zone movement in *Mus musculus* (Barton and Hewitt, 1981), *M. annua* (Buggs and Pannell, 2006) and *Limnodynastes tasmaniensis* (Littlejohn and Roberts, 1975). Such patterns can provide useful corroboration for other evidence, but might also be explained by long-range dispersal events.

Table 1 Observed cases of hybrid zone movement

Species (advancing taxa first)	Location	Evidence	Movement (km)	Time (year)	Hybrid fitness	Possible mechanism	References
<i>Plethodon glutinosus</i> – <i>Plethodon jordani</i> (salamanders)	North Carolina	Thirty-six surveys of colour pattern composition	~0.4	18	H?	Human disturbance; superiority of <i>P. glutinosus</i> ?	Hairston <i>et al.</i> (1992)
<i>Aponomma hydrosauri</i> – <i>Aponomma limbatum</i> (Ticks)	S. Australia	Annual morphological surveys	1–2	17	L	Environmental change; differential adaptation	Bull and Burzacott (2001)
<i>Allonemobius socius</i> – <i>Allonemobius fasciatus</i> (crickets)	Appalachian mountains	Annual isozyme surveys	Frequency shift over 300 km wide mosaic	14	Variable	Climate change	Britch <i>et al.</i> (2001)
<i>Solenopsis invicta</i> – <i>Solenopsis richteri</i> (fire ants)	N. America	Surveys after alien introduction; distribution of RAPD markers and cytoplasmic elements	~350	<60	?	Higher fitness of <i>S. invicta</i> , sex differences in migration or selection	Shoemaker <i>et al.</i> (1994, 1996, 2000), Goodisman <i>et al.</i> (1998)
<i>Orchelimum nigripes</i> – <i>Orchelimum pulchellum</i> (katydids)	Potomac River, E. USA	Survey after alien introduction	>25	<100	L	Mate preference	Shapiro (1998, 2000, 2001), Cabrero <i>et al.</i> (1999)
<i>Orconectes rusticus</i> – <i>Orconectes propinquus</i> (crayfish)	Northern Wisconsin lake	Survey after alien introduction; patterns of cytonuclear disequilibrium	~6.3	9	H	Skewed sex ratios	Perry <i>et al.</i> (2001)
<i>Cervus nippon nippon</i> – <i>Cervus elaphus</i> (deer)	Scotland	Surveys after alien introduction; isozymes, microsatellite markers and mtDNA RFLPs	?	~80	=?	Assortative mating, selective advantage of <i>C. n. nippon</i> genotype	Abernethy (1994), Goodman <i>et al.</i> (1999)
<i>Pseudorasbora parva</i> – <i>Pseudorasbora pumila</i> (minnows)	E. Japan	Surveys after alien introduction; 5-year allozyme study and mtDNA survey	?	~30	L	Assortative mating; male–male competition	Konishi and Takata (2003, 2004a, b)
<i>Poecile carolinensis</i> – <i>Poecile atricapillus</i> (chickadees)	Ohio	Three morphological surveys	100	60	L	Male intrasexual dominance or female preference	Bronson <i>et al.</i> (2003a, b), Woodcock <i>et al.</i> (2005), Reudink <i>et al.</i> (2006)
<i>Hippolais polyglotta</i> – <i>Hippolais icterina</i> (warblers)	Western Europe	Three morphological surveys	60–240	70	?	Cross-species learning of song parameters; differential parasite infestation	Faivre (1993), Yeatman-Berthelot and Jarry (1994), Secondi <i>et al.</i> (2003), Reullier <i>et al.</i> (2006)
<i>Vermivora pinus</i> – <i>Vermivora chrysoptera</i> (warblers)	E. N. America	Morphological surveys, patterns of mtDNA distribution	‘Substantial’	~100	?	Mate choice and habitat preference?	Remington (1968), Gill (1997), Shapiro <i>et al.</i> (2004), Dabrowski <i>et al.</i> (2005)
<i>Corvus corone corone</i> – <i>Corvus corone cornix</i> (crows)	Denmark and Germany	Two morphological surveys	19	78	?	<i>C. c. corone</i> more aggressive	Saino and Scatizzi (1991), Rolando and Giachello (1992), Haas and Brodin (2005)
<i>Sceloporus tristichus</i> – <i>Sceloporus cowlesi</i> (lizards)	Arizona	Two chromosome polymorphism surveys	>1.5	~30	?	Overgrazing	Leaché and Cole (2007)
<i>Mercurialis annua</i> diploid–hexaploid (mercuries)	Spain	Two morphological/cytological surveys	>8	?	L	Pollen swamping due to sexual system and higher fitness of diploids	Buggs and Pannell (2006, 2007), Dorken and Pannell (2007)
<i>Quiscalus quiscalus quiscula</i> – <i>Quiscalus quiscalus versicolor</i> (grackles)	Louisiana	Morphological variation of collected specimens	32	~30	L?	High dispersal ability of species suggests selection is maintaining narrow hybrid zone	Yang and Selander (1968), Moore and Dolbeer (1989)
<i>Pseudophryne bibroni</i> – <i>Pseudophryne semiararmorata</i> (frogs)	S. Australia	Five surveys of colour pattern composition; introgression of isozyme marker	<20 (colour pattern)	15	L		Woodruff (1972), McDonnell <i>et al.</i> (1978),
			<75 (isozyme introgression)	?			Woodruff (1981)

Table 1 Continued

Species (advancing taxa first)	Location	Evidence	Movement (km)	Time (year)	Hybrid fitness	Possible mechanism	References
<i>Triturus cristatus</i> – <i>Triturus marmoratus</i> (newts)	France	Two morphological surveys; one allozyme and mtDNA survey	>30	~30	L	Asymmetric mate choice?	Arntzen and Wallis (1991)
<i>Limnoporus dissortis</i> – <i>Limnoporus notabilis</i> (waterstriders)	SW Canada	Two morphological surveys	<10?	~13	=	Almost all hybrids are males, and <i>L. notabilis</i> females prefer <i>L. dissortis</i> or hybrid males	Spence (1990), Sperling and Spence (1991), Klingenberg <i>et al.</i> (2000)
<i>Heliconius erato</i> <i>hydarana</i> (butterflies)	Panama	Two morphological surveys	47	17	L?	Dominance drive; selection by predators	Blum (2002)
<i>Anartia fatima</i> – <i>Anartia amathia</i> (butterflies)	Panama	≥4 wing pattern surveys; 1 allozyme survey; 2 mtDNA surveys	50	20	L	Competitive exclusion; deforestation	Dasmahapatra <i>et al.</i> (2002)
<i>Geomydoecus aurei</i> – <i>Geomydoecus centralis</i> (lice)	New Mexico	Two morphological surveys	0.7–0.9	5	?	Competitive superiority of <i>G. aurei</i>	Hafner <i>et al.</i> (1998)
<i>Pholidobolus montium</i> – <i>Pholidobolus affinis</i> (lizards)	Ecuador	Two morphological surveys	≥30	≤12	?	Agricultural activity modifying habitat	Hillis and Simmons (1986)
<i>Helianthus annuus</i> – <i>Helianthus bolanderi</i> (sunflowers)	California	Three morphological surveys	<0.35	55	L	Human disturbance favouring <i>H. annuus</i> ; differential adaptation	Carney <i>et al.</i> (2000)

Hybrid fitness: L, lower than parents; H, higher than parents.

Patterns of molecular markers

Patterns of molecular markers have been hypothesized to provide a signature of hybrid zone movement: a moving zone will leave in its wake a tail of clines of unlinked neutral markers, 'the hybrid zone will thus appear to be asymmetrical with apparent unidirectional introgression across the zone' (Moran, 1981, p 71). Recent modelling has shown that even limited hybridization between two taxa can result in substantial introgression, when one is competitively displacing the other (Currat and Excoffier, 2005). However, these patterns are hard to interpret, as they might also be evidence for introgression of advantageous alleles away from a static hybrid zone due to selection (Moran, 1981). Where a mitochondrial or chloroplast marker has introgressed, cytoplasm-nuclear interactions or selection for nuclear but not cytoplasmic genes may play a role (Rieseberg and Soltis, 1991). Barton and Hewitt (1985) suggested that marker evidence was most unequivocal when many neutral alleles introgressed, all in the same direction. In some of the hybrid zones listed in Table 1, patterns of introgression have been studied, apparently confirming the possible value of introgressed markers in detecting hybrid zone movement.

In the case of the hybrid zone between the birds *Quiscalus quisculus quiscula* and *Quiscalus quisculus versicolor*, populations of the former are only slightly introgressed with genes from the latter, whereas those of the latter are heavily introgressed with genes from *Q. q. versicolor*. This is as we would expect given that *Q. q. quiscula* is advancing (Yang and Selander, 1968). At the frog *Pseudophryne bibroni*–*Pseudophryne semiarmorata* hybrid zone, a tail of asymmetric introgression of an *Ldh* isozyme marker diagnostic of *P. semiarmorata* populations into *P. bibroni* populations to the north of the hybrid zone also fits with the observed zone movement in favour of *P. bibroni* (McDonnell *et al.*, 1978). A hybrid zone between lizards *Sceloporus tristichus* and *Sceloporus cowlesi* has moved over 1.5 km in around 30 years in favour of the former; correspondingly, *S. cowlesi* mitochondrial DNA is found introgressed over 8 km into the current range of *S. tristichus* (Leaché and Cole, 2007). Introgression between newts *Triturus cristatus* and *Triturus marmoratus* is found in the area of recent species replacement, but is absent in other areas (Arntzen and Wallis, 1991). At a hybrid zone between two warbler species, predominantly *Vermivora chrysoptera* mtDNA haplotypes are found in hybrids at the leading edge of a *Vermivora pinus* expansion (Dabrowski *et al.*, 2005) and cytonuclear disequilibrium is also found at a crayfish *Orconectes rustica*–*Orconectes propinquus* hybrid zone. Two studies of deer, *Cervus elaphus* and alien *Cervus nippon nippon*, show introgression in both taxa (Abernethy, 1994; Goodman *et al.*, 1999), but the expanding alien taxon shows higher levels of introgression which are uniform across its range, while introgression is lower in *C. elaphus* and more common near the region of overlap (Goodman *et al.*, 1999).

Interpretation of introgression in terms of hybrid zone movement has consistently generated controversy. Moran's paper (1981) suggesting the idea contained eight possible examples, only two of which had been identified as such by the original investigators. In three of the cases above, where historical observation appears to confirm evidence for movement from genetic markers, alternative

explanations have still been suggested. In the case of *P. bibroni* and *P. semiarmorata*, Woodruff (1981) questioned the colour pattern data of McDonnell *et al.* (1978) and suggested that the distribution of the *Ldh* marker might be a northward introgression due to *P. semiarmorata* male dominance. It has been suggested that the pattern of introgression in *Cervus* could be due to hybridization far into the *C. nippon nippon* range, or an ancestral polymorphism (Goodman *et al.*, 1999). Given the difficulty of interpreting marker evidence in cases like the above, where historical evidence is available, caution is needed in drawing conclusions from genetic marker evidence alone.

Several recent examples of hybrid zones in the literature show patterns of markers that have been discussed by investigators in terms of hybrid zone movement, where confirmatory historical observation does not appear to be available. In some of these cases, factors have been observed which are likely to promote movement. Below, I describe three well-studied cases where zone movement has been postulated and discuss the difficulties involved in interpreting the evidence, then list 13 other possible cases. Details of these 16 hybrid zones can be found in Supplementary Table 1.

A sharp hybrid zone north of Brisbane between 'Moreton' and 'Torresian' chromosomal races of the grasshopper *Caledia captiva* appears to be a tension zone, but 'Moreton' rDNA and mtDNA extend up to 450 km north into the 'Torresian' regions (Shaw and Wilkinson, 1980; Arnold *et al.*, 1987; Marchant, 1988; Marchant *et al.*, 1988; Shaw *et al.*, 1993). While this asymmetrical introgression could be due to selective incorporation of 'Moreton' genes at the hybrid zone, a balance of evidence points to the markers being neutral, and the introgressed genes being the result of southward hybrid zone movement in favour of the 'Torresian' race (Marchant, 1988; Marchant *et al.*, 1988; Shaw *et al.*, 1993) and biased gene conversion (Arnold *et al.*, 1988). Short-term studies of the hybrid zone's dynamics have not shown ongoing movement. Over a 6-year period, the zone appeared to be in stasis (Shaw *et al.*, 1985), and in a 4-year study of four allozyme markers there was a 200 m shift northwards towards an area of reduced gene flow (Kohlmann and Shaw, 1991). It is suggested that the past southward movement was due to climate change (Shaw *et al.*, 1990).

Complex patterns of molecular markers are found in the plant species *Piriqueta caroliniana* in Florida, at a hybrid zone between morphotypes: *caroliniana* (to the north) and *viridis* (to the south). Sharp clines in *caroliniana* markers occur over an ~100-km wide zone, coincident with high levels of gametic disequilibrium indicating ongoing hybridization. Introgression of *viridis* traits is found to the north of this area, extending ~300 km into the *caroliniana* range. To the south, almost all *viridis* populations contain low frequencies of markers associated with *caroliniana*. It is proposed that this pattern has emerged due to the arrival of the *viridis* morphotype in southern Florida since the last Pleistocene glaciation (Maskas and Cruzan, 2000). The sharp clines are thought to indicate a tension zone (Cruzan, 2005). Presence of *caroliniana* alleles in the *viridis* populations (Martin and Cruzan, 1999; Cruzan, 2005) is thought to be due to northwards movement of the tension zone and presence of *viridis* alleles in the *caroliniana* range (Martin

and Cruzan, 1999) due to selective introgression north of the tension zone (Cruzan, 2005). However, to illustrate the ambiguity of introgression data even in such a well-studied system as this, the data might hypothetically also be interpreted in terms of a southward movement of a contact zone initially established in northern Florida. The widespread *viridis* markers to the north of the sharp cline could be due to genetic assimilation by invading *caroliniana* morphotypes. This scenario incorporates two factors: first, a lack of disequilibria among diagnostic genetic markers in the northern hybrid populations, which suggests that introgression of *viridis* alleles into *caroliniana* morphotypes has slowed or stopped (Cruzan, 2005); and second, asymmetric hybridization in favour of the *caroliniana* morphotype in experimental studies (Wang and Cruzan, 1998).

Mouse subspecies *Mus musculus musculus* and *Mus musculus domesticus* meet at a hybrid zone stretching across Europe. Mitochondrial DNA introgression has been studied at five widely spaced transects. In three of these, introgression of *domesticus* mtDNA was found in *musculus* populations, and in two, introgression of *musculus* mtDNA was found in *domesticus* populations (Božíková *et al.*, 2005 and references therein). A study of ten allozyme loci showed asymmetry always in the direction of *domesticus* into *musculus* (Raufaste *et al.*, 2005). Several studies have found that *musculus* females prefer *musculus* males, but *domesticus* females display no breeding preference (Smadja and Ganem, 2002; Smadja *et al.*, 2004; Bimova *et al.*, 2005; Ganem *et al.*, 2005). Hybrids appear to be of low fitness (Britton-Davidian *et al.*, 2005). The hypothesis that the zone could be moving in favour of *musculus*, leaving a trail of *domesticus* markers, was discussed 25 years ago but rejected as the zone appears to have been stable from 1960 to 1980 and the distribution of the subspecies on islands close to the mainland suggest movement in the opposite direction (Barton and Hewitt, 1981). More recently this hypothesis has been raised again (Smadja *et al.*, 2004; Raufaste *et al.*, 2005).

In a further 13 hybrid zones, patterns of introgression might be interpreted as evidence for movement: gulls *Larus glaucescens* and *Larus occidentalis* (Bell, 1996; Gay, 2006); pocket gophers *Thomomys townsendii* and *Thomomys bottae* (Patton, 1993; Patton and Smith, 1993); *Thomomys bottae actuosus* and *Thomomys bottae ruidosae* (Ruedi *et al.*, 1997); fish *Gambusia affinis* and *Gambusia holbrooki* (Reznick, 1981; Scribner, 1993; Scribner and Avise, 1993; Scribner and Avise, 1994a,b); hares *Lepus granatensis/Lepus europaeus* and *Lepus timidus* (Thulin and Tegelström, 2002; Melo-Ferreira *et al.*, 2005, 2007); salamander *Chioglossa lusitanica* North and South forms (Sequeira *et al.*, 2005); mussels *Mytilus galloprovincialis* and *Mytilus edulis* (Gardner and Skibinski, 1988; Skibinski and Roderick, 1991; Willis and Skibinski, 1992; Gardner *et al.*, 1993; Wilhelm and Hilbish, 1998; Bierne *et al.*, 2003); beetles *Carabus albrecti* and *Carabus lewisianus* (Takami and Suzuki, 2005); lizard *Sceloporus grammicus* chromosomal races F5 and FM2 (Sites *et al.*, 1996; Marshall and Sites, 2001); warblers *Dendroica townsendii* and *Dendroica occidentalis* (Pearson, 2000; Pearson and Rohwer, 2000; Rohwer *et al.*, 2001; Owen-Ashley and Butler, 2004); plants *Iris innominata* and *Iris douglasiana* (Lenz, 1959; Young, 1996); plants *Ipomopsis aggregata* and *Ipomopsis tenuituba* (Wu and Campbell, 2005);

cottonwoods *Populus angustifolia* and *Populus fremontii* (Keim *et al.*, 1989; Paige *et al.*, 1991; Martinsen *et al.*, 2001).

In some of these, patterns of introgression are accompanied by a putative mechanism (see column 4 in Supplementary Table 1) known to drive hybrid zone movement in other systems (see next section). For example, there is evidence that asymmetrical hybridization may be occurring in eight of the hybrid zones as shown in Supplementary Table 1. When two lines of evidence concur in this way, it seems reasonable to take zone movement as a working hypothesis. Controversy arises because different researchers have different expectations and place more weight on different lines of evidence. Some, like Dasmahapatra *et al.* (2002) set out to look for introgression of neutral markers to test the hypothesis that a zone is moving. Others, such as Gay (2006) find concordant asymmetric introgression at multiple neutral loci but suggest movement in the same direction as the neutral markers due to other lines of evidence such as the distribution of morphological intermediates. Patterns of markers can provide useful information and it is advantageous that data suggesting zone movement can be collected at a single time point by one research group. However, interpretation is difficult and the conclusions drawn may be less reliable than historic observational data.

Identifying causes of hybrid zone movement

As described in Introduction, multiple factors may in theory be implicated in causing hybrid zone movement. The number of empirical studies of moving hybrid zones now available allows some assessment of these factors in nature. The discussion below will mainly draw on studies where there is some observational evidence for movement (Table 1).

In several of these examples, the fitness of hybrids has been assessed: 11 appear to involve hybrids of low fitness, and 3 involve hybrids of equal or greater fitness than their parents. The higher number of zones with low fitness hybrids may reflect a greater propensity of such zones to move, although the observational evidence may be biased because tension zones are easier to detect empirically due to a sharp boundary.

Asymmetrical crossing appears to be playing a role in the movement of zones with both high and low fitness hybrids. In a hybrid zone between chickadees *Poecile atricapillus* and *Poecile carolinensis*, dominance of *P. carolinensis* males, or their preference by *P. atricapillus* females may aid the zone's movement in favour of *P. carolinensis* (Bronson *et al.*, 2003b; Woodcock *et al.*, 2005; Reudink *et al.*, 2006). Katydid *Orchelimum nigripes* females show a conspecific mate preference, whereas *O. pulchellum* females show no clear preference; this may cause movement in favour of *O. nigripes* (Shapiro, 2001). Waterstrider *Limnoporus notabilis* females prefer *Limnoporus dissortis* and hybrid males, giving movement in favour of *L. dissortis* (Spence, 1990; Sperling and Spence, 1991; Klingenberg *et al.*, 2000). In a 5-year allozyme study, all hybrids between the minnows *Pseudorasbora pumilla* and *Pseudorasbora parva* have *P. pumilla* mtDNA suggesting that this tension zone moves in favour of *P. parva* due to asymmetrical hybridization (Konishi and Takata, 2004a). Sexual system differences between diploid

and hexaploid plants of *M. annua* cause asymmetrical hybridization at their hybrid zone and movement in favour of the diploid (Buggs and Pannell, 2006). Asymmetrical hybridization is suggested in a hybrid zone between butterflies *Anartia fatima* and *Anartia amathea* by deviations from Hardy–Weinberg and linkage disequilibria (Dasmahapatra *et al.*, 2002). These recent findings suggesting a role for asymmetrical hybridization in hybrid zone movement fit well with the predictions of Hewitt (1975), Endler (1977) and Barton (1979).

The apparent role of asymmetrical hybridization in the above moving hybrid zones suggests that movement may well have occurred in the eight hybrid zones as shown in Supplementary Table 1 where such asymmetries occur. Researchers have also discussed the possibility of hybrid zone movement solely on the basis of evidence for asymmetrical hybridization in the species *Eucalyptus risdonii* and *Eucalyptus amygdalina* (Potts, 1986; Potts and Reid, 1985) and *Chorthippus parallelus parallelus* and *Chorthippus parallelus erythropus* (Bella *et al.*, 1992). However, this evidence is not compelling in isolation, as the effect of asymmetric hybridization may be countered by other factors (Barton and Hewitt, 1985).

A role for ecological differentiation between taxa, on which natural selection acts, has been suggested in driving the movement of several of the zones as shown in Table 1, with both high and low hybrid fitness. The most reliable indicator of natural selection at hybrid zones is by reciprocal transplant experiments. These have been used in the case of *M. annua*, where the advancing diploid plants were found to be fitter than the hexaploids in all environments used (Buggs and Pannell, 2007). In other zones, selection has been inferred from observational evidence. The rate of spread of salamanders *P. glutinosus* into the range of *P. jordani* appears too great to be explained by random diffusion, suggesting selection for *P. glutinosus* characters (Hairston *et al.*, 1992). *Heliconius erato hydara* butterflies appear to have a slight advantage over *Heliconius erato petiverana* and selection by predators has been inferred (Blum, 2002). A competitive advantage for the advancing taxon has also been inferred in the movement of hybrid zones between: chickadees *P. atricapillus* and *P. carolinensis* (Bronson *et al.*, 2003b; Woodcock *et al.*, 2005; Reudink *et al.*, 2006), butterflies *A. fatima* and *A. amathea* (Dasmahapatra *et al.*, 2002), lice species *Geomydoecus aurei* and *Geomydoecus centralis* (Hafner *et al.*, 1998), and crows *Corvus corone* and *Corvus corone corone* (Saino and Scatizzi, 1991; Rolando and Giachello, 1992). Differential parasite infestation may play a role in a hybrid zone of warblers *Hippolais polyglotta* and *Hippolais icterina* (Reullier *et al.*, 2006). A strong role for ecological differentiation and natural selection at moving hybrid zones would uphold predictions made by Key (1968), but more experimental evidence is needed in several of the cases above. Also, selection may be slowing some moving hybrid zones: estimates of dispersal in the grackle *Quiscalus quisqualis* suggest that it can occur at 100 km per year, and the much slower movement of the narrow *Q. q. versicolor*–*Q. q. quiscula* hybrid zone has been interpreted as indicating a role for stabilizing selection (Moore and Dolbeer, 1989); and the cricket *A. fasciatus*–*A. socius* hybrid zone appears to be maintained partly by differential adaptation (Howard and Waring, 1991; Britch *et al.*, 2001).

Dominance drive may be assisting the movement of a hybrid zone between butterflies *H. e. hydara* and *H. e. petiverana*, as the dominant black hindwing allele spreads and replaces the recessive yellow bar allele (Mallet, 1986; Mallet and Barton, 1989; Blum, 2002). The observed rate of movement fits very well with the theoretical expectation (Blum, 2002).

A direct effect of environmental change has been invoked in explaining the movement of five zones. Increased rainfall may have favoured tick species *A. hydrosauri* at a hybrid zone with *A. limbatum* (Bull and Burzacott, 2001) and climate fluctuations may have caused movement in a *T. b. actuosus*–*T. b. ruidosae* hybrid zone (Ruedi *et al.*, 1997). Human-induced climate change appears to have caused movement of the *Pholidobolus montium*–*Pholidobolus affinis* (lizards) hybrid zone, when fields which had been rocky with numerous agaves were cleared of rocks, irrigated and planted with crops (Hillis and Simmons, 1986), and hybridization between salamanders *P. jordani* and *P. glutinosus* may have increased due to intense timbering (Hairston *et al.*, 1992). Ecological changes due to overgrazing may have caused movement in a hybrid zone between lizards *S. cowlesi* and *S. tristichus* (Leaché and Cole, 2007). Global warming was tentatively invoked to explain the movement of a hybrid zone between crickets *A. fasciatus* and *A. socius* (Britch *et al.*, 2001).

Few empirical studies have measured population density in the context of hybrid zone movement. In the case of the diploid–hexaploid hybrid zone in *M. annua*, hexaploid populations were found to be smaller and more scattered than diploid populations (Eppley and Pannell, 2007). This may fit Barton and Hewitt's (1985) prediction that a tension zone will move down a density gradient, although adaptation of the hexaploids sexual system to its population structure may be slowing the movement of the zone (Dorken and Pannell, 2007). It is possible that differences in population density are a proximate cause of some hybrid zone movements, attributed to ecological differentiation or climate change above. More studies are needed that measure this attribute.

Discussion

In 1985, Barton and Hewitt found five hybrid zones in the literature that appeared to be unstable. Publications since then allow a review of 23 hybrid zones in diverse groups that have compelling historical evidence for movement and a further 16 with possible evidence from patterns of molecular markers. This suggests that movement of hybrid zones in the present and recent past could be a widespread phenomenon, deserving more attention in ecological and evolutionary studies. Thus far, empirical approaches have been somewhat disparate. This is to some extent inevitable due to the different types of historical evidence available, and the diversity of taxonomic groups studied, but there is a need for long-term, structured surveys that trace the dynamics of hybrid zones over several decades.

Interpreting patterns of molecular markers

Growth in the use of molecular markers in assessing hybrid zone movement is an exciting development, but caution is needed in its interpretation. This review

identifies 16 studies in animals and plants where patterns of molecular markers might be understood in terms of movement in the absence of firm historical evidence. Barton and Hewitt's (1985) suggestion that marker evidence was most unequivocal when many neutral alleles introgressed in the same direction deserves to be better known, and could prevent some misleading conclusions. However, the patterns in some natural zones are complex, with different markers introgressing in different directions. Sometimes, further light may be shed by comparative studies in space, or locally at different scales, but only repeated sampling over time and use of historical evidence, and manipulative experiments on the processes acting in the hybrid zone can resolve dynamics precisely.

Most of the moving hybrid zones reviewed here are between two taxa with well-defined differences that give rise to well-demarcated hybrid zones. A wide range of related situations may arise where a hybrid zone is harder to define. In some natural zones, different phenotypic characters or regions of the genome may show contrasting spatial patterns and it may be difficult to define a single current hybrid zone location about which introgression may have occurred.

Evolutionary implications

Moving hybrid zones provide excellent examples of evolution in action, but much work is needed to characterize the processes responsible for their dynamics. A wide range of both natural and human-induced processes appear to have been involved and no single factor has a universal dominant effect in all zones. When examined, multiple causes are often shown to be involved within a single zone, but few empirical studies have thus far systematically disentangled them. Our knowledge of the interplay of factors is limited and there is a general lack of empirical data on some crucial factors, such as local adaptation and population density. Ideally, long-term, quantitative experimental studies of hybrid zones are needed that incorporate reciprocal transplants (to test hypotheses of local adaptation), hybridization experiments (to test the fitness of hybrids and asymmetries in hybridization dynamics) and regular surveys of population density and molecular and morphological markers at a range of scales.

The study of hybrid zone movement has survived related controversies over stasipatric speciation (Rieseberg, 2001; Navarro and Barton, 2003) and Wright's shifting balance (Coyne *et al.*, 1997, 2000) hypotheses. Most zones discussed here appear to be secondary and so do not necessarily provide support for these hypotheses. The study on the *H. e. hydara*–*H. e. petiverana* hybrid zone was recently discussed in terms of phase III of Wright's shifting balance model, but does not fully correspond to all the conditions (Blum, 2002). Hybrid zones have also been examined in search for evidence for reinforcement of reproductive isolation (Howard, 1993). In this context, asymmetry of hybridization has sometimes been interpreted as the ongoing evolution of new pre-zygotic reproductive barriers that could end in stable species coexistence. However, conditions for this to occur are stringent (Servedio and Kirkpatrick, 1997; Tiffin *et al.*, 2001) and asymmetry seems more likely to lead to hybrid zone movement and the elimination of one taxon.

Untested assumptions of hybrid zone stasis may lead to mistaken conclusions in evolutionary studies. This is most obviously the case for studies of introgressive hybridization, where failure to detect zone movement, if present, could result in the inference of selection for a gene which is in fact neutral. This could affect the use of hybrid zones as systems in which statistical analysis of genome scans can identify locus-specific selection (Rieseberg and Buerkle, 2002; Lexer *et al.*, 2004; Murray and Hare, 2006) when assumptions about the evolutionary equilibrium or otherwise of the zone affect the models used.

To what extent can recent movements in a hybrid zone be extrapolated to shed light on long-term patterns of migration or genetic exchange? When a currently moving zone shows a trail of introgression over a larger distance than the observed movement, researchers may infer that the movement can be to some extent extrapolated into the past (McDonnell *et al.*, 1978; Leaché and Cole, 2007). In some cases, the limits of the neutral introgression may indicate the location where the initial hybrid zone was formed, but little certainty can be placed on this inference unless multiple neutral markers show a concurrent limit when examined at a range of spatial scales. However, it is likely that many hybrid zones have undergone spatial fluctuations during their history, as illustrated by the case of *Caledia captiva*, where the recent movement of a hybrid zone is in a different direction to past movement inferred from molecular markers (Shaw *et al.*, 1985). Some indication of whether recent hybrid zone movements may be extrapolated into the past may be provided by assessment of the factors causing recent movement. Factors such as deforestation or overgrazing may have started recently, so recent movements will be atypical of the hybrid zone's history. On the other hand, a difference in sexual system between the hybridizing taxa may have a more ancient origin so that recent movements may be representative of those in the past. It is worth noting that it may be unwise to disregard records of movement from the recent past on the assumption that a hybrid zone is many thousands of years old, as the estimated age of a hybrid zone between *T. b. connectens* and *T. b. opulentus* was revised from 10 000 years to 50 years when flood records were examined (Hafner *et al.*, 1998). Overall, while studies of hybrid zone dynamics in the past few decades may help in the modelling of long-term phylogeographic patterns and genetic exchanges, they do not provide a panacea for the difficulties involved in reconstructing past events.

Hybrid zone movement could have the effect of accelerating the rate of evolution in the advancing taxon, in two ways. First, Klopstein *et al.* (2006) show in a simulation study that mutations occurring on the edge of a range expansion can 'surf' on the wave of advance and thus reach a larger spatial distribution and a higher frequency than would be expected in stationary populations. Second, hybrid zone movement may increase introgression of positively selected traits into the advancing taxon from the retreating relative. Traits under positive selection are known to be able to cross hybrid zones (Parsons *et al.*, 1993), and movement may decrease the threshold level of selection needed for introgression to occur (as witnessed by the introgression of neutral markers) and increase the rate at which it occurs. Increased rates of evolution might aid the advancing taxon in overcoming the home-range advantage of the retreating taxon.

Conservation implications

Hybrid zone movements are simultaneous invasions and extinctions, and at times conservation effort may be needed to protect one taxon. The studies above demonstrate some practical difficulties of detecting such movement. This contrasts to the comparative ease with which introgression—a consequence of hybridization which is a conservation concern in its own right (Rhymer and Simberloff, 1996)—may be detected using modern methods. This presents two potential pitfalls. First, if hybrids are of very low fitness, providing an impermeable barrier to gene flow, a survey at a single time point will appear to show the coexistence of two taxa, which have retained their genetic integrity; even if one taxon is being eliminated. Second, in a moving hybrid zone where barriers to gene flow are permeable, the effect of introgression will be most marked in the advancing taxon, with the declining taxon remaining genetically pure. Conservation effort focussed on preventing introgression could inadvertently protect the invading taxon, to the neglect of the declining taxon.

There is some evidence that 11 of the 39 cases of hybrid zone movement reviewed here are to some extent due to local human activity. Hybrid zones seem to have arisen by the human introduction of *C. nippon nippon*, *Solenopsis invicta*, *O. nigripes*, *Orconectes rusticus* and *P. parva* to alien environments. Local, short-term ecological changes to environments by humans via agriculture or forestry may have contributed to the movement of hybrid zones between *P. glutinosus* and *P. jordani*, *P. montium* and *P. affinis*, *L. glaucescens* and *L. o. occidentalis*, *Helianthus annuus* and *Helianthus bolanderi*, *A. fatima* and *A. amatheia*, and *S. tristichus* and *S. cowlesi*.

Global warming has been suggested as a 'very preliminary hypothesis' as a cause for the movement of one transect in an *A. socius*–*A. fasciatus* hybrid zone in the recent past (Britch *et al.*, 2001). Past movements evidenced by introgression patterns in the *L. granatensis*–*L. europaeus* (Melo-Ferreira *et al.*, 2007), *T. b. actuosus*–*T. b. ruidosae* (Ruedi *et al.*, 1997) and *Caledia captiva* (Shaw *et al.*, 1993) hybrid zones have been attributed to Pleistocene climate changes. This suggests that hybrid zone movements could provide biological indicators of climate change, an application that could be of public interest in coming years. For a good understanding of where climate change is implicated, development is needed in both the quality and quantity of moving hybrid zone studies. More thorough characterization of hybrid zones than is currently available in many cases is needed, as many factors must be carefully disentangled before firm conclusions can be drawn about the causes of hybrid zone movement. Many studies are needed as multiple species must demonstrate a similar trend before climate change can be reliably identified as a causative factor (Parmesan and Yohe, 2003). At present there is little evidence that climate change is causing current hybrid zone movements, but this may owe more to our ignorance of the latter, rather than lack of the former.

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