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Hybridization but No Evidence for Backcrossing and Introgression in a Sympatric Population of Great Reed Warblers and Clamorous Reed Warblers

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Abstract

Hybridization is observed frequently in birds, but often it is not known whether the hybrids are fertile and if backcrossing occurs. The breeding ranges of the great reed warbler (Acrocephalus arundinaceus) and the clamorous reed warbler (A. stentoreus) overlap in southern Kazakhstan and a previous study has documented hybridization in a sympatric population. In the present study, we first present a large set of novel microsatellite loci isolated and characterised in great reed warblers. Secondly, we evaluate whether hybridization in the sympatric breeding population has been followed by backcrossing and introgression. We isolated 181 unique microsatellite loci in great reed warblers. Of 41 loci evaluated, 40 amplified and 30 were polymorphic. Bayesian clustering analyses based on genotype data from 25 autosomal loci recognised two well-defined genetic clusters corresponding to the two species. Individuals clustered to a very high extent to either of these clusters (admixture proportions ≥0.984) with the exception of four previously suggested arundinaceus–stentoreus hybrid birds that showed mixed ancestry (admixture proportions 0.495–0.619). Analyses of simulated hybrids and backcrossed individuals showed that the sampled birds do not correspond to first–fourth-generation backcrosses, and that fifth or higher generation backcrosses to a high extent resemble ‘pure’ birds at this set of markers. We conclude that these novel microsatellite loci provide a useful molecular resource for Acrocephalus warblers. The time to reach reproductive isolation is believed to be very long in birds, approximately 5 Myrs, and with an estimated divergence time of 2 Myrs between these warblers, some backcrossing and introgression could have been expected. However, there was no evidence for backcrossing and introgression suggesting that hybrids are either infertile or their progeny inviable. Very low levels of introgression cannot be excluded, which still may be an important factor as a source of new genetic variation.


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Introduction

Hybridization and introgression can lead to the creation of novel genotypes and phenotypes and are therefore important processes in the evolution of animals and plants [1,2]. Hybridizing species and hybrid zones provide excellent opportunities to examine evolutionary processes such as adaptation, gene flow and, ultimately, speciation [3–6]. Determining the degree and pattern of introgressed genetic material between recently diverged species may be particularly interesting from an evolutionary point of view, since they typically show incomplete reproductive isolation.

Studies of hybrid zones have indicated that natural hybridization is most likely to take place in intermediate habitats, which are often found at the ecological limits of the species’ distributional ranges, and where both taxa are found in close proximity to each other [4]. If some of the interspecific matings lead to fertile first-generation (F₁) hybrids, then there is a possibility that these will backcross with at least one of the parental genotypes, with introgression as a consequence. If the resulting backcrossed individuals subsequently mate with the most similar parental genotype, novel genes and gene complexes can be particularly rapidly introduced into the new genetic background [7]. In some cases, stable and long-lasting hybrid zones are formed as a consequence of spatial range overlap between two species [8–10]. However, another possible scenario is that one of the two species, or possibly even the new hybrid cross, becomes more successful and replaces one or both of the original taxa [11].

In birds, several well-characterised hybrid zones are known, e.g. between carrion and hooded crows (Corvus corone ssp.) [12], wood warblers of the genus Dendroica [13], and Darwin’s finches (Geospiza ssp.) [14]. Avian hybridization seems to be quite commonly occurring when two related species meet and one of them is rare [15,16]. In such situations, individuals that remain unpaired might choose heterospecific mates. Alternative hypotheses postulate that hybridizing females are attracted to heterospecific males when these are larger in size than the conspecific males, or that heterospecific song and plumage characteristics sometimes act as supernormal mate choice stimuli [17]. Hybridization might also result from general mistakes in mate recognition [17].

The great reed warbler (Acrocephalus arundinaceus) and the clamorous reed warbler (A. stentoreus) are closely related passerines in the family Sylviidae [18]. They are similar in morphology and behaviour, and have partly overlapping breeding ranges in the
Middle East and southern Central Asia [19,20]. The great reed warbler is a long-distance migrant throughout its range, whereas clamarous reed warblers are either sedentary or perform a short-distance migration. Morphologically the two species are distinguished most easily on differences in wing characters (length and shape) [19]. In addition, males are easily distinguished by their song: the great reed warbler has a variable and high-pitched song, whereas the clamarous reed warbler has a monotone song of low frequency ([19]; B. Hansson, personal observation). In southern Central Kazakhstan, great reed warblers (subspecies A. a. zarudnyi) are at their south-eastern range limit, whereas clamarous reed warblers (subspecies A. s. brunnecens) are at their northern range limit [19,20]. In this region, the clamarous reed warbler has expanded its range northwards during the last three decades, with increasing numbers in the newly colonized areas [21]. Currently, the breeding ranges of the two species overlap over a zone 500 x 1400 km wide and several sympatric breeding populations are known [20,21]. We have previously detected that viable hybrids between these two species occur in a sympatric breeding population in Kazakhstan [21]. Birds with intermediate morphology were identified as hybrids: four of the examined individuals were stored in SET buffer (0.15 m NaCl, 0.05 m Tris, 0.001 m EDTA). Genomic DNA was extracted using a standard phenol/chloroform protocol [29]. In a previous study [21], hybrids had been verified by genotyping at a Z-linked microsatellite marker (Aes50 [30]), the species identity of the mother had been verified by sequencing a part of the mitochondrial control region (using the primers BCML4 and 12SH1 [31]), and the sex of the birds had been identified by amplifying a Z- and W-linked locus (CHD12/Z/W using the primers 2530F and 2716R [32]).

Microsatellite isolation

A microsatellite-enriched library was constructed from a single female ‘pure’ great reed warbler sampled at Lake Kvismaren, Sweden (see e.g. Hasselquist 1998 [26]). The library was constructed at NERC Biomolecular Analysis Facility at the University of Sheffield. The method of Armour et al. [33] was used and the MboI fragments were enriched separately for the following di- and tetra-nucleotide microsatellite motifs: (GT)n, (CT)n, (GTAA)n, (TTC)n and (GATA)n and their complements, which had been denatured and bound to magnetic beads following Glenn & Schable [34]. Transformant colonies were not screened for the presence of a repeat region but were directly sequenced by the NERC Biomolecular Analysis Facility at Lake Kvismaren, Sweden (see e.g. Hasselquist 1998 [26]). The library was constructed at NERC Biomolecular Analysis Facility at the University of Sheffield. The method of Armour et al. [33] was used and the MboI fragments were enriched separately for the following di- and tetra-nucleotide microsatellite motifs: (GT)n, (CT)n, (GTAA)n, (TTC)n and (GATA)n and their complements, which had been denatured and bound to magnetic beads following Glenn & Schable [34]. Transformant colonies were not screened for the presence of a repeat region but were directly sequenced by the NERC Biomolecular Analysis Facility at the University of Edinburgh. Clones were sequenced in the forward and reverse orientation and a consensus sequence created. A total of 181 unique great reed warbler microsatellite sequences were isolated (EMBL accession numbers: FM678097–FM678277; Table S1). The location of these loci on the zebra finch (Taeniopygia guttata) genome assembly (3.2.4, build 1.1; [35]), based on BLAST analyses ([E-value<1E-10); is provided in Table S1 and illustrated in Figure S1. PCR primers were successfully designed for most of the 181 loci (Table S2) using PRIMER3 [36], and 41 loci were tested for amplification and polymorphism in four unrelated great reed warbler individuals from Lake Kvismaren (Table S2). All loci were PCR-amplified using Quagen Multiplex PCR kit (Quagen, Ltd.). The following PCR conditions were used: pre-heating for 95 °C for 15 min, then 35 cycles at 94 °C for 30 s, annealing temperature (Ta) for 90 s, 72 °C for 60 sec, followed by 60 °C for 30 min and an ambient hold temperature (locus specific Ta is given in Table S2).
PCR products were separated using an ABI Prism 3730 capillary Sequencer and analyzed with GENEMAPPER 4.0 (Applied Biosystems).

We genotyped 28 great reed warblers, 15 clamorous reed warblers and the 4 previously detected hybrids in the Kazakhstan population, using 19 of the newly isolated loci and four other published microsatellite loci known to be polymorphic in great reed warblers (Table S3). The amplification conditions were as described above and Te is given in Table S2.

**Population genetic analyses**

Each locus was tested for deviation from Hardy-Weinberg equilibrium using the software FSTAT version 2.9.3 [37], and estimates of null allele frequencies (Oosterhout’s estimate) were conducted using MICRO-CHECKER [30]. FSTAT was further used to calculate several basic measures of genetic diversity, including expected heterozygosity (HEXP), number of alleles and Wright’s inbreeding coefficient (FIS).

To detect potential hybrids and backcrosses, we performed ‘admixture models’ in STRUCTURE (ver. 2.3.3; [23]). Allele frequencies were allowed to be ‘correlated’ in the models. We started each run with a ‘burn-in’ period of 50,000 replicates, followed by a sampling period of 50,000 replicates. In this study we were particularly interested in the results from the runs with two clusters (K = 2), corresponding to the two species. However, we also tested K from 1 to 5, and as expected these analyses confirmed that K = 2 is the most likely K in our data (see Results). The admixture proportion (±90% credible intervals) of each individual to the genetic clusters reflects the degree of genetic similarity to the two species, and hybrids are expected to show intermediate values and genetically pure individuals values close to one (cf. [24,25]).

To understand the power to detect hybrids and backcrosses with our set of markers and degree of divergence of the two species (cf. [25]), we generated simulated genotypes of hybrids and backcrosses with the program HYBRID-LAB [39] using the genotypes of the 28 individual great reed warblers and the 15 clamorous reed warblers as initial inputs. We generated 100 genotypes of each of the following crosses: first-generation hybrid (F1), and first to fourth generation backcross to both parental species. We then evaluated the admixture proportions (±90% credible intervals) of these artificial crosses with STRUCTURE using similar admixture models but this time we used the ‘population flag’ option, which allows clusters to be based on allele frequencies from pre-specified reference populations; in our case great reed warblers and clamorous reed warblers, hence K = 2 (cf. [24,40,41]).

**Results**

**Genetic variation at the loci**

Of the 41 novel microsatellite loci tested, 40 (98%) amplified and 30 (73%) were polymorphic in four unrelated great reed warbler individuals from Sweden (Table S2).

In the 28 great reed warblers from Kazakhstan categorised as pure species based on morphology, the number of alleles per locus ranged from 2 to 26 with a mean of 7.96 at a set of 23 autosomal loci (19 of the newly isolated loci and four other published microsatellite loci known to be polymorphic in great reed warblers; Table S3). Expected heterozygosity ranged from 0.14 to 0.97, and FIS was low to moderate for all loci (Table S3). Significant deviation from Hardy-Weinberg equilibrium due to homozygous excess was found for locus Aar39 (FIS = 0.25; P = 0.016), and the MICRO-CHECKER analyses suggested the presence of null alleles at this locus at a frequency 12% (Table S3).

All 23 primer pairs cross-amplified in the clamorous reed warbler and the number of alleles ranged from one to 12 with a mean of 5.57, whereas the expected heterozygosity ranged from 0 to 0.97 with a mean of 0.55 (Table S3). Significant deviation from Hardy-Weinberg equilibrium due to homozygous excess was found at two loci, Aar33 and Aar57, in clamorous reed warbler (Table S3).

**Bayesian clustering analyses**

The STRUCTURE analyses detected strong genetic differentiation between the two species. The estimated likelihood probability of the data, LnPD, for K = 1–5 was as follows: −3494.4, −3064.5, −3509.7, −3175.8, and −3256.8. Thus, K = 2 was the most likely number of genetic clusters in the group of individuals genotyped.

The individual admixture proportions indicate that there are no backcrossed individuals present in the sample and there is no evidence for introgression of genetic material between the species (Figure 1). The 28 great reed warblers had admixture proportions ≥0.984, and for the clamorous reed warblers the corresponding values were ≥0.991 (Figure 1). In contrast, the four individuals that were categorised as hybrids based on intermediate morphology (and the genetic signature at one mitochondrial and a single microsatellite locus [21]) had admixture proportions of between 0.495–0.619 to the cluster corresponding to the great reed warbler genotypes (Figure 1).

The analyses of the artificial hybrid and backcross genotypes (Figure 2) suggest that the four hybrids are similar to genotypes
expected for F1 hybrids and less likely to be first or higher
generation backcrosses, and furthermore that the individuals
categorised as pure species based on morphology are genetically as
pure or purer than fifth generation backcrosses (Figure 1; Figure 2).

Discussion

In the present study, we have presented a large set of novel
microsatellite loci isolated from and characterised in the great reed
warbler. In total, 181 loci were isolated and, among 41 tested for
amplification, 73% were polymorphic in a small set of great reed
warbler individuals. Moreover, we used a set of 23 autosomal
microsatellites to evaluate whether ongoing hybridization in a
sympatric breeding population in Kazakhstan has been followed
by backcrossing and led to significant introgression of genetic
material between the species. The clamorous reed warbler has
expanded its range northwards in Kazakhstan during the last three
decades and sympatric breeding populations have been recorded
since 1981 [21]. Within a sympatric locality, the two species show
no or little habitat separation and they take up neighbouring
territories within their preferred reed habitat (B. Hansson, pers.
obs.). Thus, there should have been plenty of opportunities for
backcrossing and introgression in those areas where the two
species overlap.

We used Bayesian clustering analyses in the program Struc-
ture to recognise two genetic clusters corresponding to the two
species, and all individuals either clustered to a very high extent to
either of the species cluster (i.e. ‘pure’ species) or showed a mixed
ancestry (i.e. hybrids). There was neither any evidence for
backcrossed individuals nor introgressed genetic material in the
population, suggesting that the hybrids are either infertile or their
progeny inviable. We cannot of course exclude very low levels of
backcrossing and old introgression events in the study populations
(cf. [25]), which still may be an important factor as a source of new
generic and phenotypic variability [3,42]. Nevertheless, there seem
to be little potential adaptive significance of introgression in these
Acrocephalus warblers.

In vertebrates, hybridization is particularly common in fish,
where several hundred interspecific and intergeneric crosses have
been reported, and in birds with roughly 10% of all species known
to have bred in the wild with another species (e.g. [4,16,43]). As
mentioned above, the breeding ranges of great reed warblers and
clamorous reed warblers overlap in southern Kazakhstan and a
previous study has documented the occurrence of hybrids in a
sympatric population [21]. Occasionally, heterospecific matings
and/or viable hybrids have been documented also between other
Acrocephalus species [19,44], for example, between reed warbler and
marsh warbler, A. scirpaceus and A. palustris [45], and between reed
warbler and great reed warbler [46,47].

Previous work on plants [48,49] and animals [16] has suggested
that directional hybridisation usually occurs between the females
of the rare species and the males of a common species, but not vice
versa. Consequently, under such a condition, the rare species is
usually the maternal parent of the hybrids. This is not the case in
the present study system, where females of both the rarer species
great reed warbler and the more common species (clamorous
reed warbler) are known to engage in hybrid matings [21].
Interestingly, three of the four hybrids in the data set were
previously found to carry clamorous reed warbler mitochondria,
and, hence, had clamorous reed warbler mothers [21]. At the
breeding locality, there were about eight times more clamorous
reed warblers than there were great reed warblers, but despite this
both species were common. There was no indication of any
difference in sex-ratio between species (B. Hansson et al.,
unpublished). Therefore, the data from this population neither
support the hypothesis suggesting that females of the rarer sex
should be engaged in hybrid matings, nor the hypothesis
proposing that hybridization happens when either species is rare
[15,16,21].

The cytochrome b sequence divergence between great reed
warbler (GenBank sequence accession record: AJ004784) and
clamorous reed warblers (AJ004788) is approximately 4% which
may correspond to a divergence time of approximately 2 Myrs
[50]. The time to reach complete reproductive isolation, with

Figure 2. Admixture proportions and 90% credible regions to two genetic clusters of simulated hybrids (F1) and first–fifth
generation backcrosses (1-5BC; 100 individuals in each category) between great reed warblers and clamorous reed warblers. The
higher the admixture proportion, the higher the similarity to the genetic cluster corresponding to a ‘pure’ great reed warbler genotype.
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hybrids of both sexes being fully infertile, is very long in birds; it was recently estimated to be approximately 5 Myrs based on data from several taxa [43]. Although this estimate should be taken only as a rough indication in each particular case, with an estimated divergence time of 2 Myrs between great and clamorous reed warblers backcrossing and introgression would not have been unlikely. In some other similar study systems a low degree of introgression has in fact been detected. For instance, in icterine and melodious warblers (Hippocites icterinus and H. polyglottos), and between collared and pied flycatchers (Ficedula albicollis and F. hypoleuca) introgression occurs at low frequencies [10,51].

We conclude that our novel microsatellite markers provide a useful molecular genetic resource for this group of birds, and that there is no evidence for backcrossing and introgression in the study population, which in turn suggests that hybrids between these two warbler species are either infertile or their progeny inviable. We cannot however exclude very low levels of introgression, which could potentially be an important factor as a source of new genetic variation in the species.

Supporting Information

Table S1 Summary of BLAST analyses of 181 great reed warbler (Acrocephalus arundinaceus) microsatellite sequences and four other avian microsatellite loci used in the present study against the zebra finch genome assembly (tgz3.2.4, build 1.1). BLAST hit statistics and chromosomal locations in the zebra finch genome are included. (PDF)

Table S2 Characteristics of 181 great reed warbler (Acrocephalus arundinaceus) microsatellite loci isolated and characterized in this study. Primer sequences, expected and observed product size, melting (Tm) and annealing (Ta) temperatures, 5′-fluoro-label, and amplification success in four test individuals are shown. (PDF)

Table S3 Number of alleles, range of fragment length (bp), expected and observed heterozygosity, Wright’s FIS, and two-tailed P-value for deviations of Hardy-Weinberg equilibrium (PHW) shown when P<0.1 in great and clamorous reed warblers. Also given are null allele frequencies in the great reed warbler. (PDF)

Figure S1 Chromosomal locations of great reed warbler (Acrocephalus arundinaceus) microsatellite loci and four other avian microsatellite loci included in the present study (Table S1) on the zebra finch (Taeniopygia guttata) genome. (PDF)

References