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NATURAL HYBRID ZONES AS A SOURCE OF GENETIC DIVERSITY

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Abstract

The paper is devoted to experimental evaluation of influence of hybridization on genetic variation in the natural populations. The widespread common species were taken as an example: wild mice and crows, both proved to be the convenient models for evolutionary-genetic studies. We found increased karyological variation in the populations of Siberian hybrid zone of crows, combined with appearance of some new allozyme variants. High varyability was revealed in each of three proposed hybrid zones of wild mice in Primorye region, Low Amur region and Sakhalin island. Usually this variation does nor correspond to allozyme diversity in the same population. Each of the region of hybridization studied fits well to the model of mozaic hybrid zone.

Introduction

Natural hybridization and particularly hybrid zones are quite widespread among plants and animals. Its influence on genetic variability and speciation is underestimated. Among birds, from one third to half of the total number of species are connnected by hybrid zones (Hewitt, 1989). Using of the chromosomal, allozyme and molecular markers, more and more hybrid species are discovering among both invertebrates and vertebrates. Hybridization not only increases genetic variability but also produces new evolutionary lineages which can lead to speciation events under some conditions. Thus study of the hybrid zones would be important not only for investigation this phenomenon itself but also for forecasting their evolutionary fate.

Carrion and Hooded crows (*Corvus corone, C. cornix*) form two narrow stable hybrid zones in Europe and Siberia appeared presumably after the ice ages. The populations of hybrid zones are highly variable phenotypically, however it was unknown if these variations was concerned with genetic one. The distinct forms of the superspecies *Mus musculus* met each other after development of agriculture and commensalization resulted in appearance of the hybrid zones in Western Europe, Transcaucasus, Japanese Islands and Russian Far East. Regarding the latter, we had to reveal its genetic structure and subdivision, and find what taxa participated in its formation.

Material and Methods

We studied karyotypes of 7 hooded crows, 6 carrion crows and 9 their natural hybrids taken from the zone of their overlapping and hybridization in West Siberia. The blood samples for electrophoresis were taken from the following populations: 1) The mixed population from the central part of the zone of sympatry and hybridization, settl. Tisul', Kemerovo region, 34 samples; 2) Population of phenotypically pure hooded crows from Novosibirsk city, 62 samples; 3) Population of phenotypically pure carrion crows from vicinity of Krasnoyarsk city, 76 samples; 4) Population of phenotypically pure carrion crows from Cherga settl., Altai region, 24 samples. Proteins were separated in polyacrilamide gel. Five proteins of blood serum were analysed: Alb, pAlb-1, Tf, pTf-1 and Est-1, by using the known techniques. Concerning wild mice, 144 animals were studied from 21 localities in Primorsky region, 65 samples from 10 points in Low Amur region, and 34 mice from 5 localities in Sakhalin Island. Chromosomes were prepared by standart technique with subsequent C- and Q-H banding staining. While allozyme analysis, we considered such polymorphic systems as Hbb, Aat-1, Sod-1 and Idh-1.

Results

Karyotypes of the both species of crows proved to be identical with 2n=80. However we found heteromorphism in 2 males originated from the hybrid zone. Usually this pair looks as subtelocentric but in these birds one chromosome was subtelocentric and the other acrocentric. These crows were mosaic, with content of unusual cells being 27% and 22%, correspondingly. Allozyme analysis of the crows revealed several polymorphic protein systems. Posttransferrin 1 (Ptf-1), a high polymorphic protein was studied only in the mixed population in which 6 phenes of Ptf-1 was found. Among them, only 4 were met as in pure as in hybrid animals while two - only in hybrids. Crows with the mixed plumage that were undoubted hybrids had additional variants of albumine (Alb-98/100) and two new variants of esterase 1 (Est-100/104 and Est-96/100). However the same allele Alb-98 was found in the population of hooded crows of Novosibirsk city. In addition, this population obliged the third more fast allele Alb-102 not found elsewhere. In the both cases, the rare alleles were found in one sample from 62 studied. Several variants of esterase 1 (i.e., Est-96/100 and Est-100/104) were revealed not only in hybrid samples but also in the neighboring pure populations. Besides, new variant of postalbumine 1 – pAlb-N/S – was found in the Krasnoyarsk population of pure carrion crows. Anyway, in spite of presence of several rare alleles and different portions of genotypic variants, while populations were compared for heterogeneity, the Pirson test showed no differentiation among all populations in respect of all polymorphic proteins studied.

In the karyological analysis of the wild mice, we used the following characters: quantity and distribution of heterochromatin (H); numbers of marker chromosomes with superlarge C-blocks; variants of C-segmentation of X-chr: C-positive (X+) *domesticus*-like or *castaneus*-like and C-negative (X-) *musculus*-like type of staining. According to the content and distribution of heterochromatin (H) we have divided all mice into four karyomorphs: L (large content of H), AU (average content and uniform distribution of H), AN (average content with nonuniform distribution of H) and S (small content of H). The all four karyomorphs were found in Primorye region, with C+ and C- X-chr and marker chromosomes. For the main part of Primorye region, the karyomorph H, C- proved to be the main, with absence of any marker chromosomes. However in the western part, near the borderline with China and Korea, karyomorphs L and AU could be met often which predominate over the karyomorph H, while the marker chrs number 5, 10, 12, 14, 15, 17–19 found here in every population in different composition. The special attention should be paied to the markers 17 and 18, which have been met not only in western Primorye but sometimes in the remaining part of the region as well. These markers can serve as the "namecard" of *M. m.gansuensis* of the Central Asia, which contributes to the originating of the fauna of Primorye region also. In general, we suppose five taxa of superspecies *Mus musculus* may contribute to the hybrid zone of Primorye region (Yakimenko et al., 2000). The populations of wild mice from Primorye region oblige high allelic diversity. In difference from the pattern of karyological variation, it is impossible to determine the main biochemical variants. We found here combinations of alleles being usual for the biochemical forms *musculus, castaneus* and even *domesticus* (Frisman et al., 1990; Yakimenko et al., 2000). We have shown that the karyomorph L, C-preyails in Middle Amur region and in most part of Primorye. Karyologically, these mice are similar to those of Primorye region and we suggest them as belonging of the same hybrid zone. The mice from the other part of Amur region are highly variable in respect of their karyotypes. It is difficult to nominate the dominating karyomorph because each of four can be met at similar portions. The portion of C+ is high, which may indicate, as presence of the karyomorph H, to the possible tracks of *castaneus* and *domesticus.* This is supported by the data of Yonekawa et al. (1998) who discovered here the *castaneus*-type of mtDNA. In each sample of Amur region, the mice bear the marker chromosomes (2, 5–7, 9–13, 15 and 19) and often their portion is high. Mice with the markers nither 17 nor 18 were found in Amur region. Thus *M.m.gansuensis* did not penetrate to Amur region in spite of connection of the Low Amur region with North China existed along Amur river from 18th century. The karyotypes of the Sakhalin's mice were studied by using of C-banding only. Therefore we can state the presence of all four karyomorths in about equal portion, high portion of C+ and high content of the marker chromosomes 1, 2, 3, 5 and 19 (Korobitsyna et al., 1997), however we can identify only the markers 1, 2 and 19 for sure. Nevertheless, the pattern of the extreme high karyotypic heterogeneity of the Sakhalin's mice is clear and similar to that of Amur region. The patterns of the allozyme variation of the mice in Amur region and Sakhalin are similar as well, and their common property is the incomplete allelic content while their sets are characteristic to the biochemical form *musculus.* It should be mentioned that allozyme monomorphism does not correspond to the pattern of high karyological variability of the wild mice of Amur region and Sakhalin Island.

Discussion

Most of the hybrid zones studied by this time may be characterysed by not only increased variability but also appearance of some new alleles called "hybrizymes" (Barton, Hewitt, 1985; Woodruff, 1989). Variability in different kinds of features is sometimes connected, but there are some examples when mitochondrial and nuclear markers, for example, are distributed independently. The main property of the crow hybrid populations is their high phenotypic variability (Kryukov, Blinov, 1989). Also polymorphism of some chromosomes and new alleles were found there, however in other characters they are similar to parental populations, othervise their quantative differences are not significant that may reflect close relations of carrion and hooded crows. For wild mice, increasing karyotypic variability is apparent, not concordant with the allozyme one. These rodents may examplify the common property of animals with expressed commensalism: their hybrid zones may be involved by many taxa. For all hybrid zones studied by us the secondary contact is supposed, appeared after development in allopatric conditions. Antropogenic factor could influence on occurring the contact not only between mice but crows as well. In general, hybrid zones of crows and wild mice correspond to the meaning of mosaic hybrid zones (Harrison, Rand, 1989). Their further fate may be different. For crows, maintenance of the stable narrow hybrid zone is expected due to assortative mating and phylopatry of the birds, while for mice, distinct parental forms may fuse resulting in appearance of unique hybrid population in each settlement and city.

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