GENETIC STRUCTURE IN FOUR SELECTED PIG POPULATIONS OF CZECH REPUBLIC USING MICROSATELLITE MARKERS

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Introduction

The goal of this study has been to investigate the genetic diversity of four czech pigs breeds, explain their genetic relationship and assess their integrity and degree of admixture. There have been included populations of commercial breeds (Large White – father line – LWF, Large White – mother line – LWM, Czech Meat – CM) and a native breed – genetic resource (Prestice Black Pied – PC).

The 10 microsatellite markers have been used to the study of genetic diversity of breeds in which have been included markers recommended by the Food and Agriculture Organization and the International Society of Animal Science for a tracking a diversity of pigs.

Material and Method

Blood samples were collected on farms in Czech Republic from 2002 to 2011. Representative groups of four breeds LWF, LWM, CM and PC of boars were sampled i.e. 100 of following breeds, except CM. Finally, DNA from 357 animals was used. Every animal was genotyped for 10 microsatellite markers (S0107, S0386, SW353, S070, S0355, S0068, SW24, SW936, SW72 and TNFB).

The mean number of alleles per locus (MNA), polymorphism information content (PIC), allele frequency, observed heterozygosity (H_O) and expected heterozygosity (H_E) were obtained across different loci and populations using the Excel Microsatellite Toolkit v. 3.1.1. add-in utility for Microsoft Excel (Park, 2001). The software package Fstat v. 2.9.3.1 (Goudet, 2001) was used to calculate Wright's F_{IS} index according to Weir and Cockerham (1984). Genetic differentiation and population subdivision were tested by algorithm of Pritchard et al. (2000) implemented in software Structure v. 2.2. Individual animals were assigned to two or more subpopulations on their multilocus 10 microsatellite genotypes.

Results and Discussion

The total number of alleles found for 10 microsatellite markers was 107 with mean number of alleles per locus 10.7, ranging between six (SW72) to 17 alleles (S0070). All loci in this study were observed polymorphic for each breed. On the other hand, MNA ranged between 6.7 in CM and 7.5 in LWM boars (Table 1). By focusing on different populations of boars, the greatest PIC was 0.691 in PC and lowest 0.565 in LWF (Table 1). Six out of 10 microsatellite markers exceeded PIC value 0.7 in S0068, S0107, SW24, SW936, S0070, and TNFB. Four markers S0355, S0386, SW72 and SW353 were close to 0.7. For all loci expected heterozygosity exceeded observed heterozygostiy. Negative Wright's coefficient indicates a significant difference of FIS smaller than zero, suggesting an excess of heterozygotes due to non-random mating. Negative FIS coefficient was estimated only in CM breed. However, relatively high diversity values (MNA, HE) were observed in all breeds. Especially, genetic resource and native breed PC has the highest HE, which illustrating no risk status of this breed

The Structure algorithm was applied to measure the population structure and degree of admixture. All runs from K = 2 to K = 5 showed a pattern allowing a meaningful interpretation (Figure 1). The contribution of the assumed ancestral populations to the 4 breeds under study is graphically presented in Figure 1, for values of K ranging between 2 and 5. As is obvious from Figure 1, when K = 2, CM together with PC were separated from LWF and LWM. When K = 3, CM and PC were already separated from each other, while LWF and LWM appeared as a one ancestral population. Even if K = 4 or 5, there is still no clear divergence of LWF and LWM. Genetic differences between mother and father lines of Large White were not significant. Assuming K = 4, the proportional contribution of the assumed ancestral populations to each one of the current breeds was computed.

Population	N	H_O[1]	H_E[1]	MNA[1]	PIC	BDHW	F_{IS}
LWF	100	0.628 (0.016)	0.614 (0.048)	7.10 (2.08)	0.565	0.0000	0.051
LWM	100	0.669 (0.012)	0.688 (0.034)	7.50 (2.46)	0.641	0.3163	0.019
CM	57	0.698 (0.017)	0.692 (0.053)	6.70 (2.11)	0.646	0.2199	-0.007
PC	100	0.712 (0.015)	0.738 (0.025)	7.40 (2.59)	0.691	0.0125	0.025

Table 1. Genetic diversity within 4 pigs populations. Observed heterozygosity (H_O), expected heterozygosity (H_E), mean number of alleles per breed (MNA), polymorphism information content (PIC), proportion of breed not complying with the Hardy-Weinberg equilibrium at P < 0.05 (BDHW), and F_{IS} per locus. Significance of the F_{IS} values are indicated by asterisks (*p < 0.01)
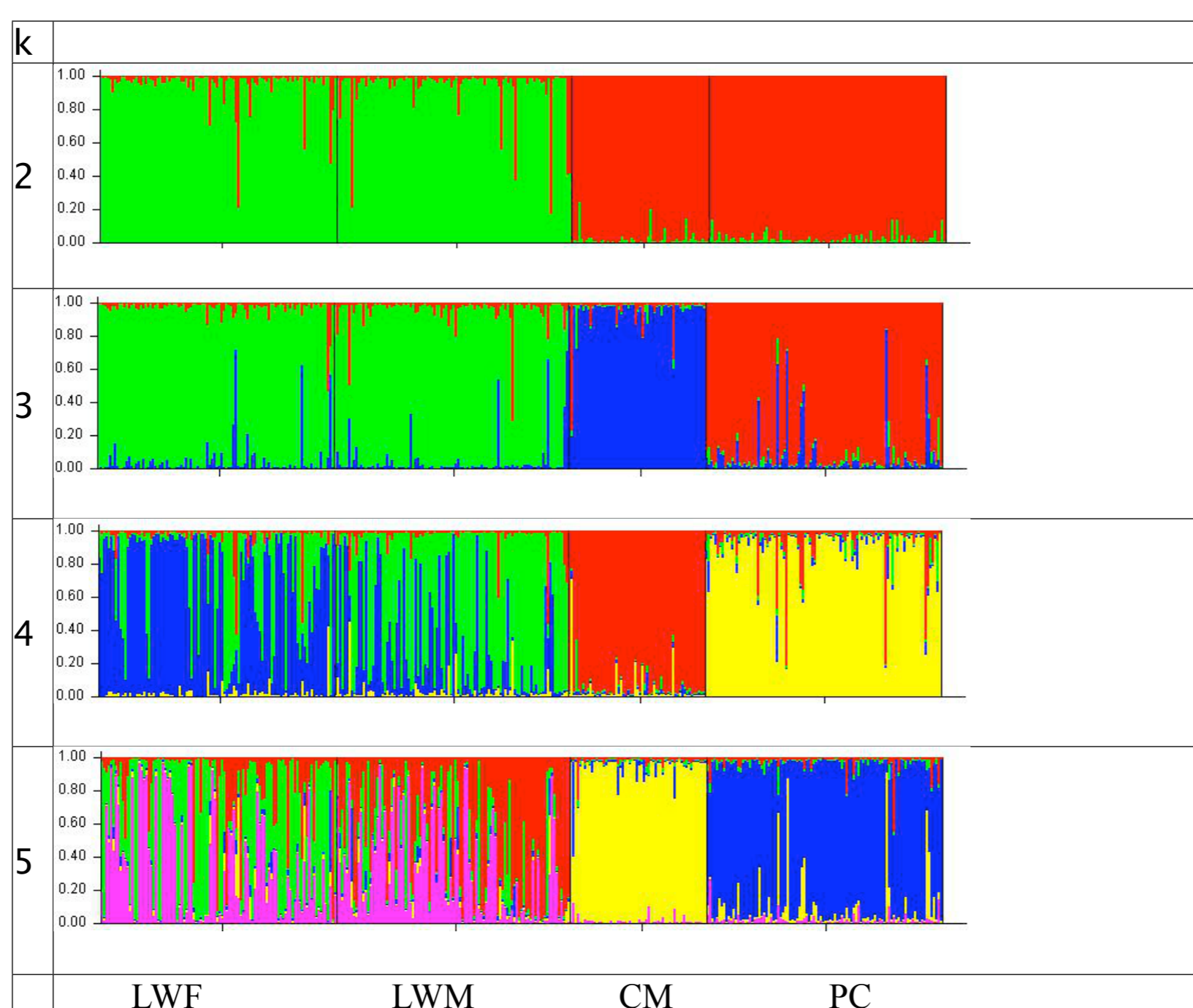

Figure 1. Graphical representation of the estimated membership fractions of individuals of the breed analyzed in each of the K inferred clusters, for K = 2 to K = 5.

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