

BIODIVERSITY CONSERVATION THROUGH PATERNITY ANALYSIS IN INDIGENOUS SHEEP POPULATIONS

Kocho Porchu, Vladimir Dzabirski, Dragoslav Kocevski and Zoran Popovski

Faculty of Agricultural Sciences and Food, Skopje, Republic of Northern Macedonia, North Macedonia

koco_porcu@yahoo.com



SHAPLANINIAN (SHAR)



OVCHEPOLIAN (OVCH)



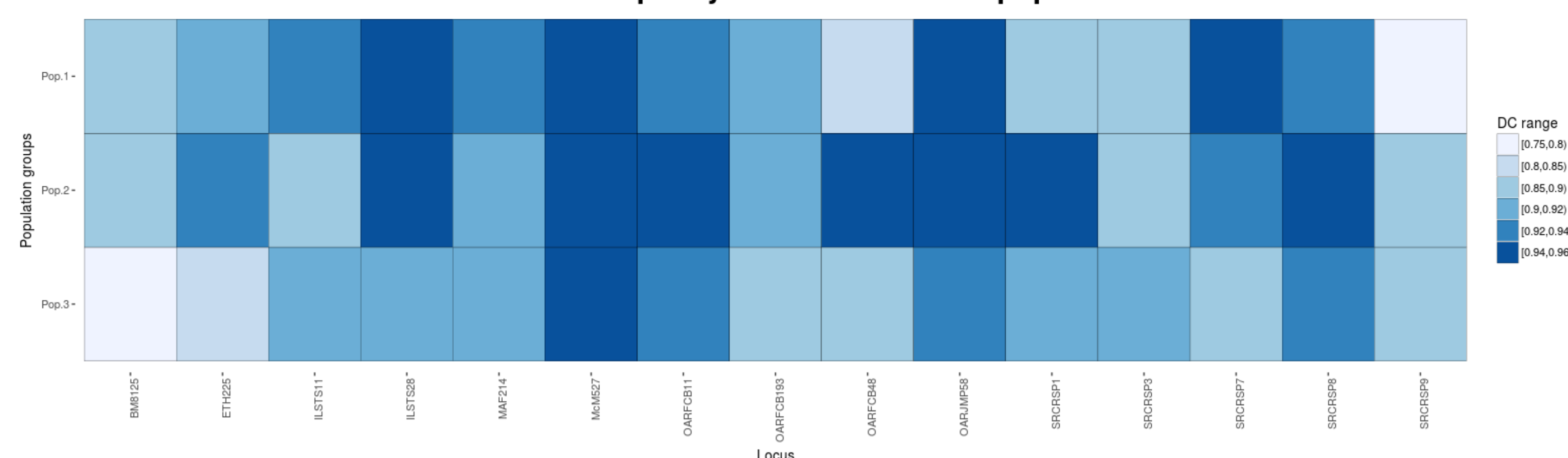
KARAKACHANIAN (KARA)

The genome of Sharplaninian, Ovchepolian and Karakachanian sheep population, 35 samples per population, was analyzed with 15 DNA microsatellites. The power of discrimination (PD), power of exclusion (PE), paternity index (PI) and match probability (MP) were calculated for each microsatellite marker. Combined power of exclusion (CPE) and combined power of discrimination (CPD) were calculated for the whole set of studied markers. Statistical analysis were performed by PowerStatsV12 software.

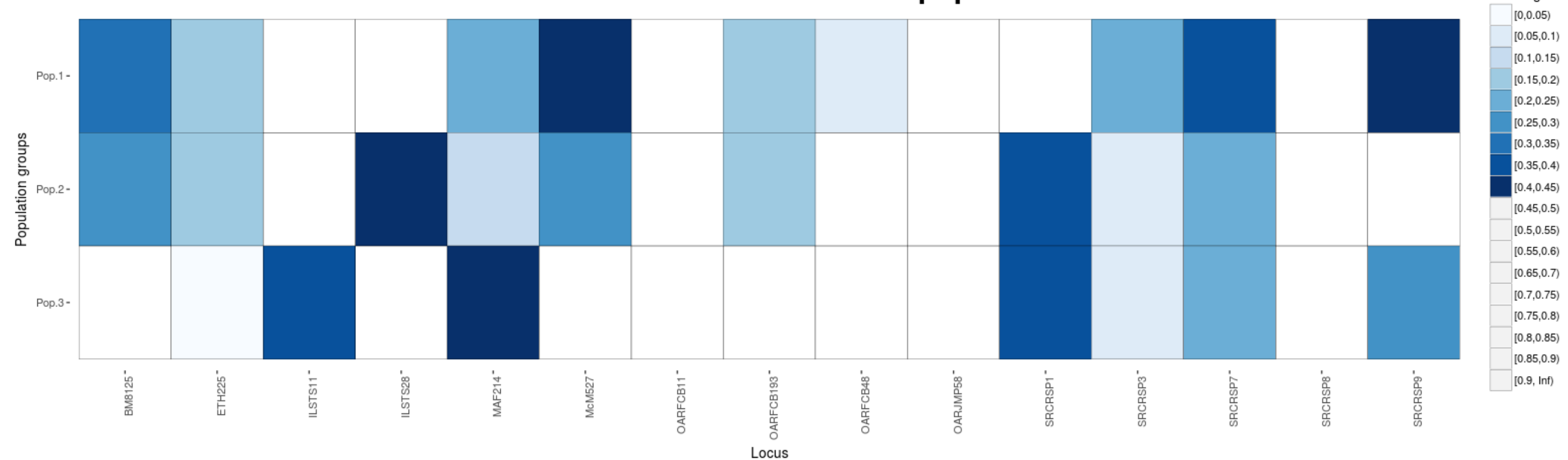
PD ranged from 0.795 (McM527) up to 0.957 (SRCRSP3) in the Sharplaninian, 0.859 (McM527) up to 0.957 (SRCRSP7) in the Ovchepolian and from 0.789 (BM8125) up to 0.952 (SRCRP3) in the Karakachanian sheep. PE was in the range of 0.097 (SRCRSP9) up to 0.942 (OARFCB11), 0.070 (OARFCB193) up to 0.825 (MAF214) and from 0.047 (ILSTS11) up to 0.942 (OARFB11) in the Sharplaninian, Ovchepolian and Karakachanian, respectively. The range of PI was from 0.795 (OARFCB48) up to 17.5 (OARJMP58) in the Sharplaninian, 0.729 (SRCRSP3) up to 5.83 (SPRCRSP8) in the Ovchepolian and 0.673 (ETH225) up to 17.5 (OARJMP58) in the Karakachanian sheep. Detected MP was in the range from 0.043 (McM527) up to 0.205 (SRCRSP 9), 0.043 (OARJMP58) up to 0.141(SRCRSP 9) and 0.048 (McM527) up to 0.211(BM8125) in the Sharplaninian, Ovchepolian and Karakachanian, respectively. The CPE (0.9999, 0.9997 and 0.9999) and CPD (1.0, 1.0 and 0.9999) was very high when all 15 markers were used in combination.

The results in this study enable proper forensic analysis of the genomes of selected populations, the data indicate the possibilities offered by molecular studies in the protection of the biodiversity and further genome characterization.

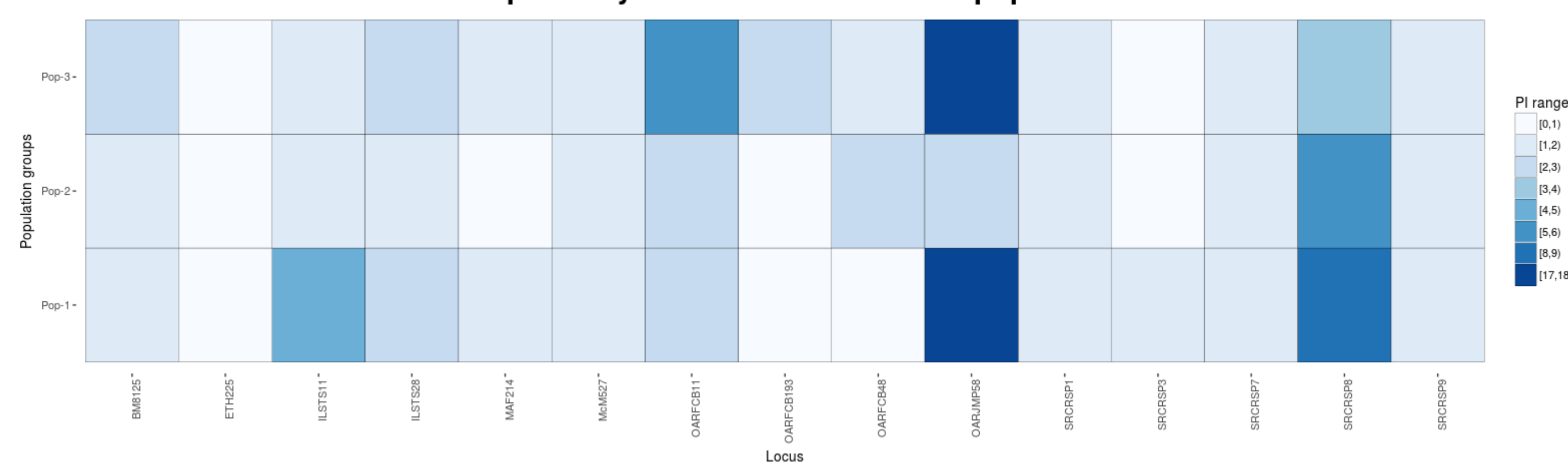
Discrimination capacity of each loci within populations



Power of exclusion of loci within populations



The paternity index of all loci in each population



Match probability of loci between populations

