Genetic diversity of three local chicken breeds using high-density SNP-data

S. Gfeller¹, S. Joller², A. Burren¹, M. Neuditschko³, E. Kump⁴, P. Ammann⁴, A. Spiri⁵, C. Drögemüller²; C. Flury¹

¹Bern University of Applied Sciences, School of Agricultural, Forest- and Food Sciences HAFL, Länggasse, 3052 Zollikofen, Switzerland, ²University of Bern, Vetsuisse Faculty, Institute of Genetics, Brengartenstrasse, 3012 Bern, Switzerland, ³Agroscope, Swiss National Stud Farm, Les Long Prés, 1580 Avenches, Switzerland, ⁴ProSpecieRara, Unter Brüglingen, 4052 Basel, Switzerland, ⁵ZUN, Bühlstrasse, 9217 Neukirch an der Thur, Switzerland

Introduction

Appenzell Barthuhn (AB), Appenzell Spitzhauben (AS) and Schweizerhuhn (SH) are the three local Swiss chicken breeds.

Goal: analysis of genetic diversity and estimation of genomic inbreeding coefficients for these three breeds using high-density SNP-genotypes

Results

<table>
<thead>
<tr>
<th>ROH Chromosome</th>
<th>AB</th>
<th>AS</th>
<th>SH</th>
</tr>
</thead>
<tbody>
<tr>
<td>CHR1</td>
<td>0.238 ± 0.074</td>
<td>0.397 ± 0.109</td>
<td>0.181 ± 0.06</td>
</tr>
<tr>
<td>CHR2</td>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>CHR7</td>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
</tr>
<tr>
<td>CHR8</td>
<td>0.0</td>
<td>0.0</td>
<td>0.0</td>
</tr>
</tbody>
</table>

Figure 1: Estimated population structure of the three local chicken breeds, separated by breed and feather colour

Figure 2: Proportion of individuals of the three breeds (AB: blue line; AS: orange line; SH: red line) having a SNP in a ROH for Chromosome 1, 2, 7 and 8.

Conclusions

• Cluster analysis supports the assumption that admixture with additional breeds is frequent in AB
• Breeding on different plumage colours resulted in sub-structures in the AS breed
• Genomic inbreeding coefficients at remarkable level were found for all three breeds; being highest in AS followed by AB and SH
• The majority of SH-individuals has the region between 14.6-21.8 Mb on CHR7 in a ROH. Structural changes in this region are described in the context of the rose comb phenotype

Material and Methods

After quality control genotypes of 152 chicken and 309'428 SNPs were available. ADMIXTURE was applied for structure analysis. Runs of homozygosity were derived with PLINK and used for the estimation of genomic inbreeding coefficients (FROH).