

**P67 Model and demonstration project – cryopreserve of the chicken**

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The majority of biodiversity in the domestic chicken is in the care of hobby breeders. Because of a small population size and breeders giving up their stocks, the existence of some breeds is threatened. To maintain the genetic diversity, a cryopreservation of cock sperm should be built up as part of the national cryopreservation of Germany. All 12 selected breeds are endangered and had once a great importance in agriculture depending on their breeding focus: layer, dual purpose and meat-type breeds. The goal are 150 hatching eggs per breed from as many breeders as possible, to hatch a minimum of 15 preferably unrelated cocks which represent the breed standard. To date hatching eggs of four breeds Creeper (N=293), East Frisian Gull (N=459), Sachsenhuhn (N=398) and Westfälischer Totleger (N=322) were incubated. We found significant differences of fertilization rates between the breeds ( $p \leq .001$ ), whereby East Frisian Gull has the highest (92.4 %) in contrast to the other breeds (70.9–82.2 %). Relationships of the cocks were checked by molecular analysis and phenotype was evaluated by judges. From the selected cocks, sperm will be taken and conserved in liquid nitrogen tanks. At the same time, laying performance of the hens will be recorded. Different parameters such as feed consumption, fertilization and hatching rates are also of interest. All information gained will reinforce the individual sperm cryopreservation to support Animal Genetic Resources in Germany.

**P68 Identification of genes related to beak deformity in Beijing-You chickens using digital gene expression profiling**

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The deformed beaks and normal-shaped beaks in full-sibs in chicken are used to build digital gene expression together (DGE), and identification by qPCR technology; At the same time, to determine the tissue specificity of the differentially expressed genes and screened teratogenicity candidate genes, the expression profiles of most up-regulated gene and down-regulated gene were established. The results show that there were 1156 differentially expressed genes, 409 up-regulated and 747 down-regulated. Using GO enrichment analysis, the differentially expressed genes were significantly enriched in the cytoskeleton GO term, which contained many keratin family members in chromosome 25. Differentially expressed genes were also significantly enriched in pathways of unsaturated fatty acid biosynthesis and glycerol acid metabolism. Subsequent validation tests, using qPCR, essentially confirmed the trends shown by digital gene expression sequencing. From these results, 12 candidate genes including gene BMP4, CK19, LOC426217, LPL, ALDH7A1, GLA and so on, which could be linked with the deformed beaks were selected and gene LOC426217 will be the first candidate gene for further research. The unsaturated fatty acid biosynthesis pathway and glycerol acid metabolism pathways could be target pathways in the development of beak deformity.