

(Submission for poster session)

Hybrid genome assembly of Ogye (*Gallus gallus domesticus*) using short and long reads and annotations of noncoding genes.

Kyoungwoo Nam¹, Jang-il Sohn¹, Hyosun Hong¹ and Jin-Wu Nam^{1,2,*}

¹Department of Life Science, College of Natural Sciences, Hanyang University, Seoul 133-791, Republic of Korea

²Research Institute for Natural Sciences, Hanyang University, Seoul 133-791, Republic of Korea

Background: Because of ongoing decrease in cost of high-throughput sequencing (HTS), studies for genome assembly and noncoding gene annotations have been getting popular for not only model organisms but also non-model organisms. Ogye, a Korean traditional *Gallus gallus* breed, is well known for its unique phenotypical characteristics of black leather, skin, fascia, and sclera, and also have strong immune resistance against some specific diseases, such as Marek's disease and avian influenza, in the Korean poultry industry.

Results: To study of the phenotypical characteristics of Ogye in genome level, we first sequenced Illumina (60X paired-end and 170X mate-pair) and PacBio libraries (11X) of Ogye genome, and assembled a draft genome using our hybrid genome assembly pipeline, which consists of ALLPATHS-LG, SPACE-LongRead, OPERA-LG, PBJelly, LoRDEC, etc. The resulting draft genome of Ogye displayed a high quality of N50 (133 Kbp for contig and 21.2 Mbp for scaffold), and the scaffold N50 length of which is better than that of *Gallus gallus* (Galgal4.0). We also constructed noncoding transcriptome maps on the draft genome and profiled their expression across 20 different tissues including the skin, fascia, and eye by sequencing RNA-seq and small RNA-seq. As a result, we found 23 microRNA (miRNA) and 316 long intervening ncRNAs (lincRNAs) specifically expressed in the black tissues.

Conclusions: We expect that our genomic and transcriptomic resources could provide insights of the genomic evolution during *Gallus gallus* *subspeciation* and of the medical implication for the viral infection and immune-related diseases.

* Corresponding author: jwnam@hanyang.ac.kr

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