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**WPSA Indonesia Branch-Faculty of Animal Science Univ. of Andalas
Padang, West Sumatra, Indonesia**



PROCEEDINGS

**The 1st Poultry International Seminar 2012
The Role of Poultry in Improving Human Welfare**

ORGANIZED BY:

**FACULTY OF ANIMAL SCIENCE, UNIVERSITY OF ANDALAS, PADANG
WEST SUMATRA INDONESIA**

AND

WORLD'S POULTRY SCIENCE ASSOCIATION INDONESIA BRANCH



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5. BENGKULU ENDEMIC BURGO CHICKEN GENETIC ASSESSED BY mtDNA D-loop REGION

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ABSTRACT

One of Bengkulu Province endemic faunal species is burgo chicken. Burgo chicken is crossbreed of male red jungle fowl (*Gallus gallus* or *Gallus bankiva*) with female kampung chicken (*Gallus domestica*). However, there is less scientific information revealed, specifically on its fundamental genetic information and the genetic linkage to its progenitor. This study would be the preliminary study for burgo chicken genetic. The purpose of this study was to trace burgo's genetic information particularly on maternal phylogenetic kinship with its parental species by using PCR and DNA sequencing protocol. There were 10 samples of male burgo, 2 samples of male kampung and 2 samples of male red jungle fowl chicken used in this study. All individual samples were sexually mature and healthy condition. Twenty grams of meat from each sample was collected in a plastic bag and immediately stored in a refrigerator with temperature of -20° C. Few days prior to mtDNA D-loop region analysis, samples were dried and evaporated under sunlight for 8 hours during 3 days of treatment. Each sample was extracted by spin-column method and amplified by a thermal cycler. The Fpri and Rpri used was chickenMt_H408F (20-CTC TCG TGA GGT GGA CGA TC) and chickenMt_L16750R (20-AGG ACT ACG GCT TGA AAA GC), consecutively. The extracts were electrophorated by 3% agarose gel and then treated by a Wizard SV Gel PCR clean-up system. The data was analyzed by using BioEdit Sequence Alignment Editor program (Version Lhapus 1.26). The PCR results showed that the average of Burgo's nucleotide sequence length was 400 bp. It shorter than Kampung and Red Jungle Fowl's sequences length, 428 bp and 413 bp, consecutively. The result of TreeView program showed that genetically, burgo chicken was maternal phylogenetically close to red jungle fowl and maternal phylogenetically distant to kampung chicken. Furthermore, burgo and red jungle chicken were in the same cluster. We can concluded that burgo chicken nucleotide sequence length is shorter than its parental and burgo has a closer linkage to red jungle fowl.

I. INTRODUCTION

Previous studies by Putranto (2011a, b) and Putranto *et al.* (2010, 2012) reported that Indonesia is well known as a rich biodiversity country with various sub-species of native chickens. Unfortunately when they are captured, this rare sub-species would easily suffered from stress, low reproductive status and could be suffered for loss of feed intake which resulted in a high mortality rate. Furthermore, its low reproductive and low growth rate status of those indigenous sub-species have lead into a low population growth situation.

Lately, Bengkulu Province began to promote a new sub-species of native chicken called burgo chicken or also wellknown as Rejang chicken (Nurmeliastari, 2003; Setianto, 2009; Setianto *et al.*, 2009; Putranto, 2011a, b; Putranto *et al.*, 2010, 2012). Burgo chicken is

an endemic indigenous chicken of Bengkulu, a province which is located in Southern Sumatera island. They have been kept by rural communities for many generations in Rejang Lebong Regency of Bengkulu Province, therefore it is also known as Rejang chicken (Setanto, 2009; Setianto *et al.*, 2009; Warnoto and Setianto, 2009).

Farmers in rural area of Bengkulu keep burgo chicken live naturally by a backyard farming system. However, similar to their parental characteristics (kampung chicken and wild red forest chicken) which is low reproductive rate and low growth rate have resulted in a low population growth rate (Putranto *et al.*, 2010). Similar to other wild sub-species chicken, they are also difficult to domesticated and could not easily adapt to a captivity condition. This sub-species of chicken can be categorized as one of Indonesia biodiversity treasure and should be conserved immediately (Putranto 2011a, b; Putranto *et al.*, 2010, 2012).

II. MATERIALS AND METHODS

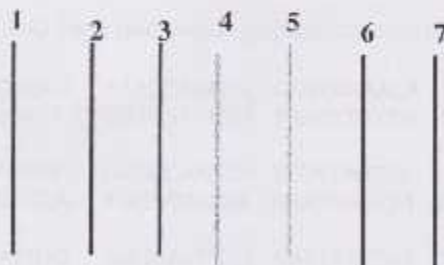
The main objective of this study was to trace Burgo's genetic information particularly on maternal phylogenetic kinship with its parental species by using PCR and DNA sequencing protocol. This study was conducted at Department of Animal Science, Faculty of Agriculture, University of Bengkulu, Indonesia and Matsumura Laboratory, Faculty of Applied Biological Sciences, Gifu University, Japan.

There were 10 samples of male Burgo, 2 samples of male Kampung and 2 samples of male Red Jungle fowl chicken used in this study. All individual samples were sexually mature and healthy condition. Twenty grams of meat from each sample was collected in a plastic bag and immediately stored in a refrigerator with temperature of -20° C. Few days prior to mtDNA D-loop region analysis, samples were dried and evaporated under sunlight for 8 hours during 3 days of treatment.

Each sample was extracted by spin-column method and amplified by a thermal cyclor. The Fpri and Rpri used was chickenMt_H408F (20-CTC TCG TGA GGT GGA CGA TC) and chickenMt_L16750R (20-AGG ACT ACG GCT TGA AAA GC), consecutively. The extracts were electrophorated by 3% agarose gel and then treated by a Wizard SV Gel PCR clean-up system. The data was analyzed by using BioEdit Sequence Alignment Editor program (Version Lhapus 1.26).

III. RESULTS

The following figures are the PCR result for samples used such as kampung chickens, red jungle fowls and burgo chickens (Figure 1 and Figure 2).



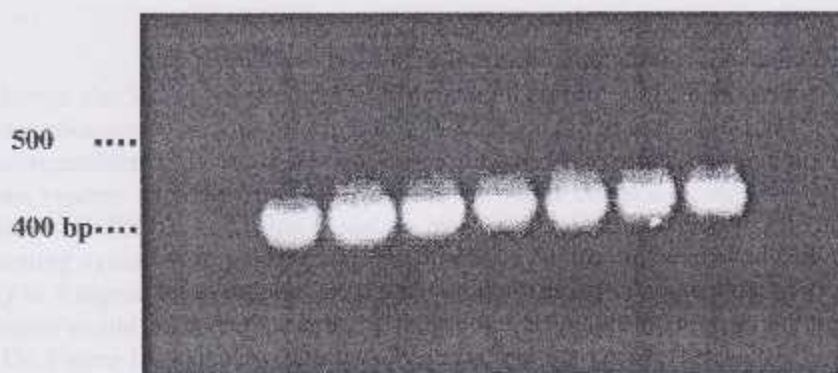


Fig 1. PCR result for 6 samples (1: DNA Ladder , 2: kampung #1, 3: kampung #2, 4: jungle fowl #1, 5: jungle fowl #2, 6: Burgo #1, 7: Burgo #2).

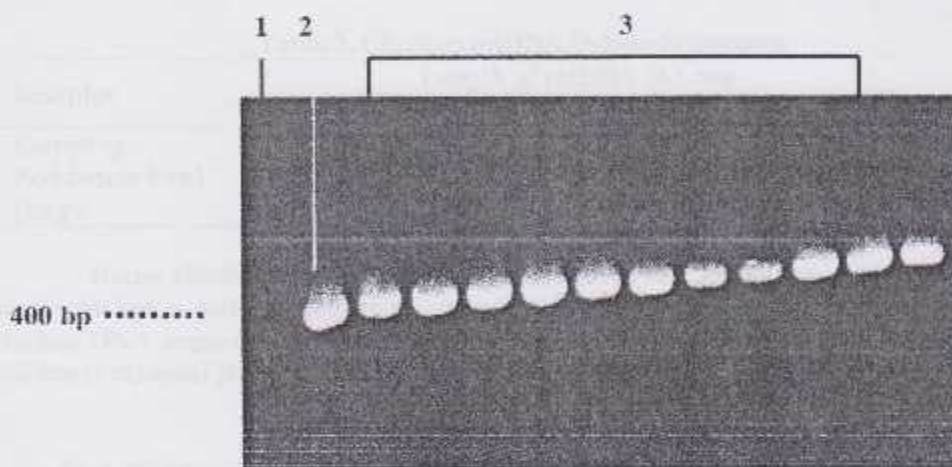


Fig 2. PCR result for 6 samples (1: kampung #1 , 2: jungle fowl #2, 3: from left to right, Burgo #1, 2, 3, 4, 5, 6, 7, 8, 9 and 10).

The following table contains burgo chicken mtDNA D-loop nucleotide sequencing result (Table 1).

Table 1. Burgo chicken mtDNA D-loop nucleotide sequencing result

| | | | | | |
|-----|------------|------------|------------|------------|------------|
| 1 | TCCATCTGAT | ACGACGAGCA | TAACCAAATG | GGTTAGAACA | TGGTAGTTAA |
| 51 | GTGTATGTCC | TGTAACCAAT | CATAGTTAGG | TGACTTGTTG | GGGGAGGAG |
| | | | | | C |
| 101 | AATGAGAGTG | AGATTTATGT | CCTGCAACCA | TTCATAGTTA | GGTGACTTGG |
| 151 | TAGTGGTTTG | GAGCTGTCTA | TGGGGAGGG | GAATGAGTAT | GTCTGGATC |
| | | | | | T |
| 201 | ATGCATAGAA | TGGACATTGG | GAGAAATGTG | GAATATAGAT | TAATGCCCGT |
| 251 | ATACATATAA | TGGGTTTACT | ACATATATAG | TATATATTAG | CGGTACCATA |
| 301 | ATATATGTGG | TATATAAATG | TATGCACGAT | TATGCATAGT | ATACCCCCCC |
| 351 | TGGGGGGGAA | AGGGGGGGTA | CACTTACTAG | GGGAGTTAGG | TAAAAAATAT |
| 401 | AATGT | | | | |

IV. DISCUSSION

Burgo chicken is genetically a crossmated chicken with some specific phenotypical characteristics and beautiful feather colour. Unfortunately, there are limited reports on burgo chicken reproductive physiology (Putranto, 2011a, b; Putranto *et al.*, 2010, 2012). There were previous reports informed about population of burgo chicken in Rejang Lebong Regency (Nurmeiliasari 2003), population based on macro environment, altitude, temperature, rainfall and farming system type (Setianto *et al.*, 2009) and the population percentage and population density in 5 regencies in Bengkulu Province (Putranto, 2011a, b; Putranto *et al.*, 2010, 2012). This report would be the first and preliminary study of burgo chicken genetic information.

On Figure 1 and 2, there were 6 and 12 samples with approximately length of 400 bp, consecutively. However, DNA sequencing result has shown a different length for each subspecies of chicken. Kampung chicken sample length was approximately 413 bp, burgo chicken sample was approximately 405 bp (Table 1). Based on DNA sequences, those 3 subspecies samples have shown a similarity of nucleotide with some minor differences (Table 2).

Table 2. Chicken mtDNA D-loop Sequences

| Samples | Length of mtDNA D-Loop | | | | | | |
|-----------------|------------------------|-----|-----|-----|-----|-----|-----|
| | 16 | 282 | 306 | 311 | 344 | 356 | 393 |
| Kampung | - | G | - | T | G | T | C |
| Red Jungle Fowl | A | A | T | C | A | C | T |
| Burgo | - | G | T | C | A | C | T |

Burgo chicken DNA sequence was similar to red jungle fowl. We assumed that burgo chicken is maternal phylogenetically close to red jungle fowl. In comparison, burgo chicken DNA sequence was unsimilar to kampung chicken. Therefore, we assumed burgo chicken is maternal phylogenetically distant to kampung chicken.

V. CONCLUSION

As a preliminary report, we assumed that burgo and red jungle chicken were in the same cluster. We can concluded that burgo chicken nucleotide sequence length is shorter than its parental and Burgo has a closer linkage to red jungle fowl.

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