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GENETIC DIVERSITY IN THE NATIVE CHICKEN POPULATION AT UPTD TAMPAKSIRING, GIANYAR, BALI

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ABSTRACT

This study aimed to analyze the phenotypic distribution, allele frequency, and genetic diversity based on qualitative traits of native chickens at UPTD Tampaksiring, Gianyar Regency, Bali. The study used 207 chickens, consisting of 67 males and 140 females. Observations were conducted on eight qualitative traits, including plumage colour, plumage pattern, plumage barring, plumage sheen, shank colour, comb type, muffs and beard, and crest. Data were analyzed descriptively through phenotypic distribution, allele frequency, and expected heterozygosity (He). The results showed that the coloured plumage phenotype (other than white) dominated the population, accounting for 86.57% in males and 88.57% in females, respectively. The rose comb type also dominated, at 82.09% in males and 88.57% in females. The highest heterozygosity was found in the plumage pattern trait, at 0.57 ± 0.04 in males and 0.66 ± 0.07 in females, whereas the lowest was found in the muffs and beard trait. These results indicate that diversity based on qualitative traits varies among traits and sexes. This information can serve as a preliminary basis for the documentation and conservation of native chickens, with further research using molecular markers to confirm their genetic diversity.

Keywords: Native Chicken, Allele Frequency, Heterozygosity, Qualitative Traits, Genetic Diversity.

1 INTRODUCTION

Native chicken is one of the local poultry germplasms that plays an important role in Indonesian livestock development. Its adaptability to tropical environments as well as the variation in its phenotypic traits make native chicken a genetic resource that needs to be conserved [1]. In Bali, native chicken is not only utilized as a source of animal protein and holds economic value, but also has social and cultural roles in the implementation of religious ceremonies, such as *Bhuta Yadnya* and *caru*. Plumage colour is one of the traits considered in selecting chickens for ritual purposes. This indicates the importance of native chicken as a local genetic resource possessing food, economic, social, and cultural values [2].

The genetic diversity of native chickens can be observed through variations in phenotypic traits associated with inherited genetic characteristics. Qualitative traits, such as plumage colour and plumage colour pattern, comb type, shank colour, and beak colour, are traits that can be used to identify phenotypic variation within a population [3]. Variation in plumage colour pattern is also an interesting trait to study because it can be associated with genetic inheritance, adaptation, and natural selection [4]. Observations of these traits can form part of population diversity studies, although determining the genetic condition requires the analysis of appropriate genetic parameters.

Genotype distribution, allele frequency, and heterozygosity are parameters that can be used to describe the genetic diversity of a population. Genotype distribution shows the proportion of each genotype at the observed locus, whereas allele frequency describes the proportion of each allele within the population. Heterozygosity is used to estimate the level of genetic diversity based on allelic variation at the analyzed locus. Information regarding these parameters is important for understanding the genetic composition of the population as well as providing a scientific basis for the management and conservation of native chicken genetic resources.

The native chicken population at UPTD Tampaksiring, Gianyar Regency, Bali, is a genetic resource that needs to be studied to obtain information regarding its genetic characteristics. Documentation of genotype distribution, allele frequency, and the level of genetic diversity in this population is required to describe genetic variation based on the analyzed traits. This study aimed to analyze the genotype distribution, allele frequency, and genetic diversity in the native chicken population at UPTD Tampaksiring, Gianyar Regency, Bali. The analysis was conducted to obtain an overview of the genotype composition, allele proportions, and the level of genetic diversity based on the observed loci or traits. The results of this study are expected to provide scientific information as a basis for the documentation, management, and conservation of native chicken genetic resources in Bali.

2 MATERIALS AND METHODS

2.1 Materials and Equipment

This study used 207 native chickens reared at UPTD Tampaksiring, Gianyar Regency, Bali, consisting of 67 male chickens and 140 female chickens. The equipment used included a camera or smartphone for documenting phenotypic traits, stationery, observation sheets, and a laptop for data processing and analysis.

2.2 Research Methods

Data collection was conducted through direct observation of the qualitative traits of each individual chicken. The observed traits included plumage colour, plumage pattern, plumage barring, plumage sheen, shank colour, comb type, presence of muffs and beard, and presence of crest. Documentation was carried out using a camera to assist in the identification and recording of phenotypic traits. Observations were performed separately based on sex, namely males and females.

Each phenotypic trait was subsequently grouped based on the observed categories and identified using genotype symbols in accordance with the relevant patterns of trait inheritance. The determination of genotype symbols and estimation of allele frequencies referred to the chicken genetics references used in this study, taking into account autosomal traits, sex-linked traits, and traits controlled by multiple alleles where relevant.

This study aimed to analyze and identify the genotype distribution in Merawang Cross chickens. Genotype data of visible genes were analyzed based on the characteristics of autosomal alleles (plumage colour and comb type), multiple alleles (plumage pattern), and sex-linkage (plumage barring, plumage sheen, and shank colour). In addition, expected heterozygosity (*he*) and mean heterozygosity (*e*) were calculated in this study to observe genetic diversity in the visible genes of Merawang Cross chickens.

The allele frequencies of autosomal alleles were calculated using the mathematical formula from [5] as follows:

$$p = 1 - q$$

$$q = \sqrt{\frac{\sum n_{ii}}{N}}$$

Where:

p = frequency of the dominant gene
q = frequency of the recessive gene
nii = number of chickens with the recessive genotype

N = total number of chickens

Allele frequencies for multiple alleles were calculated using the mathematical formula from [5] as follows:

$$p = 1 - q - r$$
$$q = \sqrt{\frac{\sum n_W + \sum n_C}{N}} - r$$
$$r = \sqrt{\frac{\sum n_C}{N}}$$

Where:

p = frequency of allele E
q = frequency of allele e+
r = frequency of allele e
n_w = number of chickens with wild-type plumage
n_c = number of chickens with Columbian plumage
N = total number of chickens

The allele frequencies of sex-linked alleles were calculated using the mathematical formula from [5] as follows:

$$\text{Males } = p = 1 - q \text{ and } q = \sqrt{\frac{\sum n_{ii}}{N}}$$

$$\text{Females } = p = 1 - q \text{ and } q = \sqrt{\frac{\sum n_{ii}}{N}}$$

p = frequency of the dominant gene
q = frequency of the recessive gene
nii = number of chickens with the recessive genotype
N = total number of chickens

Expected heterozygosity (*he*) and mean heterozygosity (*e*) were calculated using the mathematical formula from [6] as follows:

$$H_e = 1 - \sum_{i=1}^{n} Pi^2 \quad SE(h) = \sqrt{\frac{2}{2n(2n-1)}\left\{2(2n-2)\left[\sum q_1^2 - \sum q_1^3\right] + \sum q_1^2\right\}}$$

$$\bar{H}_e = \frac{\sum h_e}{r} \qquad SE(\bar{H}) = \sqrt{\frac{\sum h_e^2 - r\bar{H}^2}{r(r-1)}}$$

Where:

he = expected individual heterozygosity
$_e$ = mean individual heterozygosity
Pi = frequency of the i-th allele
qi = frequency of the i-th gene
SE = standard error
qi = heterozygosity of the i-th locus
r = number of phenotypic traits
n = number of chickens

The genetic composition in Merawang Cross chickens based on White Leghorn (WL), Rhode Island Red (RIR), and Barred Plymouth Rock (BPR) chickens was calculated using the following formulas [7] :

QWL = qI

QRIR = qId – qB

QBPR = qB – qI

QT = QWL + QRIR + QBPR

Q = 1 - (QWL + QRIR + QBPR)

Where:

QWL = introgression value of White Leghorn chicken
QRIR = introgression value of Rhode Island Red chicken
QBPR = introgression value of Barred Plymouth Rock chicken
QT = total introgression value
qId = frequency of the white-yellow shank colour gene
qI = frequency of the white plumage colour gene
qB = frequency of the barred plumage pattern gene

The original genetic composition of Merawang Cross chickens not derived from WL, RIR, and BPR chickens was calculated using the following formula [7]:

qE = qE-qB

qe+ = qe+

qe = qe - QRI

qS = qS – qB

qs = qs - QRI

qId = qId

qp = qp - qId

qP = qP

Note:
qE = Frequency allele E
qB = Frequency allele B
qe+ = Fekuensi allele e+
qe = Frequency allele e
qS = Frequency allele S
qs = Frequency allele s
qId = Frequency allele Id
qP = Frequency allele P
qp = Frequency allele p
QRI = Nilai intogresi ayam RIR

3 RESULTS

The results of genotype frequency and allele frequency for qualitative traits in Merawang Cross chickens obtained in this study can be seen in Table 1 and Table 2 below.

Table 1: Percentage frequency of qualitative traits in native chickens in Gianyar, Bali

No	Phenotype	Genotype	Amount		Frequency (%)	
			Male (N=67)	Female (N=140)	Male (N=67)	Female (N=140)
1	Plumage Colour:					
	White	I_	9	18	13.43	12.86
	Coloured	Ii	58	124	86.57	88.57
2	Plumage Pattern:					
	Black	E_	1	20	1.49	14.29
	Wild-type	e^{+}-	43	87	64.18	62.14
	Columbian	ee	13	9	19.40	6.43
3	Plumage Barring Pattern:					
	Barred/Lurik	B_	46	90	68.66	64.29
	Non-barred	bb	21	50	31.34	35.71
4	Plumage Colour (Silver/Gold):					
	Silver	S_	48	40	71.64	28.57
	Gold	ss	18	101	26.87	72.14
5	Shank Colour:					
	Yellow/White	I^{d}	45	102	67.16	72.86
	Black/Grey	$i^{d}I^{d}$	22	38	32.84	27.14
6	Comb Type:					
	Pea	rrP_	0	2	0	1,43
	Singel	rrpp	12	10	17.91	7.14
	Rose	R_pp	55	124	82.09	88.57
	Walnut	R_P_	2	2	2.99	1.43
7	Muffs and Beard:					
	Present	Mb	2	3	2.99	2.14
	Absent	mb^{+}	65	137	97,01	97,86
8	Crest:					
	Present	Cr_	5	34	7.46	24.29
	Absent	cc	62	104	92.54	75.71

Note: Coloured plumage encompasses all colour variations other than white, including wild-type, Columbian, and barred patterns, as well as colour variations recognized in Balinese native chicken nomenclature, such as *ijo*, *hitam*, *buik*, *klawu*, *biying*, and *wangkas*.

Table 2: Percentage allele frequency of qualitative traits in native chickens in Gianyar, Bali

Phenotype	Allele Type	Allele	Frequency (%)	
			Male (N=67)	Female (N=140)
Plumage Colour	Autosomal	I	0.07	0.06
		i	0.93	0.94
		E	0.09	0.37
Plumage Pattern	Multiple alleles	e^+	0.47	0.38
		e	0.44	0.25
Plumage Barring Pattern	Sex-linked	B	0.44	0.64
		b	0.56	0.36
gold plumage sheen	Sex-linked	S	0.48	0.28
		s	0.52	0.72
Shank Colour	Sex-linked	I^d	0.43	0.73
		i^d	0.57	0.27
		P	0.88	0.68
Comb Type	Autosomal	p	0.12	0.32
		Rp	0.89	0.92
		rP	0.11	0.08
Muffs and Beard	Autosomal	Mb	0.02	0.02
		Mb^+	0.98	0.98
Crest	Autosomal	Cr	0.04	0.24
		c	0.96	0.76

The expected heterozygosity and mean expected heterozygosity values can be seen in Table 3. The genetic constitution values relative to European breeds and native chickens can be seen in Table 4 and Table 5.

Table 3: Heterozygosity (H) and mean heterozygosity values for qualitative traits in native chickens in Gianyar, Bali

Phenotype	Heterozygosity	
	Male	Female
Plumage Colour	0.13±0.03	0.11±0.02
Plumage Pattern	0.57±0.04	0.66±0.07
Plumage Barring Pattern	0.49±0.03	0.46±0.06
gold plumage sheen	0.50±0.02	0.40±0.06
Shank Colour	0.49±0.04	0.40±0.06
Comb Type	0.02±0.01	0.15±0.01
Muffs and Beard	0.03±0.02	0.04±0.01
Crest	0.07±0.02	0.37±0.02

Table 4: Original genetic constitution (Q) of native chickens in Gianyar and genetic introgression of chickens

Genetic Integration	Male	Female
$Q_{wl} = qI$	13.43	12.86
$Q_{RI} = qI^d - qB$	-1.50	8.57
$Q_{PR} = qB - qI$	55.23	51.43
$Q_T = Q_{WL} + Q_{RI} + Q_{PR}$	67.16	72.86
$Q = 1 - (Q_{WL} + Q_{RI} + Q_{PR})$	-66.16	-71.86

Keterangan: qI; dominant plumage colour frequency, qId; dominant shank colour frequency, qB; dominant plumage barring frequency $Q_{wl;\ White\ leghorn}$, $Q_{RI;\ rhode\ island\ red}$, $Q_{PR;\ barred\ Plymouth\ rock}$

Table 5: Gene frequency of native chickens in Gianyar without genetic constitution from European chicken breeds (White Leghorn, Rhode Island Red, and Barred Plymouth Rock)

Gene Frequency (q_n)	Male	Female
$q_E = qE - qB$	-0.35	-0.27
$q_{e+} = q_{e+}$	0.47	0.38
$q_e = qe - Q_{RI}$	1.94	-8.32
$qs = qS - qB$	0.04	-0.36
$q_s = qs - Q_{RI}$	2.02	-7.85
$q_{id} = qi^d$	0.43	0.73
$q_p = qp - qI^d$	-0.30	-0.65
$qp = qp$	0.12	0.08

Note: q; frequency, E; dominant plumage pattern, e+; wild-type plumage pattern, e; Columbian plumage pattern, p; single comb type, P; pea comb type, s; silver plumage sheen, S; gold plumage sheen, id; recessive shank colour

4 DISCUSSION

Morphogenetic characterization through the observation of qualitative traits is used to describe phenotypic variation and allele distribution in native chicken populations. This study included eight traits, namely plumage colour, plumage pattern, plumage barring, plumage sheen, shank colour, comb type, muffs and beard, and crest. The analysis was conducted by comparing phenotype distribution, allele frequency, and expected heterozygosity (*He*) between male and female chickens. The results of this study indicate that the native chicken population at UPTD Tampaksiring, Gianyar, Bali, has different levels of diversity for each trait. Plumage pattern exhibited the highest heterozygosity, whereas plumage colour, comb type, and muffs and beard showed relatively low diversity.

4.1 Plumage Colour

The plumage colours of the native chickens observed included *buik*, *klawu*, *biying*, *ijo*, *wangkas*, *selem*, *serawah*, *brumbung*, and white. Non-white plumage phenotypes dominated the population, accounting for 86.57% in males and 88.57% in females, whereas white plumage was found at 13.43% and 12.86%, respectively. The frequency of allele *i* reached 0.93 in males and 0.94 in females, whereas allele *I* was 0.07 and 0.06, respectively. According to [8], the *I* gene acts as a pigmentation inhibitor, whereas the *i* gene is associated with plumage colour expression. These results show a similar trend to the study by [9] on Merawang Cross chickens, which showed the dominance of coloured plumage. The heterozygosity value for plumage colour of 0.13 ± 0.03 in males and 0.11 ± 0.02 in females indicates that diversity in this trait is relatively low compared to several other traits.

4.2 Plumage Pattern

Plumage pattern was analysed based on the frequencies of alleles E, e+, and *e*. The frequency of allele *E* was 0.09 in males and 0.37 in females, allele *e+* was 0.47 and 0.38, and allele *e* was 0.44 and 0.25, respectively. These differences indicate variation in allele composition between male and female chickens. According to [10], the *Extension* locus plays a role in regulating pigment distribution in chicken plumage. These results differ from [9], who reported the dominance of the Columbian pattern in male chickens and the wild-type pattern in female Merawang Cross chickens. Plumage pattern had the highest heterozygosity values, namely 0.57 ± 0.04 in males and 0.66 ± 0.07 in females. These values

indicate that the plumage pattern trait possesses relatively high genetic diversity and has the potential to serve as one of the important traits in the conservation of native chickens.

4.3 Plumage Barring

Plumage barring was differentiated into barred and plain. The barred pattern dominated the population, accounting for 68.66% in males and 64.29% in females. The frequency of allele *B* was 0.44 in males and 0.64 in females, whereas allele *b* was 0.56 and 0.36, respectively. According to[10], the *Barred* (*B*) gene is located on the Z chromosome, so its inheritance is sex-linked. The results of this study differ from [9], who reported the dominance of plain plumage in Merawang Cross chickens. The heterozygosity value for plumage barring of 0.49 ± 0.03 in males and 0.46 ± 0.06 in females indicates that this trait still possesses relatively high genetic diversity.

4.4 Plumage Sheen

Plumage sheen was analysed through the frequencies of alleles *S* and *s*. The frequency of allele *S* was 0.48 in males and 0.28 in females, whereas allele *s* was 0.52 and 0.72, respectively. These results indicate that allele s had a higher frequency in both groups, especially in females. Compared to the study by [9], which reported the dominance of gold plumage sheen in Merawang Cross chickens, the results of this study need to be interpreted by considering the consistency of the allele symbols and phenotype categories used. The heterozygosity value for plumage sheen of 0.50 ± 0.02 in males and 0.40 ± 0.06 in females indicates relatively high diversity, with a higher value in male chickens.

4.5 Shank Colour

The frequency of allele *Id* for shank colour was 0.43 in males and 0.73 in females, whereas allele id was 0.57 and 0.27, respectively. Thus, allele *id* was higher in males, while allele *Id* was higher in females. Shank colour is one of the qualitative traits that can be used to identify phenotypic variation in native chickens [3]. The heterozygosity value of 0.49 ± 0.04 in males and 0.40 ± 0.06 in females indicates that this trait possesses relatively high diversity, especially in the male group.

4.6 Comb Type

The rose comb type was the dominant phenotype, found in 82.09% of male chickens and 88.57% of female chickens. Based on allele analysis, the frequency of *P* was 0.88 in males and 0.68 in females, whereas *p* was 0.12 and 0.32, respectively. In the other allele pair, the frequency of *Rp* was 0.89 and 0.92, whereas *rP* was 0.11 and 0.08, respectively. According to [10], comb shape in chickens is influenced by the interaction of two genetic loci. The heterozygosity value for comb type of 0.02 ± 0.01 in males and 0.15 ± 0.01 in females indicates relatively low diversity, especially in the male group.

4.7 Muffs and Beard

The non-muffed and beardless phenotype dominated the population, accounting for 97.01% in males and 97.86% in females. The frequency of allele *Mb* was 0.02 in both groups, whereas allele *Mb+* reached 0.98. The muffs and beard trait is associated with the *Muffs and Beard* (*Mb*) gene, which influences the growth of extra feathers around the chicken's face [10], The heterozygosity value of 0.03 ± 0.02 in males and 0.04 ± 0.01 in females indicates that the genetic diversity of this trait is relatively low.

4.8 Crest

Non-crested chickens dominated the population, accounting for 92.54% in males and 75.71% in females. The frequency of allele *Cr* was 0.04 in males and 0.24 in females, whereas allele *c* was 0.96 and 0.76, respectively. According to [10], the crest trait is associated with the *Crest* (*Cr*) locus. The heterozygosity value for crest of 0.07 ± 0.02 in males and 0.37 ± 0.02 in females indicates that the genetic diversity of this trait is higher in the female group.

4.9 Genetic Diversity Based on Heterozygosity

Expected heterozygosity (*He*) values indicate the level of genetic diversity based on allele frequencies. In male chickens, the highest value was found in plumage pattern (0.57 ± 0.04), followed by plumage sheen (0.50 ± 0.02), plumage barring (0.49 ± 0.03), and shank colour (0.49 ± 0.04). In female chickens, the highest value was also found in plumage pattern (0.66 ± 0.07), followed by plumage barring (0.46 ± 0.06), plumage sheen (0.40 ± 0.06), and shank colour (0.40 ± 0.06). Conversely, plumage colour and muffs and beard showed relatively low heterozygosity values. These results demonstrate that genetic diversity is not evenly distributed across all traits. These findings are consistent with [11], who reported variation in heterozygosity in Indonesian native chicken populations. Differences in diversity among traits may be associated with allele frequencies, population history, mating systems, selection, and gene flow. However, heterozygosity based on phenotypic traits only describes variation in the specific traits and calculation system used, rather than overall genomic variation.

4.10 Implications for the Conservation of Native Chickens at UPTD Tampaksiring

The results of this study indicate that the native chicken population at UPTD Tampaksiring possesses morphogenetic variation with differing levels of diversity. The dominance of non-white plumage and rose comb, as well as the high heterozygosity of plumage pattern, provides important information for documenting population characteristics. Based on the genetic constitution analysis in the thesis, the estimated genetic contribution of Barred Plymouth Rock reached 55.23% in males and 51.43% in females. These results indicate a possible external genetic influence. However, because these estimates are based on gene frequencies derived from phenotypic traits, the results cannot yet be considered direct evidence of genomic composition.

Overall, the results of phenotype distribution, allele frequencies, and heterozygosity can serve as an initial basis for the management and conservation of native chickens in Gianyar, Bali. Directed mating management and the avoidance of inbreeding need to be considered to maintain genetic variation. Further research using molecular markers, such as SNPs or microsatellites, is needed to confirm the genetic diversity and the influence of external genetic sources on the population.

5 CONCLUSION

The native chicken population at UPTD Tampaksiring, Gianyar, Bali exhibits morphogenetic trait variation based on the eight qualitative traits observed. The highest genetic diversity was found in the plumage pattern trait, with heterozygosity values of 0.57 ± 0.04 in male chickens and 0.66 ± 0.07 in female chickens. The results of this study demonstrate variation in allele frequencies and genetic diversity between male and female chickens, which can serve as a basis for the conservation and maintenance of native chicken genetic resources.

STATEMENTS ON COMPLIANCE WITH ETHICAL STANDARDS

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Disclosure of conflict of interest

The author confirms that no financial or personal interests exist that could have influenced the outcomes or interpretation of the present study.

Statement of ethical approval

The use of 207 native chickens in this study was approved by the Animal Ethics Committee of the Faculty of Veterinary Medicine, Udayana University, Badung, Bali, Indonesia.

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