Doctoral Thesis

Molecular Phylogeny of Junglefowls, genus *Gallus*
and
Monophyletic Origin of Domestic Fowls

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Abstract

With the aim of elucidating the evolutionary origin of junglefowls and their domestication processes, I conducted molecular evolutionary analyses of mitochondrial DNAs for various kinds of birds belonging to the subfamily Phasianinae. I then found that the real matriarchic origin of all the domestic fowls examined in the present study was an Asian continental population of *Gallus gallus gallus.* The phylogenetic analysis conducted in this study also suggested that the continental population of *Gallus gallus gallus* is the monophyletic ancestor of all domestic fowls. These findings resolve the long-time controversy concerning monophyletic versus polyphyletic origin theories of domestic fowls.

The present thesis is composed of four chapters. In Chapter 1, as an introduction, I described the evolutionary significance of the domestication processes of junglefowls and the overview of taxonomical problems of birds within the subfamily Phasianinae, particularly junglefowls and domestic fowls.

In Chapter 2, attention is focused on the molecular phylogeny of the subfamily Phasianinae. Comparisons of DNA sequences for mitochondrial control regions among 16 avian species belonging to the subfamily Phasianinae, revealed the following: (1) Generalized perdicine birds (quails and partridges) are descended from ancient lineages. Even the closest pair,

the common quail of the Japanese subspecies (*Coturnix coturnix japonica*) and the Chinese bamboo partridge (*Bambusicola thoracica*), maintained only a 85.71% identity. (2) The 12 species of phasianine birds previously and presently studied belong to three distinct branches. The first branch is made up exclusively of members of the genus *gallus*, while the second branch is made up of pheasants of the genera *Phasianus, Chrysolophus* and *Syrmaticus*. Gallopheasants of the genus *Lophura* are distant cousins to these pheasants. The great argus (*Argusianus argus*) and peafowls of the genus *Pavo* constitute the third branch. Members of the fourth phasianine branch, such as tragopans and monals, were not included in the present study. (3) The one perdicine species, *Bambusicola thoracica*, is more closely related to the phasianine genera *Gallus* and *Pavo* than to members of other perdicine genera. The above might indicate that *Bambusicola* belongs to one stem of the perdicine lineage which later split into two sublineages that yielded phasianine birds; one evolving to *Gallus*, while the other differentiated toward *Pavo* and related genera. (4) Tandem duplication of the 60-base unit was established as a trait unique to the genus *Gallus,* which is shared neither by pheasant nor by quail.

In Chapter 3, I discuss evolutionary relationships between red and green junglefowls. The noncoding control region of the mitochondrial DNA of various gallinaceous birds was studied with regard to its RFLP (restriction fragment length polymorphism) and sequences of the first 400 bases. Unlike its close ally green junglefowl, the red junglefowl *Gallus gallus* is a genetically very diverse species; a 7.0% sequence divergence was seen between those from Thailand *(Gallus gallus gallus* and *Gallus gallus spadiceus)* and that of the Indonesian island of Java *(Gallus gallus bankiva).* Furthermore, the divergence increased to 27.83% when each transversion was regarded as an equivalent of 10 transitions. On the other hand, a mere 0.5-3.0% difference (all transitions) separated various domestic breeds of chicken from two subspecies of *Gallus gallus gallus* of Thailand, thus indicating a single domestication event in the area inhabited by this subspecies, with the red junglefowl being the origin of all domestic breeds. Only transitions separated six diverse domesticated breeds. Nevertheless, a 2.75% difference was seen between RFLP type I breeds (white leghorn and nagoya) and a RFLP type VIII breed (*ayam pelung*). The above data suggest that although the mitochondrion of RFLP type V is the main contributor to domestication, hens of other RFLP types also contributed to this event.

Finally, in Chapter 4, the evolutionary origin and dispersal patterns of domestic fowls are discussed from various aspects of molecular evolution and human history. With the aim of elucidating in more detail, the genealogical origin of the present domestic fowls of the world, I determined mitochondrial DNA (mtDNA) sequences of the D-loop regions for a total of 21 birds which belong to the red junglefowl (*Gallus gallus*) comprising three subspecies (6 *Gallus gallus gallus,* 3 *Gallus gallus spadiceus* and 3 *Gallus*

gallus bankiva) and 9 birds representing diverse domestic breeds (*Gallus gallus domesticus*) . I also sequenced mtDNAs from 4 green junglefowl (*Gallus varius*), 2 Cingalese junglefowl (*Gallus lafayettei*) and 1 grey junglefowl (*Gallus sonnerati*). I then constructed a phylogenetic tree for these birds using nucleotide sequences, choosing the Japanese quail (*Coturnix coturnix japonica*) as an outgroup. Moreover, I found that a continental population of *Gallus gallus gallus* was the real matriarchic origin of all the domestic species examined in the present study. It is also of particular interest to note that there were no discernible differences among *Gallus gallus* subspecies; *Gallus gallus bankiva* being a notable exception. This was because *Gallus gallus spadiceus* and a continental population of *Gallus gallus gallus* formed a single cluster in the phylogenetic tree. One obvious and distinct feature that customarily separates *Gallus gallus gallus* from *Gallus gallus spadiceus* is the color of their ear lobes: white for the former and red for the latter. The fact that domestic breeds of the chicken are of two kinds as to color of ear lobes is a clear reflection of the contribution made by *Gallus gallus gallus* as well as by *Gallus gallus spadiceus* to their ancestry. *Gallus gallus bankiva*, on the other hand, is a distinct entity, thus, deserving its subspecies status. This implies that a continental population of *Gallus gallus gallus* was the monophyletic ancestor of all domestic breeds. I also discuss the possible significance of the initial dispersal pattern of present domestic fowls, utilizing the phylogenetic tree.

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Chapter 1

Introduction

In our ever increasingly mechanized society, the fond memory of intimate tie that existed between man and his domesticated animals is rapidly fading. Yet the lasting impact that the domestication event exerted upon our history can easily be realized by recalling 16th century tragedies that befell the two great empires of the new world with wondrous architectural skills; Aztec in the middle and Inca to the south.

Horses of the genus *Equus* originally evolved in the new world and eventually their range expanded to the central Asia. This expansion was probably through the Bering landbridge during the initial Gunz period of the great ice age. It is a historical injustice of extreme proportion that by the time, the first wave of migrants from the Asia began to arrive in the new world some 30,000 years ago also through the Bering landbridge, horses were already extinct from the continent of their origin. At the same time, the domestication of wild horses in the central Asian plains was yet to take place in the ancestral land of these migrants. Because of the above two tragic coincidences, ameridians were condemned to remain *gentis sans* *equus.* Gazing at the magnificent temple city ruins of Teotihuacan and Machu Picchu, one can not help but wonder how it was possible to move and pile such enormous stones without help from beasts of the burden.

It is this condemnation which enabled two spaniards, Hernando Cortes and Francisco Pizarro, to conquer the two great new world empires possessing well organized armies with less than 200 horsemen each.

It now appears that the domestication of junglefowls was no less a historical significance. Only man-made artefacts recognizable from high-orbiting manned spacecrafts is said to be the Great Wall of China. This enormous architectural project was started around 220 B. C. by Shi-huangdi, the first emperor of Qin. Many archeologists now believe that labors that built the Great Wall of China were sustained by proteins furnished by the domesticated chicken.

Needless to say, only modern man *Homo sapiens* managed to domesticate wild animals. Accordingly, the recent revelation that although our predecessors such as *Homo erectus* inhabited outside of Africa as well as Africa itself (e.g., Peking man and Java man), modern man originated in Africa only half a million years ago or so and that a small band of them moved out to the near East about 100,000 years ago or thereabout and began migration toward West, North and East was a precious gift to the students of all domestication events. This is because 100,000 years became the upper time limit of all domestication events that occurred aside of Africa.

With the aim of elucidating the evolutionary origin of junglefowls and their domestication processes, I conducted molecular evolutionary analyses of mitochondrial DNAs for various kinds of birds belonging to subfamily Phasianinae. In particular, I sequenced the noncoding D-loop region of the mitochondrial genome for the birds.

In the case of the noncoding D-loop region of the mitochondrial genome, 2% sequence difference became the upper limit marker, for this is the difference seen among all ethnic groups of man. Accordingly, one is not expected to see greater than 2% sequence difference among domestic breeds of any species, as far as the D-loop region is concerned.

The present thesis is composed of four chapters. Except Introduction in Chapter 1, three chapters from Chapter 2 to Chapter 4 describes the results of my studies. In Chapter 2, I discuss molecular phylogeny of the subfamily Phasianinae and its implications to evolution of junglefowls. In particular, I focus the discussion on phylogenetic relationships between the tribes perdicine and phasianine.

First of all, duplication of the 60-base-long unit within the D-loop region was established as a trait unique to the genus *Gallus*. If in the future, a particular perdicine (quail or partridge) species is identified that has this duplication, that quail or partridge indisputably belongs to the perdicine lineage that gave rise to the genus *Gallus* and to no phasianine birds. Inasmuch as I have already identified the Chinese bamboo partridge as a close relative of this lineage, it will be possible to identify the species soon.

In Chapter 3, I would clarify the evolutionary relationships between red and green junglefowls, the noncoding control region of the mitochondrial DNA with regard to its restriction fragment length polymorphism (RFLP) and sequences of the first 400 bases.

In Chapter 4, I would make an attempt to elucidate the evolutionary origin and dispersal patterns of domestic fowls, in order to understand the domestication processes of junglefowls.

In this chapter, I make clarification of subspecies status within the red junglefowl (*Gallus gallus*). Although it has generally been accepted that diverse domestic chicken breeds originated from the red junglefowl, this species is thought to be comprised of five subspecies. Accordingly, the question of which is the ancestral subspecies remained.

When the famous 4000-year-old Mohenjo-Doro site was thought of as the original site of chicken domestication, the expectation fell on one particular subspecies *Gallus gallus murghi* whose range included the Indus valley. When 8000-year-old remains of domesticated chicken were found along the Huang He (yellow river) in northern China which has never been the habitat of junglefowls, the expectation moved further to East and South and fell upon a number of red junglefowl subspecies inhabiting the area comprised of south China, Thailand and Indochinese regions.

I have shown that *Gallus gallus spadiceus* inhabiting the Malay peninsula bisects the habitat of *Gallus gallus gallus*. *Gallus gallus gallus* of Indochinese regions in the Asian mainland was separated from *Gallus gallus gallus* of the Sumatra island. Furthermore, I have shown that continental *Gallus gallus gallus* and *Gallus gallus spadiceus* was a single genetic entity quite distinct from the Sumatran *Gallus gallus gallus,* and that diverse breeds of the domestic chicken fall into this newly recognized combined continental entity. Only discernible feature separating *Gallus gallus gallus* from *Gallus gallus spadiceus is* white ear lobes versus red ear lobes. Understandably, this dichotomy has been transmitted to domestic breeds of the chicken, for they are either white ear lobed or red ear lobed.

Among the red junglefowls, excluded from the ancestry of the domestic chicken were the Sumatran *Gallus gallus gallus* population as well as *Gallus gallus bankiva* inhabiting Indonesian islands. Although *Gallus gallus murghi* has not been studied, it can qualify as an ancestor, only if it is genetically indistinct from the afore-mentioned new combined entity.

At the end, I believe that these noted above are very important for understanding the phylogeny of junglefowl and the evolutionary origin of domestic fowls and their dispersal patterns.

Chapter 2.

Molecular Phylogeny of the Subfamily Phasianinae and its Implications to Evolution of Junglefowls, Genus Gallus

2.1 Introduction

2.1.1 Purpose of Study

In this study, I established duplication of a 60-base-long unit within the mitochondrial control (D-Loop) region characteristically unique to the genus *Gallus* among phasianine birds. Furthermore, base sequence comparison of this maternally derived noncoding region revealed that as diverse as domestic breeds of chicken are, they could only have been derived from a continental subspecies (e.g., *Gallus gallus gallus, Gallus gallus spadiceus*) but not an island subspecies (*Gallus gallus bankiva*) of the red junglefowl , *Gallus gallus* (Fumihito *et al*, 1994). Excluded from the ancestry of domesticated chicken were three other species of junglefowls; the green (*Gallus varius*), the grey (*Gallus sonnerati*) and the Cingalese (*Gallus lafayettei*).

In this study, I wish to define the position of the genus *Gallus* within the subfamily Phasianinae in relation to other members.

2.1.2 Systematic Classifications of the Subfamily Phasianinae

Because of their ornamental value, large pheasant-like birds of the subfamily, Phasianinae are widely kept and propagated in various zoological gardens of the world as well as by private fanciers. This is not the case with diverse generalized perdicine birds (quails and partridges) of the same subfamily. When a few of them are kept and propagated, they are maintained only as exotic game birds. Accordingly, I was able to secure blood samples from only five species, albeit from four (five) different genera, of the generalized perdicine birds which are said to consist of 103 species belonging to 22 different genera (Johnsgard, 1986). They were the common quail of the Japanese subspecies, *Coturnix coturnix japonica*, the blue-breasted quail (*Coturnix chinensis*, also known as *Excalfactoria chinensis*) the Chinese bamboo partridge, *Bambusicola thoracica*, the chukar partridge, *Alectoris graeca chukar* and the European grey partridge, *Perdix perdix perdix*. In sharp contrast, there were no difficulties in securing 12 species of the large pheasant-like birds of the subfamily Phasianinae representing 8 different genera, thus, 11 of the 49 extant species were sampled (Johnsgard, 1986). In addition to the red (*Gallus gallus*) and green (*Gallus varius*) previously reported (Fumihito *et al.*, 1994), the genus *Gallus* was represented by two additional junglefowl species; the grey (*Gallus sonnerati*) and Cingalese (*Gallus lafayettei*) junglefowls. Pheasants, as such, were represented by three species; the green (*Phasianus versi color*), the golden (*Chrysolophus pictus*) and Mrs. Hume's (*Syrmaticus huminae*). Other large bodied birds of this subfamily that were also called pheasants for want of more descriptive words, were the silver gallopheasant (*Lophura nycthemera*), the Burmese peacock-pheasant (*Polyplectron bicalcaratum*), and the great argus pheasant (*Argusianus argus*) which is as large as a peafowl. The peafowl of the genus *Pavo* is represented by the common peafowl; (*Pavo cristatus*) and the green peafowl (*Pavo muticus*).

Unfortunately, I was unable to secure samples of one important group of phasianine birds represented by tragopans, monals and others. Also, in this study, I did not deal with members of the four other subfamilies that together with Phasianinae constitute the family Phasianidae. They were turkeys of the new-world subfamily Meleagridinae, guineafowls of the African subfamily Numidinae and toothed quails and partridges of the new-world subfamily Odontophorinae. Grouses of the old-world subfamily Tetraoninae were also excluded.

2.2 Materials and Methods

Preparation of Cell Lysate and Extraction of DNA.

DNA were extracted from blood samples obtained from live birds with no apparent harm to them.

At least 5 μl of peripheral blood was blotted on a small piece of filter paper (approximately 5 × 5 mm) and kept dry during transportation. Blood was eluted from a filter paper in 500 μl of phosphate-buffered saline. After centrifugation at 5,000 rpm for 2 min, cell pellets were suspended in 100 μl of 10 mM Tris · HCI (pH 8.3) buffer containing 50 mM KCl, 1.5 mM $MgCl_2$ gelatin, 0.45% Nonidet P-40, 0.45% Tween 20, and 200 μg of proteinase K per ml. The suspension was incubated for 30 min at 60° C and was heated at 94° C for 15 min to stop the reaction. The cell lysate was then extracted twice with 400 μl of phenol/chloroform/isoamyl alcohol (25:24:1) and total DNA was dissolved in 200 μl of 10 mM Tris · HCI (pH7.5) buffer containing 1 mM EDTA.

Polymerase Chain Reaction(PCR).

A conserved primer pair, H1255 (5' -CATCTTGGCATCTTCAGTGCCC-3') and L16750 (5' -AGGACTACGGCTTGAAAAGC-3'), was used to amplify the control region for RFLP analysis. L and H refer to light and heavy chains and the number designates the position of the 3' end of the primer in the reference sequence (Desjardins & Morais, 1990).

Two microliters of total DNA or cell lysates was subjected to 35 amplification cycles using *Taq (Thermus aquaticus)* DNA polymerase (Takara Shuzo Co. Ltd.) according to the manufactures' instructions, with denaturation at 94° for 1 min, annealing at 55° C for 1 min, and extension at 72° C for 2 min.

Nucleotide Sequencing.

Because of the presence of an EcoRI site within, the primer HI1254 (5'-ATGAATTCTTGGCATCTTCAGTGCCA-3') was used instead of H1255 to obtain PCR products for cloning. The base sequence of another primer already given, L16775, did contain a *Hind*III site. When the above H1254/L16775 pair was used for PCR amplification, 3.0 mM $MgCl_2$ replaced the 1.5mM concentration recommended. PCR products were digested with *Eco*RI and *Hind*III and purified by agarose gel electrophoresis. Ligation of the DNA segments into the *Eco*RI/*Hind*III site of the cloning vector pUC118, transformation of *Escherichia coli* JM109, and single-strand DNA preparation using the helper phage M13K07 were performed as previously described (Desjardins & Morais, 1991). To minimize errors introduced by *Taq* DNA polymerase during PCR, two or three clones obtained from each sample were used for sequencing. Sequencing was carried out with the BcaBEST dideoxynucleotide sequencing kit (Takara Shuzo Co. Ltd.) using a fluorescein isothiocyanate labeled M13 forward primer (Shimazu Co. Ltd.) and DNA sequencer DSQ1 (Shimazu Co. Ltd.).

Phylogenetic tree reconstruction

The nucleotide sequences obtained were aligned with each other (Figure 2-1), and the number of nucleotide substitutions were estimated by the six-parameter method (Gojobori et al., 1982). A phylogenetic tree was constructed by the neighbor-joining method, using the substitution numbers estimated (Saitou & Nei, 1987). Statistical significance was evaluated by the bootstrapping method (Felsenstein, 1985).

2.3 Results and Discussion

2.3.1 Evolutionary relationships between perdicine and phasianine birds

Sequences at the 392 positions of the mitochondrial control region of 14 species were aligned and are shown in three parts in Figures 2-1 and 2-2 (Fumihito *et al.*, 1994). The 60-base-long unit containing the nearly invariant tetradecamer, AACTATGAATGGTT in its center is duplicated only in members of the genus *Gallus* and no other. Accordingly, the interspecific sequence comparison presently carried out only involved the original of this 60-base-long unit. Further, the roughly 50-base-long region immediately in front of this 60-base-long region or its duplicated copy is hypervariable in all species (Fumihito *et al.*, 1994). In as much as liberal introduction of gaps was needed to maximize interspecific homology of this hypervariable region, it was thought advisable to eliminate this region from the present sequence comparison. Accordingly, the dendrograms of perdicine and phasianine birds shown in Figures 2-1 and 2-2 were drawn based upon differences at a total of 392 positions; positions 1 to 192 and then positions 241 to 441 (307 to 507 or 370 to 570) in the case of *Gallus*, depending upon numbers of copies of the 60-base-long unit individual birds possessed.

2.3.2 The antiquity of generalized perdicine lineages

The antiquity of generalized perdicine lineages (quails and partridges).

The differences at 392 positions of the mitochondrial noncoding control region of five perdicine species are shown at the top of Figure 2-1 and the dendrogram drawn based upon these differences, is shown immediately below. It should be noted that the European grey partridge (*Perdix perdix perdix*) was separated from the rest by the greatest distance. The second in remoteness was the chukar partridge (*Alectoris graeca chukar*). Although the remaining three appeared to be cohorts of one cohesive group, the closest relationship was seen within a pair comprised of representatives of two separate tribes; *Coturnix coturnix japonica* representing the tribe Corturnicini and *Bambusicola thoracica* of the tribe Perdicini (Johnsgard, 1986). Regardless of whether the common quail of the Japanese subspecies and the blue-breasted quail belong to the same genus *coturnix* or to two separate genera, *Coturnix* and *Excalfctoria*, the two belonged to the same tribe. Yet, the distance separating the two appeared slightly greater than that between the common quail and the Chinese bamboo partridge (*Bambusicola thoracica*) in the perdicine dendrogram of Figure 2-1. At any rate, even the closest pair of perdicine species shared identical bases at only 336 of the 392 positions (a mere 85.71% identity), as shown at the bottom of Figure 2-2.

2.3.3 Three distinct branches of phasianine birds

The base sequences of the nine phasianine species are aligned in four rows from the bottom half of Figure 2-1 to the top of Figure 2-2. Adding the base sequences of red and green junglefowls (*Gallus gallus* and *Gallus varius*) previously published (Fumihito *et al.*, 1994), as well as the sequence of the green peafowl (*Pavo muticus*) shown separately at the bottom of Figure 2-2, to the present comparison, the dendrogram of 12 phasianine species was drawn and is shown at the middle of Figure 2-2. It can immediately be seen that the first major division separated the branch made of peafowls of the genus *Pavo*, the great argus and the peacock-pheasant, from the rest of phasianine birds. The remaining birds were further subdivided into two branches. One was made exclusively of members of the genus *Gallus*, while the other was a pheasant branch. In addition to those belonging to genera *Phasianus*, *Chrysolophus* and *Syrmaticus*, gallopheasants of the genus *Lophura* were included in this branch. My phasianine dendrogram shown in the middle of Figure 2-2 is in essential agreement with that previously produced on the basis of classical taxonomic studies (Figure 2-3; Johnsgard, 1986). Unfortunately, those that are thought to be members of the fourth independent branch were not included in the present study. They were tragopans, monals (*Lophophorus*) and the koklass (*Pucrasia*) (Johnsgard, 1986).

2.3.4 Perdicine versus phasianine lineages

I made a number of attempts to construct a combined dendrogram of perdicine and phasianine species studied. In the process, it was found that when two rather distantly related groups are combined, the relative positions of individual species in a dendrogram tend to shift by an addition to or a subtraction from that diagram, of a few species. In as much as my survey is by no means comprehensive, lacking representation from a few key groups as already noted, I concluded that the construction of a combined diagram at this time would be inadvisable.

2.3.5 Paradoxical genetic link between the Chinese bamboo partridge and members of the genera *Gallus* and *Pavo*

In spite of the extreme meagerness of perdicine species in the present survey, one tangible link emerged between perdicine and phasianine lineages, but this link was a paradoxical one. At the bottom of Figure 2-2, the mitochondrial DNA base sequence of *Bambusicola thoracia* is aligned with that of the green peafowl (*Pavo muticus*) on the one hand and that of the green junglefowl (*Gallus varius*) on the other. Pertinent information extracted from these alignments are shown immediately below them. It can be seen that the Chinese bamboo partridge is genetically far closer to phasianine *Gallus* (87.75% identity) and *Pavo* (89.03% identity) than to its closest perdicine ally, *Coturnix coturnix japonica* (85.71% identity).

A paradox is found in the fact that *Gallus* and *Pavo* belong to two very divergent phasiane lineages as evident in the dendrogram of Figure 2-2 as well as in the fact that there is only 85.02 % sequence identity between *Gallus varius* and *Pavo muticus* (Figure 2-2, bottom). While nearly equal affinities toward *Bambusicola thoracica* were shown by all four species of *Gallus* as well as by both species of *Pavo*, no hint of a close link was seen between *Bambusicola* and other members of the peafowl branch; i.e., *Argusianus argus* and *Polyplectron bicalcaratum*.

2.3.6 Evolutionary features of Chinese bamboo partridge

Poul A. Johnsgard, in his authoritative treatise on the subject "The Pheasants of the World" follows the customary subdivision of the subfamily Phasianinae to Perdicini and Phasianini (Johnsgard, 1986). Yet, he is of the opinion that four branches of phasianine birds sprang independently from generalized perdicine ancestors. This view is succinctly illustrated in his dendrogram shown in Figure 2-3 (Johnsgard, 1986). Indeed, the present study established one direct link between a particular perdicine lineage represented by *Bambusicola thoracica* and two phasianine genera *Gallus* and *Pavo*. The only problem was that *Gallus* and *Pavo* belong to two very divergent phasianine branches. It is quite conceivable that *Bambusicola* with only two extant species, Chinese bamboo partridge (*B. thoracica*) and Bamboo partridge (*B. fytchii*) belongs to one stem of the perdicine lineage which later split into two phasianine-yielding sublineages; one being ancestral to *Gallus*, with the other giving rise to *Pavo* and related genera. If so, one might expect to locate a species or species belonging to one or the other of the above phasianine-yielding sublineages among close relatives of *Bambusicola*. The most attractive in this respect are three species of *Galloperdix*. If the implication from its generic name holds true, they might show even closer affinity to *Gallus* than *Bambusicola*, while manifesting little affinity to *Pavo*. Unfortunately, all attempts to secure samples of *Galloperdix* which inhabit India and Sri Lanka failed.

There is however an independent line of evidence that links *Bambusicola* with *Gallus*. In 1949, Yamashina classified the chromosome complements of members of the subfamily, *Phasianinae*, to four major types. Although the karyotype of *Bambusicola*, *Coturnix* and *Gallus* were found to belong to the same type, *Pavo* was found to belong to a different type (Figure 2-4; Yamashina, 1949).

2.4 Summary

Further comparison of mitochondrial control region DNA sequences of 16 avian species belonging to the subfamily, *Phasianinae*, revealed the following: (1) Generalized perdicine birds (quails and partridges) are descended from ancient lineages. Even the closest pair, the common quail of the Japanese subspecies (*Coturnix coturnix japonica*) and the Chinese bamboo partridge (*Bambusicola thoracica*), maintained only an 85.71% identity. (2) The 12 species of phasianine birds previously and presently studied belonged to three distinct branches. The first branch was made exclusively of members of the genus *gallus*, while the second branch was made of pheasants of the genera *Phasianus, Chrysolophus* and *Syrmaticus*. Gallopheasants of the genus *Lophura* were distant cousins to these pheasants. The great argus (*Argusianus argus*) and peafowls of the genus *Pavo* constituted the third branch. Members of the fourth phasianine branch, such as tragopans and monals were not included in the present study. (3) The one perdicine species, *Bambusicola thoracica*, was more closely related to the phasianine genera *Gallus* and *Pavo* than to members of other perdicine genera. The above might indicate that *Bambusicola* belongs to one stem of the perdicine lineage which later split into two sublineages that yielded phasianine birds; one evolving to *Gallus*, with the other differentiating toward *Pavo* and related genera.

Chapter 3.

Evolutionary Relationships between Red and Green Junglefowls

3.1 Introduction

There is little doubt that the domestication of various wild animals as beasts of burden, sources of protein and fat, and instruments of war and recreation has played a pivotal role in the cultural evolution of mankind. Of special interest has been the divine rites performed in association with various domesticated animals, particularly the chicken. For documentation of so recent an event as domestication, nuclear genes with their low mutation rate would be of little use. On the contrary, the mitochondrial genome appears particularly suitable. Its high mutation rate is expected to be constant, being relatively impervious to generation time differences between species. It may be recalled that an organism does not start its life with a single copy but with hundreds of thousands of copies of the mitochondrial genome harbored in the egg cytoplasm. Accordingly, generation changes do not constitute significant epochs in the life history of mitochondrial DNA. Furthermore, an extremely useful marker for measurement was established in recent studies on two hypervariable subregions of the control region of human mitochondria. The average sequence divergence between all races of mankind was established as 2.0% and the rate of evolution was estimated to be 1% sequence divergence per 71,000-167,000 years (Cann *et al.*, 1987; Vigilant *et al.*, 1989). Under the assumption that the rate of human mtDNA divergence is almost comparable to that of domestic species mtDNA, it follows that any mitochondrial sequence divergence substantially above 2.0% within a given domesticated species creates a peculiar paradox of either domestication occurring before the emergence of mankind or at least domestication occurring within the African cradle before the exodus of certain bands to the Near East and outward.

Indeed, such a paradox was encountered in a recent study on the mitochondrial control region of various breeds of cattle. Two distinct mitochondrial lineages separated by a 5.01% sequence difference were observed. This paradox was resolved by the assumed presence of two subspecies of an ancestor of cattles, the aurochs *(Bos primigenius),* prior to the emergence of humans and the two subsequent independent domestication events after human divergence (Loftus *et al.*, 1994).

In view of the above data, I decided to study the control region light chain (L chain) of the avian mitochondria on various gallinaceous birds with regards to its restriction fragment length polymorphism (RFLP) as well as the sequence of the first 400 bases of the control region. In human studies, 64% of total polymorphism in the entire control region was found among the first 400 bases (di Rienzo & Wilson, 1991).

3.2 Materials and Methods

Materials.

Materials used for the present study are summarized in Table 3-1. Red junglefowls (*G. g. gallus* and *G. g. spadiceus*) were gifts from the Department of Forestry of the Thai government. Five specimens of *G. g. bankiva* were obtained from the Indonesian island of Java, and so are all of the green junglefowl (*Galls varius*). Four additional Thai red junglefowl sampled were from those kept in the Tama Zoological Garden (Tokyo). Of various domestic breeds, samples from all those classified as "occidental breeds" were collected at The Domestic Fowl Trust of England. As to Asiatic breeds, those starting with "*ayam*" were all Indonesian breeds and were collected there. Others were either collected in their native habitats or obtained from one of the following three institutions in Japan: Yamashina Institute for Ornithology, The Research Institute of Evolutionary Biology, or Hiroshima Animal Husbandry Experimental Station.

Detection of RFLP.

After testing 36 restriction enzymes, the following four were chosen as suitable: *Alu* I (recognition sequence, AGCT), *Mse* I (TTAA), *Mbo* II (TCTTC), And *Vsp* I (ATTAAT). RFLPs were detected on either 1.5% or 4.0% agarose gels after 30 min to 1 hr of electrophoresis at 80 V.

Most other methods, such as preparation of cell lysate and extraction of DNA, PCR and nucleotide sequencing are described in Chapter 2.

3.3 Results and Discussion

3.3.1 RFLP within the 1200- to 1300-base control region

As noted in *Materials and Methods*, four restriction enzymes recognized polymorphic cleavage sites within the control region, thus yielding different sized fragments readily distinguishable by gel electrophoresis. These four restriction enzymes were *Vsp* I, *Alu* I, *Mse* I, and *Mbo* II. Inasmuch as the last two enzymes recognized two polymorphic sites each, a total of six sites were involved in RFLP(Table. 3-1). The first four polymorphic sites are shown in Figure 3-1. Of the potential 64 (2^6) types involving the six sites, eight were found among domestic breeds and their wild ancestors, red junglefowls. Six additional types were seen among more distantly related green junglefowls. Thus, 14 of the 64 potential types are in existence today.

Table. 3-1 shows that regardless of whether they belong to breeds long established in the West (Europe and North America) or to breeds that remained in Asia, the predominant RFLP type among domesticated chickens was type V, closely followed by type I. While type V was also found in more than half of the red junglefowls of the three subspecies sampled, types I, II, and IV have not thus far been found among red junglefowls. Conversely, type VII has been confined to one subspecies of Thai red junglefowl (*G. g. spadiceus*) in spite of the sampling of >27 diverse domestic breeds. Of particular interest was type VIII. Among domesticated chickens, this type was seen only in those breeds which had originated in Indonesia. At the same time, 1 of the 19 red junglefowls exhibiting RFLP type VIII was also of Javanese origin. The above data might be interpreted as an indication of multiple sites of domestication - i.e. , Indonesia starting from the independent regional domestication of *G. gallus bankiva*. In the past, various population studies utilizing isozymes as well as blood group polymorphisms suggested such multiple and independent sites of domestication (Hashiguchi *et al.*, 1983).

The green junglefowl (*G. varius*) manifested its own polymorphism composed of six allelic forms, here designated as types A,B,C,D,E, and F. However, Table. 3-1 shows that while the second *Mbo* II site in all individuals of *G. gallus* was cleavable by the enzyme, the corresponding site in all 30 *G.varius* was not. If one excludes this second *Mbo* II site from consideration type I of *G. gallus* now becomes the same as type A of *G.varius* and the same applies to type II and type B. The above suggests that RFLP observed in *G. gallus* and *G. varius* has been a very ancient polymorphism antedating the separation of *G. gallus* from *G. varius*.

3.3.2 Tandem duplication of 60-base unit within the control region as a genus-specific trait of Gallus

Before comparison of base sequences with regard to the first 400 bases of the control region L chain, the tandem duplication of one 60-base unit in members of the genus *Gallus* as a genus-specific trait should be noted. The control region base sequence of white leghorn (Desjardins & Morais, 1990) and that of the common quail of the Japanese subspecies *Coturnix coturnix japonica* (Desjardins & Morais, 1991) have been published, and it was shown that the control region of the latter was 41 bases shorter than that of the former. My own sequencing of type I white leghorn and Japanese quail produced only one discrepancy from the published sequences noted above. The base triplet CCC underlined in the first section of Figure 3-1 was missing from the published sequences of both white leghorn (Desjardins & Morais, 1990) and Japanese quail (Desjardins & Morais, 1991).

As shown in the fifth section of Figure 3-1 (marked "Original"), the 60-base unit containing the invariant tetradecamer AACTATGAATGGTT in its center is present as a single unit in the quail, whereas tandem duplication of this unit was observed in all 11 *G. gallus* as well as all four *G. varius* individuals. In Figure 3-1, a copy of the original located immediately upstream is marked "1st copy." Also I found this duplication to be present in the third and fourth members of the genus *Gallus*: the grey junglefowl (*Gallus sonnerati*) and Cingalese junglefowl (*Gallus lafayettei*). Yet, their closest relatives, various pheasants of the genus *Phasianus*, were quail-like, having this 60-base unit in a solitary state. Among members of the family Phasianidae, pheasants were thought to be far more closely related to the chicken than quails are, as evidenced by the fact that pheasant-chicken hybrids are fully viable, albeit sterile, whereas only 0.15-2.0% of incubated eggs produce live chicken-Japanese quail hybrids (Haley, 1965). Yet, the sequence comparison between the original and its first copy on every one of the 15 sequenced individuals of *G. gallus* and *G. varius* indicated that the average difference was 20%. Interestingly the sequence difference between originals of the Japanese quail and of *Gallus* was 25%. On the basis of the above noted evidence, it appears that duplication of the 60-base-long unit has taken place immediately after the genus *Gallus* came into being. Tandem repeats within the control region of mitochondrial DNA have previously been reported in two papers: 79-base tandem repeats in three subspecies of the masked shrew (*Sorex sinreus* : Insectivora) (Stewart & Baker, 1994) and 10-base tandem repeats in canine mitochondrial DNA (Tsuchida *et al.*, 1994).

Once duplication started, further duplication would have been inevitable (Ohno, 1970). Indeed, one extra copy of the 60-base unit was found in three green junglefowl of RFLP type C, while two extra copies were found in one green junglefowl of RFLP type E (Table 3-1 and Figure 3-1). One each of these individuals with one and two extra copies was sequenced. When sequence comparisons were made between the original of green junglefowl nos. 32 and 50 and their own "second extra copies," a uniform sequence difference of 13.1% was noted. The above data revealed that the initial further duplication that produced a second extra copy from the original was a rather ancient affair, probably antedating the speciation of *G. varius*. Indeed, the presence of the second extra copy was also noted in certain individuals of *G. sonnerati* as well as *G. layfayettei*. The generation of the "third extra copy" by green junglefowl no. 50, on the other hand, was a very recent event, for it differed only by a single base substitution from the second extra copy of the same individual (Figure 3-1).

3.3.3 Sequence Differences Between *G. varius* and *G. gallus* and Affinity of All Domestic Breeds to the Thai Red Junglefowl (*G. g. gallus*).

Of the four *G. varius* individuals sequenced, two (nos. 6 and 32) were of the same RFLP type C. In spite of the fact that the latter was endowed with the second extra copy, these two demonstrated the least sequence divergence at 1.50%. Furthermore, all the substitutions were transitions (Figure 3-1). In view of the considerable antiquity of the second extra copy already discussed, this probably means the recent loss of the second extra copy by the lineage represented by no. 6. The difference between these two RFLP type C individuals and no. 2 of RFLP type D increased to 2.25%, while a 3.20% sequence difference separated no. 50 of RFLP type E from the rest. Furthermore, these differences included a few transversions (Figures 3-1 and 3-2).

In contrast to the green junglefowl (*G. varius*), which is a local species confined to the Indonesian Islands, the red junglefowl (*G. gallus*) inhabits a very large area: the Asian mainland stretching from northeastern India in the west to the western coast of China to the east. In addition, its range includes various Indonesian Islands where it is sympatric with *G. varius* as well as Hainan Island in the South China Sea. It is no surprise that *G. gallus* has often been subdivided into five subspecies (Zeuner, 1963).

As shown in Figure 3-1, when dealing with different subspecies, the same RFLP type was no indication of genetic similarity. Both red junglefowl no. 15 and the domestic breed *ayam pelung* no. 76 were typed as RFLP type VIII and they were from the same Indonesian island. Yet, a 5.75% sequence divergence separated the two. Furthermore, 9 of the 23 substitutions were transversions (Figure 3-1). The above clearly excluded the involvement of *G. gallus bankiva* from the domestication event. In sharp contrast, all three Thai red junglefowls (two *G. g. gallus* and one *G. g. spadiceus*) were very close to all breeds of domestic chicken. The closest affinity, of only 0.5% (one each of transition and deletion) difference, was seen between Thai red junglefowl no. 11 of RFLP type V and a member of the Indonesian breed, *ayam cemani,* of the same RFLP type (Figure 3-3). From phylogenetic trees constructed by the Unweighted Pairwise Grouping (UPG) method (Figure 3-2) and the Neighbor Joining (NJ) method (Figure 3-4), of three subspecies of red junglefowls, *G. g. gallus* (Thai nos. 8 and 11) was far more closely related to *G. g. spadiceus* (Thai no. 3) from the adjacent area than to *G. g.bankiva* from Java (Indonesian no. 15). Nevertheless, a transversion was involved in the difference between the first two and RFLP type VII was unique to *G. g. spadiceus.*

3.3.4 Evolutionary relationships between junglefowls and domestic fowls

Because of findings at the well-known Mohenjo-Doro site in Pakistan, it was believed for a long time that the original domestication of the chicken occurred in the Indus Valley 4,000 years ago (Zeuner, 1963). Subsequently, however, earlier signs of domestication were found in unlikely places far removed from the habitat of junglefowls-e.g., Ukraine and Spain, dated at more than 4,000 years ago (West & Zhou, 1988). Indeed, the earliest time of domestication of the chicken was pushed back to nearly 8,000 years ago. Remains of domesticated chickens were evident in 16 neolithic sites along the Huang He (Yellow River), Peiligan and Cishan, rivers in Northeast China (Figure 3-4), and some of these sites were dated to be at least 7,500 years old (West & Zhou, 1988). Inasmuch as the semiarid steppe environment of these loess highlands of North China has never been a suitable habitat for red junglefowls, the time and place of the original domestication is probably earlier and further to the south and the west. The present findings place the original site of domestication in the area inhabited by a single subspecies of the red junglefowl (*G. g. gallus*). However, as it would be shown shortly, our subsequent studies revealed no genetic distinction between continental populations of *G. g. gallus* and *G. g. spadiceus*. *G. g. gallus* inhabiting the island of Sumatra, on the other hand, was distinct from the first two.

In studying sequence divergence of the human mitochondrial DNA control region, Vigilant *et al.* (Vigilant *et al.*, 1989) noted that while all intraspecific base substitutions were transitions, the difference between humans and chimpanzees involved a number of transversions. Accordingly, the observed sequence divergence of 13.6% between the two species was converted to a 42% difference by regarding each transversion as an equivalent of 10 transitions in accordance with Nei (Nei, 1987). In the present study, I found that not only interspecific differences, but also intraspecific differences within *G. varius* involved transversions. This was also true of differences between three subspecies of *G. gallus* (*G. g. gallus* and *G. g. spadiceus* combined as one subspecies and *G. g. bankiva*). In sharp contrast, all differences within one combined subspecies (*G. g. gallus* and *G. g. spadiceus*) and diverse domestic breeds were transitions (Figure 3-3).

Among the diverse domestic breeds presently studied, the greatest sequence divergence, 2.75%, separated two breeds of RFLP type I from that of RFLP type VIII. This was considerably more than the 1.25% that separated two individual *G. g. gallus* from Thailand. The sampling of this subspecies from distant areas such as Sumatra Island is expected to expand the scope of data on intrasubspecific diversity. It would thus appear that this subspecies alone may have yielded all the diverse breeds of domestic chicken, provided that not only the mainstream RFLP type V but also a number of hens of other RFLP types contributed to the domestication event.

3.4 Summary

The noncoding control region of the mitochondrial DNA of various gallinaceous birds was studied with regard to its RFLP and sequences of the first 400 bases.

Tandem duplication of the 60- base unit was established as a trait unique to the genus *Gallus,* which is shared neither by pheasant nor by quail. Unlike its close ally, green junglefowl (*Gallus varius*), the red junglefowl *Gallus gallus* is a genetically very diverse species; the 7.0% sequence divergence was seen between those from Thailand *(G. g. gallus and G. g. spadiceus)* and that from the Indonesian island of Java *(G. g. bankiva).* Furthermore, the divergence increased to 27.83% when each transversion was regarded as an equivalent of 10 transitions. On the other hand, a mere 0.5-3.0% difference (all transitions) separated various domestic breeds of the chicken from two subspecies of *G. g. gallus* of Thailand, thus indicating a single domestication event in the area inhabited by this subspecies with the red junglefowl being the origin of all domestic breeds. Only transitions separated six diverse domesticated breeds. Nevertheless, a 2.75% difference was seen between RFLP type I breeds (white leghorn and nagoya) and a RFLP type VIII breed (*ayam pelung*). The above data suggests that although the mitochondrion of RFLP type V was the main contributor to domestication, hens of other RFLP types also contributed to this event.

Chapter 4.

Evolutionary Origin and Dispersal Patterns of Domestic Fowl

4.1 Introduction

4.1.1 Purpose of Study

There is little doubt that the successive domestication of various wild animals contributed greatly to the sustenance and cultural developments of mankind. In particular, the domestication of chickens seems to have a long history. As I mentioned in chapter 3, the earliest sign of domestication of the chicken is estimated to be nearly 8,000 years ago, because remains of domesticated chickens were evident in 16 neolithic sites along the Huang He (Yellow River) in Northeast China and some of these sites were dated to be at least 7,500 years (West & Zhou, 1988). The domestication of chickens has also been observed at the well-known Mohenjo-Doro site in the Indus Valley in Pakistan (Zeuner, 1963). Moreover, earlier signs of domestication of the chicken were found in unlikely places, far distant from the habitat of junglefowls - e.g., Ukraine and Spain (West & Zhou, 1988).

Accordingly, the question of whether the domestication of junglefowls occurred only once in a fixed site or occurred repeatedly in different locations had been raised time and again. In fact, various population studies utilizing isozyme polymorphism suggested multiple and independent sites of domestication (Hashiguchi *et al.*, 1983).

As I noted in chapter 3, I studied the noncoding region of the mitochondrial DNA of various gallinaceous birds with regard to RFLP and sequences of the first 400 bases. I then showed that while a 7.0% sequence divergence was seen between *G. g. bankiva* which inhabits the Indonesian island of Java and two other subspecies of *Gallus gallus*, both inhabitants of Thailand (*G. g. gallus* and *G. g. spadiceus*), a mere 0.5 - 3.0% difference separated three domestic breeds of the chicken from divergent geographical origins in two subspecies of *G. g. gallus* of Thailand. Thus, I indicated the strong possibility that a single domestication event took place in Thailand and its immediate surroundings (Fumihito *et al.*, 1994). In as much as the sequence divergence between two individuals of *G. g. gallus* from Thailand was 1.25%, it was concluded that this subspecies alone had been sufficient to yield all the diverse breeds of domestic chicken (Fumihito *et al.*, 1994). However, since this conclusion has been drawn from a limited number of *G. gallus* subspecies and domestic fowls, it was felt that the validity of the above conclusion should be verified by a more expanded survey.

4.1.2 Geographical distribution of junglefowls

With the aim of elucidating in more detail, the genealogical origin of the present domestic fowls in the world, I determined mitochondrial DNA (mtDNA) sequences of the D-loop regions for a total of 21 birds which belong to three subspecies of *Gallus gallus* (6 *G. g. gallus,* 3 *G. g. spadiceus* and 3 *G. g. bankiva*) and 9 domestic breeds and/or races (*G. g. domesticus*) such as white leghorn. Also, sequencing was done at the same regions of mtDNA for all other *Gallus* species (4 *G. varius*, 2 *G. lafayettei*, and 1 *G. sonnerati*). A phylogenetic tree was constructed using these sequence data. The phylogenetic tree constructed verified the previous conclusion that the genealogical origin of the domestic fowls is monophyletic descending from a combined continental population of *G. g. gallus* and *G. g. spadiceus.* I shall also discuss the possible significance of the initial dispersal pattern of the present domestic fowls, utilizing the phylogenetic tree.

4.2 Materials

The species which I examined in the present study are listed in Table 4-1. Three subspecies of *Gallus gallus* were represented by 6 specimens from *G. g. gallus*, 3 from *G. g. spadiceus*, and 3 from *G. g. bankiva.* Nine specimens were from diverse domesticated breeds. Moreover, we examined 3 other species of junglefowls of the genus *Gallus.* They were 4 specimens of *G. varius,* 2 of *G. lafayettei*, and 1 of *G. sonnerati.*

4.3 Results and Discussion

4.3.1 Evolutionary relationships among four species in the genus *Gallus*

The genus *Gallus* is comprised of four species, *G. gallus, G. varius, G. lafayettei*, and *G. sonnerati*. Their phylogenetic relationship shown in Figure 4.2 is consistent with the result of chapter 2 (Fumihito *et al.*, 1995) in which the dendrogram was constructed by using of only one specimen from each species. At first glance, *G. varius* appears to be the most divergent of the four species. However, the bootstrap value that sets this species apart is only 34.7%. Accordingly, it is likely that *G. varius, G. gallus, G. sonnerati,* and *G. lafayettei* branched out from a common stem almost simultaneously in the evolutionary time scale. Taking into account the phylogenetic tree in Figure4.2 in my previous report (Fumihito *et al.*, 1995) together with the present results, I speculate that shortly after the split, *Gallus* of the Indian subcontinent yielded *G. sonnerati* and *G. lafayettei.*

In my first paper of this series (Fumihito *et al.*, 1994), I found that a 60-base-long unit containing the nearly invariant tetradecamer, AACTATGAATGGTT in the center of the D-loop region is duplicated only in members of the genus *Gallus* and no other phasianine birds. Furthermore, more than two copies of this unit were found in three of the four *Gallus* species. In the case of *G. varius* , while 2 copies were found in two individuals, 3 and 4 copies were found in the remaining two. All specimens of *G. lafayettei* as well as *G. sonnerati* had 3 copies. Of particular significance was the fact that all 12 specimens of *G. gallus* have 2 copies, irrespective of subspecies. These observations on copy numbers of the 60-base-long unit are consistent with the above assumed order of divergence of the 4 species. All 9 domestic fowls examined had the same copy number as *G. gallus*, again implying that the genealogical origin of the domestic fowls is monophyletic descending from *G. gallus* alone.

4.3.2 A single cluster comprising a continental population of G. g. gallus and G. g. spadiceus

As shown in Figure 4-2, *G. g. gallus* and *G. g. spadiceus* do not form two separate clusters in the phylogenetic tree. It seems that *G. g. gallus* is divided into two separate populations; an island population from Sumatra which is distinct from the continental population. *G. g. spadiceus* is more closely allied with a continental population of *G. g. gallus* than an island population of *G. g. gallus* is to its continental relation. Thus, the subspecies status given to *G. g. spadiceus* might be questioned. On the other hand, *G. g. bankiva* which inhabits the Indonesian islands of Sumatra, Java and Bali is a very distinct entity that is clearly separate from *G. g. gallus* as well as *G. g. spadiceus*, thus, its subspecies status appears to be well deserved.

4.3.3 Geographical differentiation of *G. g. gallus* and *G. g. spadiceus* and domestic fowls

West and Zhou (West & Zhou, 1988) suggested that chickens were first domesticated in Southeast Asia and were taken north to become established in China, possibly spreading to European Celts via tribes of the Russian steppe. The phylogenetic tree (Figure 4-2) seems to be consistent with their contention for the following reasons.

According to the phylogenetic tree (Figure 4-2), domestic fowls including Indonesian races belong to the same cluster as continental populations of *G. g. gallus* and *G. g. spadiceus* sampled from Thailand and its adjacent areas. On the other hand, 3 specimens of *G. g. gallus* from South Sumatra form a separate cluster as already noted, yet native domestic fowls from the same island belong to the cluster in which a continental population of *G. g. gallus* and *G. g. spadiceus* from Thailand was included; e.g., two *ayam kokok balenggek* from West Sumatra. Accordingly, a domestication event in Sumatra from that of its own *G. g. gallus* can be excluded. It suggests that the original domestication took place in Thailand and its adjacent regions and subsequently dispersed to West Sumatra in Indonesia.

West Sumatra in Indonesia is known as Minangkabau. It is worth noting that the people of Minangkabau have developed a unique culture and *ayam kokok balenggek* was adopted as a symbol of the Solok prefecture in Minangkabau (Fumihito & Tanaka, 1994). It is quite possible that this domestic fowl has been highly esteemed in Minangkabau because of its novelty, implying that *ayam kokok balenggek* had been brought to West Sumatra from elsewhere. These facts support the idea that Indonesian native domestic fowls have been transferred to Indonesia from Thailand and its adjacent regions.

4.3.4 Sequence differences between *G. g. bankiva* and other *Gallus gallus* subspecies

It is clear from Figure 4-2 that *G. g. bankiva* is a very distinct entity apart from *G. g. gallus* and *G. g. spadiceus* in the phylogenetic tree as already noted. In fact, the numbers of nucleotide substitutions separating *G. g. bankiva* from other two subspecies are quite large compared with the largest individual differences seen within *G. g. gallus* as well as *G. g. spadiceus*. Thus, *G. g. bankiva* is indeed deserving of its subspecies status within the species *Gallus gallus.* Because two other subspecies of *Gallus gallus, G. g. murghi* and *G. g. jabouillei*, were not included in the present study, the validity of their subspecies status still remains an unanswered question.

Nevertheless, the monophyletic origin of domestic fowls from a continental population of *G. g. gallus* appears is evident. The Indus valley where it is evident the domestication of chicken took place at least 4,000 years ago, was and still is the domain of *G. g. murghi.* Yet, the present study indicates that if *G. g. murghi* contributed to an independent domestication event, *G. g. murghi* should be genetically close to some of the domestic fowls examined here. It naturally follows that *G. g. murghi* has to be genetically indistinct from *G. g. gallus* as well as *G. g. spadiceus* of Thailand, thus, relinquishing its subspecies status. The same applies to another subspecies not included in the present study; *G. g. jabouillei.*

4.3.5 Possible significance of the initial dispersal pattern of domestic fowls

As I have shown in the present study, it is likely that all domestic fowls have originated from a single domestication event in Thailand and its adjacent regions. The reason for the domestication of chickens is usually seen as the need to secure readily available sources of protein and fat in the form of eggs and meat. However, there are other aspects. We should not forget that since time immemorial, the chicken has often been associated with various religious services in different parts of the world; e.g. the cock as a harbinger of the sun to rise once again and cockfighting as a divine offering (Crawford, 1984 ; Stevens, 1991). The initial dispersion of domestic fowls might have been due to the religious significance attached to the chicken. In particular, the fact that cockfighting is even now wide spread throughout Southeast Asian countries appears very significant in considering the reasons for the initial dispersion of domestic fowls from the original site of domestication.

I intend to trace this initial dispersion of domestic fowls with highly polymorphic DNA markers. Inasmuch as the religious significance attached to the chicken may have been the primary reason for the initial dispersion of domestic fowls, my future work would be in the realm of ethnozoology.

4.4 Summary

With the aim of elucidating in more detail the genealogical origin of the present domestic fowls of the world, I determined mitochondrial DNA (mtDNA) sequences of the D-loop regions for a total of 21 birds which belong to the red junglefowl (*Gallus gallus*) comprising of three subspecies (6 *Gallus gallus gallus,* 3 *Gallus gallus spadiceus* and 3 *Gallus gallus bankiva*) and 9 birds representing diverse domestic breeds (*Gallus gallus domesticus*) . I also sequenced 4 green junglefowl (*Gallus varius*), 2 Lafayette's junglefowl (*Gallus lafayettei*) and 1 grey junglefowl (*Gallus sonnerati*). We then constructed a phylogenetic tree for these birds using of nucleotide sequences, choosing the Japanese quail (*Coturnix coturnix japonica*) as an outgroup. We found that a continental population of *G. g. gallus* was the real matriarchic origin of all the domestic poultries examined in the present study. It is also of particular interest to note that there were no discernible differences among *Gallus gallus* subspecies; *G. g. bankiva* being a notable exception. This was because *G. g. spadiceus* and a continental population of *G. g. gallus* formed a single cluster in the phylogenetic tree. One obvious and distinct feature that customarily separated *G. g. gallus* from *G. g. spadiceus* was a color of their car lobes: white for the former and red for the latter. The very fact that domestic breeds of the chicken are of the two kinds as to colors of their ear lobes is a clear reflection of the contribution made by *G. g.*

gallus as well as by *G. g. spadiceus* to their ancestry. An irony is that aside from this very distinct dimorphism, these two do not constitute distinct entities, thus, being undeserving of separate subspecies status. *G. g. bankiva*, on the other hand, was a distinct entity, thus, deserving its subspecies status. This implies that a continental population of *G. g. gallus* sufficed as the monophyletic ancestor of all domestic breeds. We also discussed the possible significance of the initial dispersal pattern of the present domestic fowls, utilizing the phylogenetic tree.

References

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TYP	RFLP						JUNGLEFOWLS	DOMESTIC FOWLS	
	V	A	Ms	Mb	Ms	Mb		ASIATIC	OCCIDENTAL
I	-	-	-	-	+	+		NAGOYA 1/1	WHITE LEGHORN 3/3
								GIFU-JIDORI 2/2	INDIAN GAME 2/2
								BLACK SILKY 1/3	
								THAI BANTAM 5/8	
								AYAM KATAI 1/5	
II	-	-	-	-	-	+		BLACK SILKY 1/3	
III	+	-	-	-	+	+	THAI RED 3/14	THAI BANTAM 3/8	
IV	+	-	-	+	+	+		WHITE LEGHORN(HIROSHIMA VAR.) 1/2	
								TOHMARU 1/2	
								BLACK SILKY 1/3	
V	+	+	-	+	+	+	THAI RED 7/14	WHITE LEGHORN (HIROSHIMA VAR.) 1/2	BARRED PLYMOUTH ROCK 3/3
							INDONESIAN RED 3/5	TOHMARU 1/2	WHITE PLYMOUTH ROCK 1/1
								WHITE SILKY 1/1	RHODE ISLAND RED 1/1
								DARK BRAHMA 1/1	LIGHT SUSSEX 2/2
								MALAY GAME 2/2	BUFF COCHIN 2/2
								SUMATRA GAME 2/2	PARTRIDGE COCHIN 2/2
								AYAM BANGKOK 2/2	SILVER GREY DORKING 2/2
								AYAM BEKISAR 2/4	JERSEY BLACK GIANT 2/2
								AYAM CEMANI 1/2	BROWN LEGHORN 1/1
								AYAM KEDU 2/9	LA FRECHE 1/1
								AYAM PELUNG 1/5	ARAUCANA 1/1
									HOUDAN 2/2
									FAYOMI 1/1
VI	+	+	-	+	-	+	THAI RED 1/14	AYAM CEMANI 1/2	
							INDONESIAN RED 1/5		
VII	+	+	+	+	+	+	THAI RED 3/14		
VIII	+	+	-	-	+	+	INDONESIAN RED 1/5	AYAM BEKISAR 2/4	
								AYAM KATAI 4/5	
								AYAM KEDU 7/9	
								AYAM PELUNG 4/5	
A	-	-	-	-	+	-	GREEN 1/30		
B	-	-	-	-	-	-	GREEN 1/30		
C	-	-	+	-	-	-	GREEN 18/30		
							GREEN 3/30	(60-BASE-LONG INSERTION)	
D	-	-	+	-	+	-	GREEN 2/30		
E	+	-	+	-	-	-	GREEN 3/30		
							GREEN 1/30	(120-BASE-LONG INSERTION)	
F	-	+	-	-	-	-	GREEN 1/30		

Table 3-1 Distribution of 14 RFLP types among 121 individuals of *G. gallus* (red junglefowls and domestic breeds) and *G. various* (green junglefowls) is shown. Mitochondrial control region amplified by PCR contained six polymorphic sites for four restriction enzymes. V, *Vsp* I; A, *Alu* I; Ms, *Mse* I; Mb, *Mbo* II. On the left, each RFLP type is defined as cleavable (+) or not cleavable (-) at each of the six sites. RFLP types of *G. gallus* are numbered in Roman numerals I-VIII, whereas those of *G. varius* are shown as A-F. Nevertheless, types I and II of the former and types A and B of the latter are related (see text). With regard to each wild species and subspecies as well as to each domestic breed, distribution is expressed as number of individuals of a particular RFLP type per total number studied. Aside from 14 Thai red junglefowls (10 *G. g. gallus* and 4 *G. g. spadiceus*) and 5 Indonesian red junglefowls (*G. g. bankiva*) and 30 green junglefowls, 72 individuals representing 26 diverse domestic breeds, 3 of them in 2 varieties each were studied. Although all domestic breeds are ultimately of Asiatic origin, those long established in Europe and the New World were classified as occidental in contrast to those that stayed in Asia.

Species / Subspecies / Races	**Localities**
Gallus gallus bankiva 15	Singaraja, Bali, Indonesia
Gallus gallus bankiva 18	West Jawa, Indonesia
Gallus gallus bankiva 19	Lanpung, East Sumatra, Indonesia
Gallus gallus gallus 8,10	Department of Forestry, Thailand
Gallus gallus gallus 11	Tama Zoological Garden, Tokyo, Japan
Gallus gallus gallus 39,41,58	Palembang, South Sumatra, Indonesia
Gallus gallus spadiceus 3,4,5	Department of Forestry, Thailand
Gallus lafayettei 1,2	Dehiwela Zoo, Dehiwela, Sri Lanka
Gallus sonneratii	India
Gallus varius 2,6	Singaraja, Bali, Indonesia
Gallus varius 32	Madura, Indonesia
Gallus varius 50	Banyuwangi, East Jawa, Indonesia
Gallus gallus domesticus (Ayam Cemani 1)	Surabaya Zoo, Surabaya, East Jawa, Indonesia
Gallus gallus domesticus (Ayam Kokok Balenggek 63,71)	Solok, West Sumatra, Indonesia
Gallus gallus domesticus (Ayam Pelung 76)	Bogor, Jawa, Indonesia
Gallus gallus domesticus (Barred Plymouth Rock 1)	The Domestic Fowl Trust, Worcestershire, UK
Gallus gallus domesticus (Nagoya)	Hiroshima Animal Husbandry Experimental Station, Hiroshima, Japan
Gallus gallus domesticus (Thai Bantam 8)	Thailand
Gallus gallus domesticus (White Leghorn 1)	Quotation from Desjardins & Morais (1990) J.Mol.Biol. 212,599-634
Gallus gallus domesticus (White Leghorn 2)	Hiroshima Animal Husbandry Experimental Station, Hiroshima, Japan
Coturnix coturnix japonica	Hiroshima, Japan

Table 4-1. List of the specimens and their localities.

FIGURE LEGENDS

Chapter 2

Figure 2-1. Multiple alignments and a phylogenetic tree for the mitochondrial control region sequences of five perdicine species, and multiple alignments for the mitochondrial control region sequences of nine of twelve phasianine species.

At the top, the 392 positions (Positions 1 to 192 and positions 241 to 441) of the mitochondrial control region sequences of the five perdicine species are aligned and shown in four rows. The major base of each position is shown by a large capital letter, while minor bases are shown by small capital letters adorned with asterisks. The largely invariant tetradecameric core of the 60-base-long unit is underlined with a solid bar, as is the subsequent, nearly equally invariant decameric unit. The length of the 60-base long unit is also indicated by a thin underline.

Based upon the above sequence comparison, a dendrogram of five perdicine species was drawn in accordance with the neighbor-joining method (Saitou & Nei, 1987) and is shown next. Only shared sites were dealt with and the length of each line indicates the distance from a branch point expressed as the number of base substitutions per site. The bootstrap probability of each estimated distance being correct is expressed as a percentage at each branch point based upon 1,000 replication trials.

At the bottom, nine of twelve phasianine mitochondrial sequences are aligned and continued on the top of Figure 2-2.

Figure 2-2. Multiple alignments and a phylogenetic tree for the phasianine mitochondrial sequences.

The last row of the phasianine mitochondrial sequence alignments continued from Figure 2-1 is followed by the dendrogram of 12 phasianine species. At the bottom, the sequence of the Chinese bamboo partridge (*Bambusicola thoracica*) is shown aligned with the sequence of the green peacock (*Pavo muticus*) on one hand and that of a green junglefowl (*gallus varius*) on the other. At the very bottom, the identity and differences between four pertinent pairs of species are shown. Each identity is shown as a percentage and the number of identical sites per total of 392 is shown in parentheses. Differences are shown as numbers of gaps, transitions and transversions.

Figure 2-3. Dendrogram of postulated evolutionary relationships among the species of pheasants (Illustration after Johnsgard, 1986).

Figure 2-4. Evolutionary tree of phasianidae, based on karyotype analysis (Illustration after Yamashina, 1949).

Chapter 3

Figure 3-1. Multiple alignment for the mitochondrial control region sequences of nine gallinaceous birds.

L-chain sequences of the first 400 bases of the mitochondrial control region from nine gallinaceous birds representing two wild species (*G. gallus* and *G. varius*) and three domestic breeds are aligned using the published Japanese quail (*C. coturnix japonica*) sequence as the reference (Desjardins and Morais, 1991). These nine individuals and their RFLP types are identified on the left. At each polymorphic site, the majority base is shown in a large capital letter, whereas a minority base(s) is shown in small capital letters marked by asterisks. CCC base triplets underlined in the first section were bases missed in two previous publications (Desjardins and Morais, 1990; Desjardins and Morais, 1991). Four polymorphic positions within three potential restriction sites are so indicated, *Vsp* I in the second section, *Alu* I and *Mse* I in the third section, and *Mbo* II in the bottom section. At these sites, cleavable sequences are underlined. The invariant 14-base sequence in the center of each 60-base unit is underlined and so is the invariant 10-base unit residing near the end (last section).

Figure 3-2. Phylogenetic tree constructed by Unweighted Pairwise Grouping (UPG) method, based on sequence divergence with regard to the first 400 bases of the mitochondrial control region of four *G. varius* and two *G. g. gallus* and one each of *G. g. spadiceus* and *G. g. bankiva.* Japanese quail (Desjardins and Morais, 1991) was chosen as the outgroup. Sequence difference is shown as percentage at each branch point. Often larger percentages in parentheses are derived by regarding each transversion as an equivalent of 10 transitions.

Figure 3-3. Polymorphic sites in the mitochondrial control region sequences of junglefowls and domestic fowls.

With regard to two sequenced members of *G. g. gallus* (Thai nos. 8 and 11) and one of *G. g. spadiceus* (Thai no.3) and seven individuals representing six domestic breeds and four RFLP types, individual bases at 24 polymorphic positions are identified. Asterisk at position 317 marks a single instance of transversion (A to C). All other substitutions are transitions. Shown below alignments are sequence differences in percentages of pertinent pairs.

Figure 3-4. Phylogenetic tree constructed by Neighbor Joining (NJ) method. The values given beside the branches indicate the bootstrap probabilities.

Figure 3-5. First places where the domestication occured in the world (Illustration after West & Zhou, 1988).

Chapter 4

Figure 4-1. Multiple alignment of mtDNA sequences for 32 specimens of junglefowls, domestic fowls and the common quail of Japanese subspecies.

Figure 4-2. Phylogenetic tree constructed by the Neighbor Joining (NJ) method, using nucleotide sequence data. The values given beside the branches indicate the bootstrap probabilities.

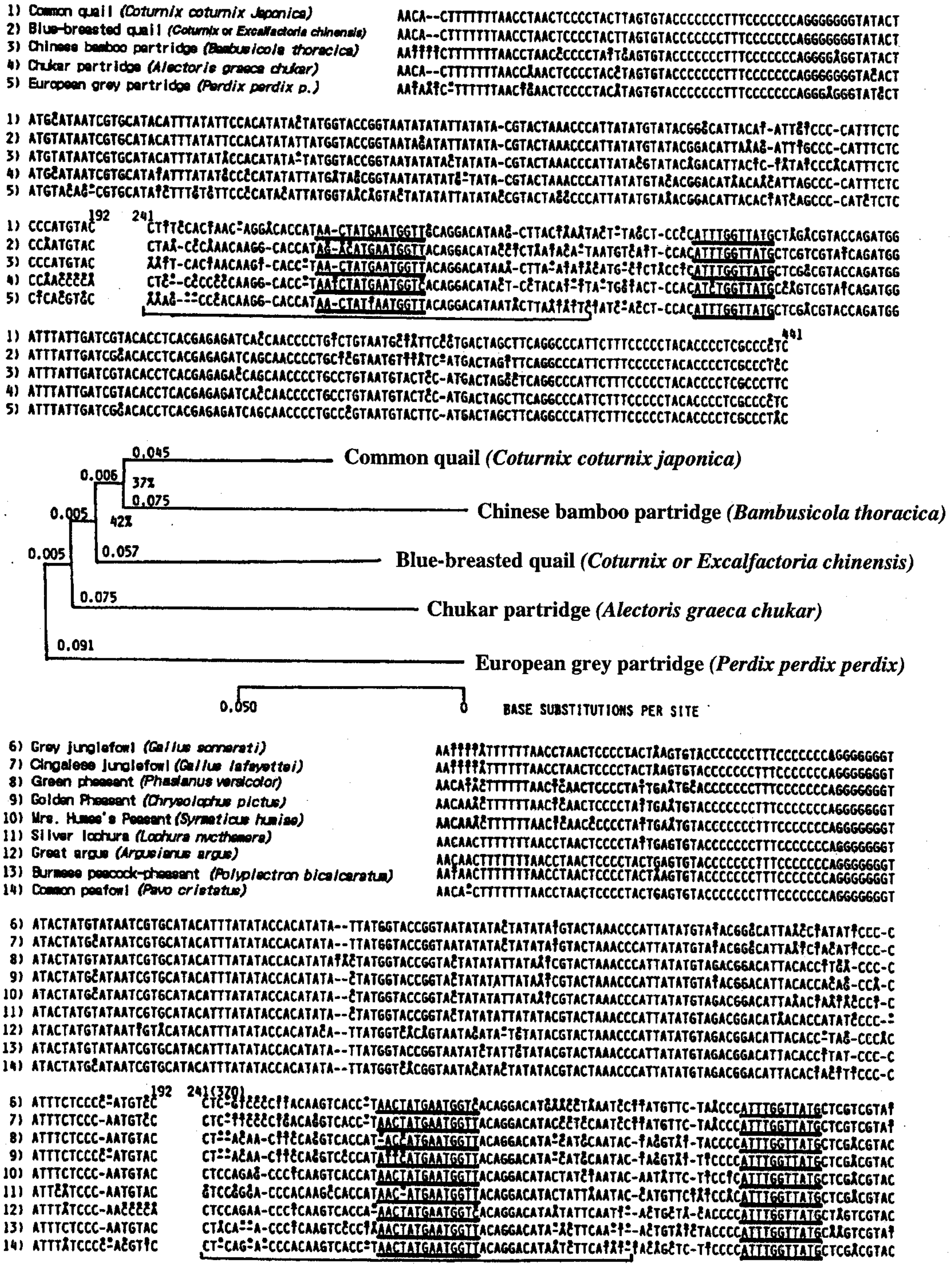
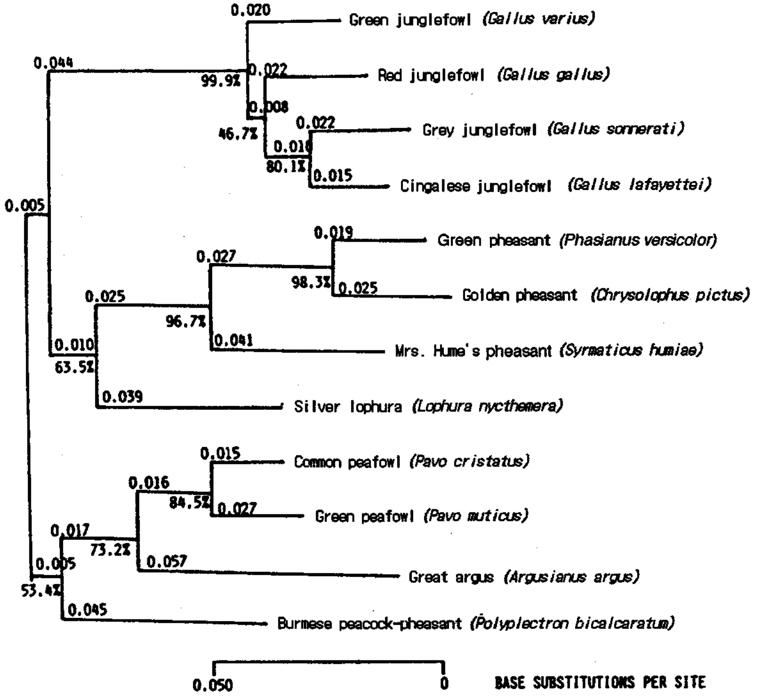

1) Common quail (Coturnix coturnix Japonica)
2) Blue-breasted quail (Coturnix or Excalfactoria chinensis)
3) Chinese bamboo partridge (Bambusicola thoracica)
4) Chukar partridge (Alectoris graeca chukar)
5) European grey partridge (Perdix perdix p.)
192
241
441
0.045
Common quail (Coturnix coturnix japonica)
0.006
37%
0.075
Chinese bamboo partridge (Bambusicola thoracica)
0.005
42%
0.005
0.057
Blue-breasted quail (Coturnix or Excalfactoria chinensis)
0.075
Chukar partridge (Alectoris graeca chukar)
0.091
European grey partridge (Perdix perdix perdix)
0.050
0
BASE SUBSTITUTIONS PER SITE
6) Grey junglefowl (Gallus sonnerati)
7) Cingalese junglefowl (Gallus lafayettei)
8) Green pheasant (Phasianus versicolor)
9) Golden Pheasant (Chrysolophus pictus)
10) Mrs. Humes's Peasant (Syrmaticus humiae)
11) Silver lochura (Lophura nycthemera)
12) Great argus (Argusianus argus)
13) Burmese peacock-pheasant (Polyplectron bicalcaratum)
14) Common peafowl (Pavo cristatus)
192
241(370)

Figure 2-1.

```
                                                                                                                 441
                                                                                                                (572)
 6) CAGATGGATTTATTGATCGTTCACCTCACGAGAGATCAGCAACCCCTGCCTGTAATGTACTTCATGACCAGTCTCAGGCCCATTCTTTCCCCCTACACCCCTCGCCCTACTTG
 7) CAGATGGATTTATTGATCGTTCACCTCACGAGAGATCAGCAACCCCTGCCTGTAATGTACTTCATGACCAGTCTCAGGCCCATTCTTTCCCCCTACACCCCTCGCCCTACTTG
 8) CAGATGGATTTATTGATCGTACACCTCACGAGAGATCACCAACCCCTGCCTATAATGTACTCCATGACTAGCTTCAGGCCCATTCTTTCCCCCTACACCCCTCGCCCTACTTG
 9) CAGATGGATTTATTGATCGTACACCTCACGAGAGATCAGCAACCCCTGCCTGTAATGTACTCTATGACTAGGTTCAGGCCCATTCTTTCCCCCTACACCCCTCGCCCCTCTTG
10) CAGATGGATTTATTAATCGTACACCTCACGAGAGATCACCAACCCCTGTCTGTAATGTATTCCGTGACCAGACTCAGGCCCATTCTTTCCCCCTACACCCCTCGGCCCTCTTG
11) CAGATGGATTTATTGATCGTACACCTCACGAGAGATCAGCAACCCCTGCCCGTAATGTACTTCATGACTAGGTTCAGGCCCATTCTTTCCCCCTACACCCCTCGC
12) CAGATGGATTTATTGATCGTACACCTCACGAGAGATCAGCAACCCCTGCC-GTAATGTACTTCATGACCAGGTTCAGGCCCATTCTTTCCCCTT
13) CAGATGGATTTATTGATCGGACACCTCACGAGAGATCAGCAACCCCTGCC-GTAATGTACGGTATGACTAGGTTCAGGCCCATTCTTTCCCCCTACACCCCTCGCCCTCCTTG
14) CAGATGGATTTATTGATCGTACACCTCACGAGAGATCAGCAACCCCTGCCTGTAATGTACTTCATGACTAGGTTCAGGCCCATTCTTTCCCCCTACACCCCTCGCCCTT
```



```
15) Green peafowl (Pavo muticus)                        AACA--CTTTTTTTAACCTAACCCCCCTACTGAGTGTACCCCCCCTTTCCCCCCCAGGGGGGGTATAC
 3) Chinese bamboo partridge (Bambusicola thoracica)    AATTTTCTTTTTTTAACCTAACCCCCCTATTGAGTGTACCCCCCCTTTCCCCCCCAGGGGAGGTATAC
16) Green junglefowl (Gallus varius)                    AATTTT-ATTTTTTTAACCCAACTCCCCTACTAAGTGTACCCCCCCTTTCCCCCCCAGGGGGGGTATAC

15) TATGCATAATCGTGCATACATTTATATACCACATACATTATGGTCACAGTAATACATACTATATACGTACTAAACCCATTATATGTAGACGGACATTACACTATCTTCCCCATTTATC
 3) TATGTATAATCGTGCATACATTTATATACCACATATATTATGGTACCGGTAATATATACTATATACGTACTAAACCCATTATACGTATACAGACATTACTCTATATCCCACATTTCTC
16) TATGCATAATCGTGTACATATTTATATACCACATATATTATGGTACCGGTAATATATACTATATATGTACTAAACCCATTATATGTATACGGACATTAACCTACATTCCCCATTTCTC

                192   241(307)
15) CCCACGTTC         CCACAACCCACAAGCCACCT AACTATGAATGGTC ACAGGACATAACGTTCA-TATTACAG CTCTCCCCCATTTGGTTATGCTCGACGTATCAGATGGAT
 3) CCCATGTAC         AATTCACTAACAAGTCACCT AACTATGAATGGTT ACGGGACATAAACTTAA-TATACATG CTCTACCTCATTTGGTTATGCTCGGCGTACCAGATGGAT
16) CCCATGTAC         CTACCCCTAACAGGTCACCT AACTATGAATGGTT ACAGGACATACATTTAACTA-CCATG ATCTAACCCATTTGGTTATGCTCGTCGTACCAGATGGAT

                                                                                                           438(503)
15) TTATTGATCGTACACCTCACGAGAGATCAGCAACCCCTGCCTGTAATGTACTTCATGACTAGCTTCAGGCCCATTCTTTCCCCCTACACCCCTCGC
 3) TTATTGATCGTACACCTCACGAGAGACCAGCAACCCCTGCCTGTAATGTACTTCATGACTAGGCTCAGGCCCATTCTTTCCCCCTACACCCCTCGC
16) TTATTGATCGTCCACCTCACGAGAGATCAGCAACCCCTGCCCGTAATGTACTTCATGACCAGTCTCAGGCCCATTCTTTCCCCCTACACCCTTCGC
```

	IDENTITY	DIFFERENCES		
		GAPS	TRANSITIONS	TRANSVERSIONS
Bambusicola thoracica *Coturnix coturnix japonica*	85.71% (336/392)	13	20	23
Pavo muticus *Gallus varius*	86.82% (336/387)	5	21	25
Bambusicola thoracica *Pavo muticus*	88.37% (342/387)	2	20	23
Bambusicola thoracica *Gallus varius*	89.15% (345/387)	3	20	19

Figure 2-2.

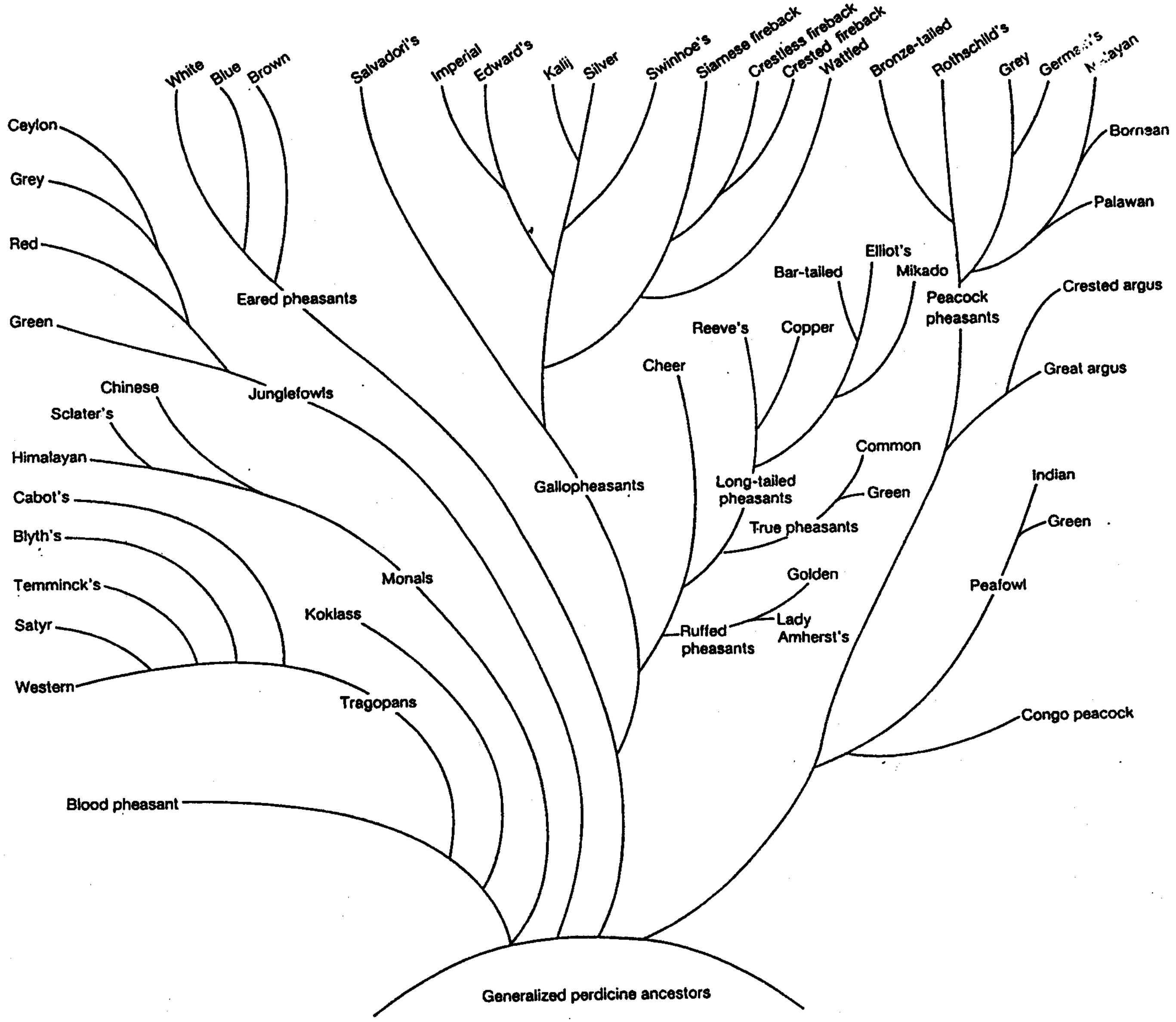

White
Blue
Brown
Salvadori's
Imperial
Edward's
Kalij
Silver
Swinhoe's
Siamese fireback
Crestless fireback
Crested fireback
Wattled
Bronze-tailed
Rothschild's
Grey
Germain's
Malayan
Bornean
Palawan
Ceylon
Grey
Red
Green
Eared pheasants
Junglefowls
Elliot's
Bar-tailed
Mikado
Peacock pheasants
Crested argus
Reeve's
Copper
Cheer
Great argus
Chinese
Sclater's
Himalayan
Cabot's
Blyth's
Temminck's
Satyr
Western
Monals
Koklass
Tragopans
Gallopheasants
Long-tailed pheasants
Common
Green
True pheasants
Indian
Green
Peafowl
Golden
Ruffed pheasants
Lady Amherst's
Congo peacock
Blood pheasant
Generalized perdicine ancestors

Figure 2-3.

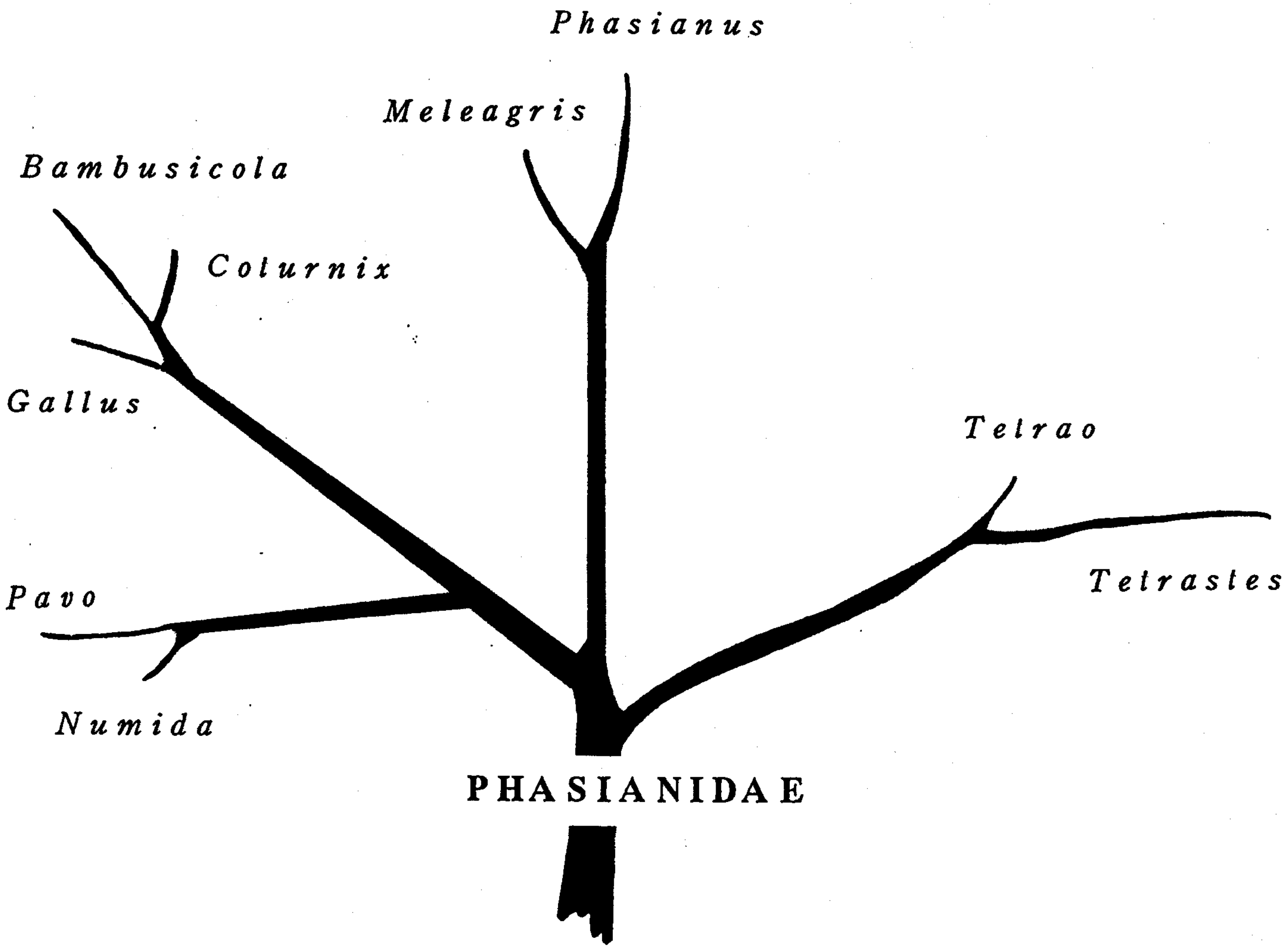
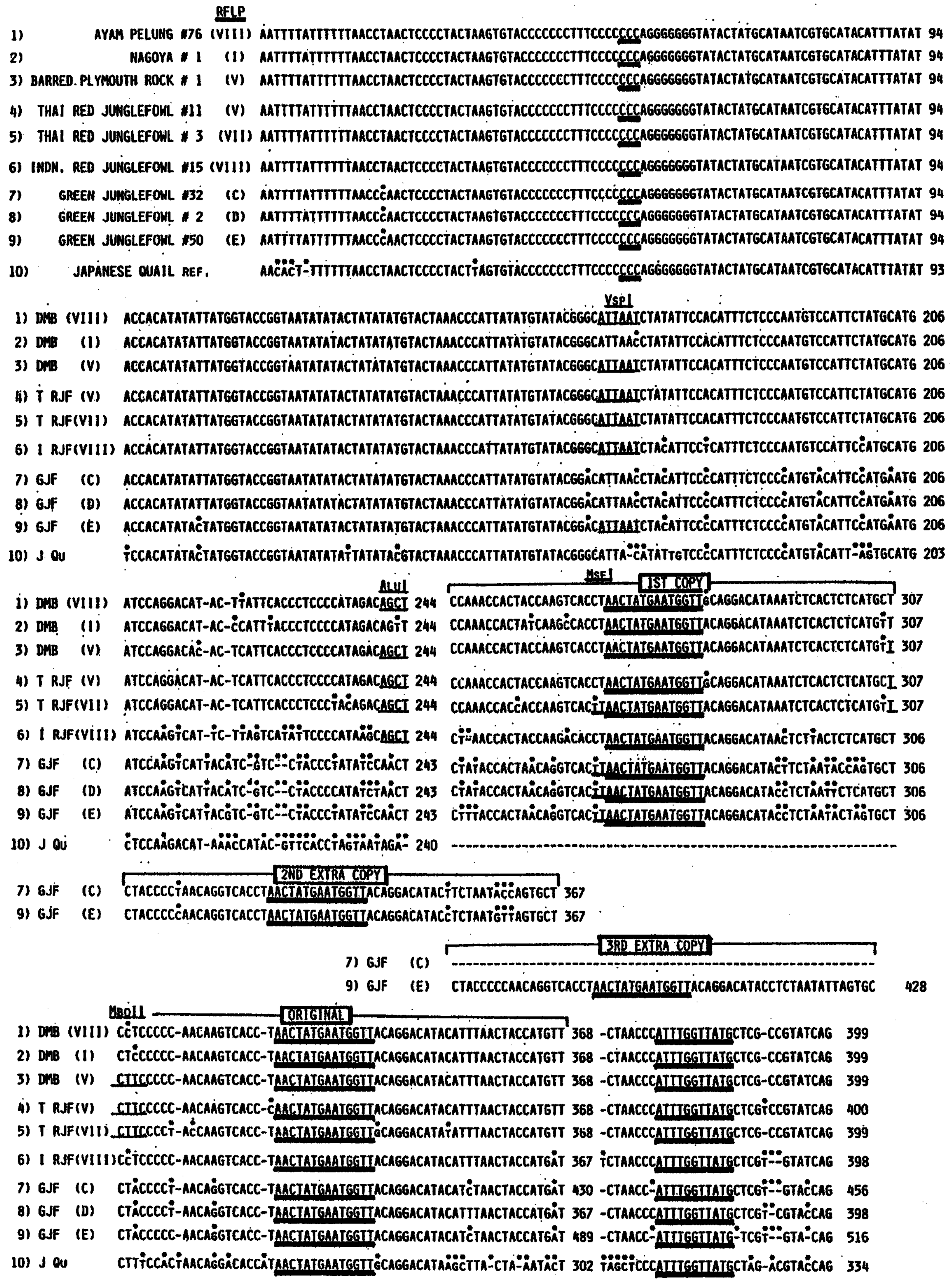

Phasianus
Meleagris
Bambusicola
Coturnix
Gallus
Tetrao
Pavo
Tetrastes
Numida
PHASIANIDAE

Figure 2-4.



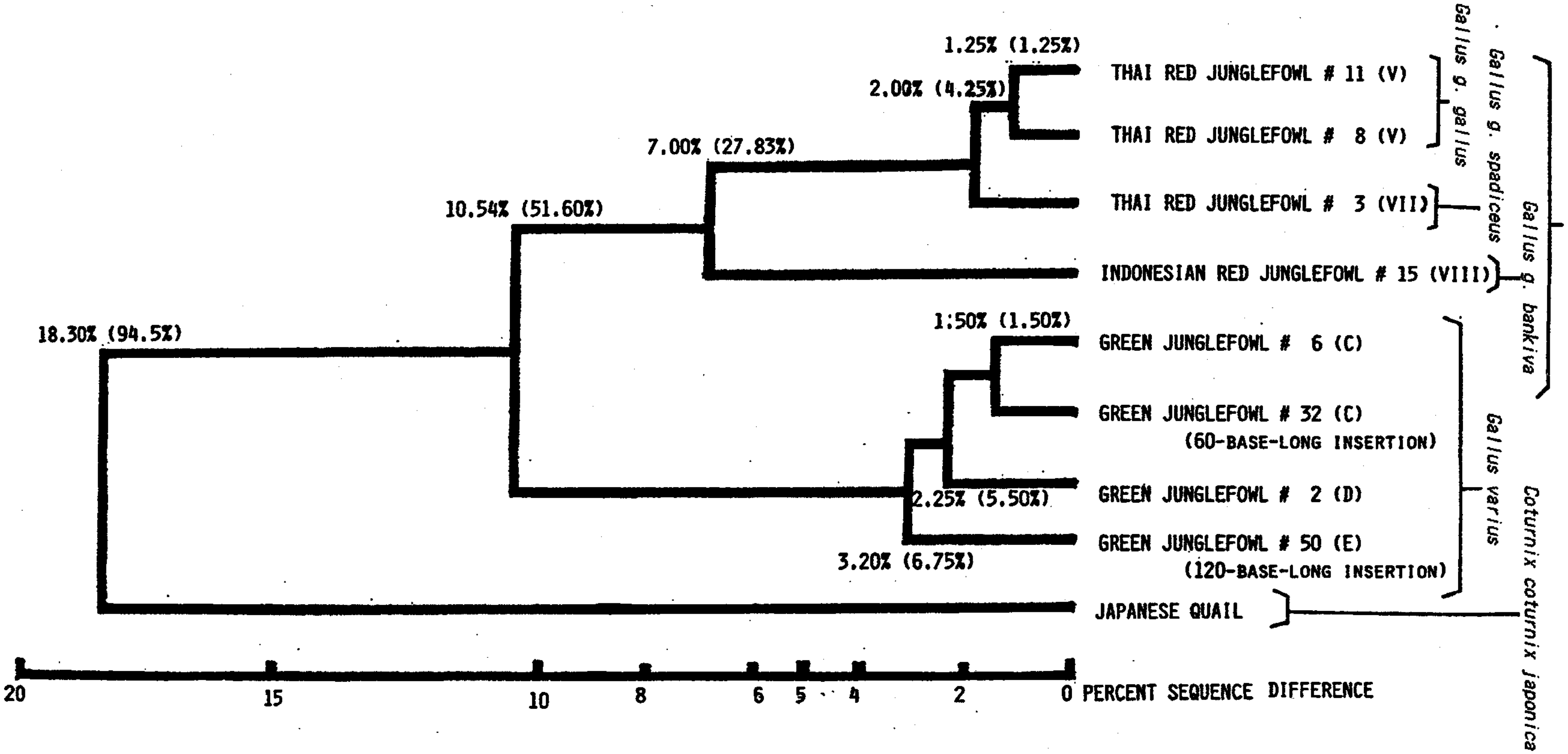

1.25% (1.25%)
2.00% (4.25%)
7.00% (27.83%)
10.54% (51.60%)
18.30% (94.5%)
1.50% (1.50%)
2.25% (5.50%)
3.20% (6.75%)
THAI RED JUNGLEFOWL # 11 (V)
THAI RED JUNGLEFOWL # 8 (V)
THAI RED JUNGLEFOWL # 3 (VII)
INDONESIAN RED JUNGLEFOWL # 15 (VIII)
GREEN JUNGLEFOWL # 6 (C)
GREEN JUNGLEFOWL # 32 (C)
(60-BASE-LONG INSERTION)
GREEN JUNGLEFOWL # 2 (D)
GREEN JUNGLEFOWL # 50 (E)
(120-BASE-LONG INSERTION)
JAPANESE QUAIL
Gallus g. gallus
Gallus g. spadiceus
Gallus g. bankiva
Gallus gallus
Gallus varius
Coturnix coturnix japonica
20
15
10
8
6
5
4
2
0
PERCENT SEQUENCE DIFFERENCE

Figure 3-2.

		167	171	210	217	220	221	225	243	246	254	256	261	265	281	282	306	309	310	315	317	327	342	391'	394'
THAI RED JUNGLEFOWL # 8	(V)	T	C	C	T	T	C	C	C	C	T	C	T	C	G	T	C	T	T	C	A	T	G	-	-
THAI RED JUNGLEFOWL #11	(V)	T	T	C	T	T	C	C	C	C	T	C	T	C	G	C	C	T	T	C	A	C	A	T	-
AYAM CEMANI	(V)	T	T	C	T	T	C	C	C	C	T	C	T	C	G	C	C	T	T	C	A	T	A	-	-
BARRED PLYMOUTH ROCK	(V)	T	T	C	C	T	C	C	C	C	T	C	T	C	A	C	T	T	T	C	A	T	A	-	-
WHITE LEGHORN(HIROSHIMA VAR.)	(V)	T	T	C	C	T	C	C	C	T	T	C	T	C	A	C	T	T	T	C	A	T	A	-	T
WHITE LEGHORN(HIROSHIMA VAR.)	(IV)	T	T	C	C	T	C	C	T	C	T	C	T	C	A	C	T	T	T	C	A	T	A	-	T
THAI RED JUNGLEFOWL # 3	(VII)	T	C	C	T	T	C	C	C	C	C	C	T	T	A	C	T	T	T	T	C	T	G	-	-
AYAM PELUNG	(VIII)	T	T	C	T	T	T	C	C	C	T	C	T	C	G	C	C	C	T	C	A	T	A	-	-
WHITE LEGHORN	(I)	C	T	T	T	T	C	T	T	C	T	T	C	C	A	C	T	T	C	C	A	T	A	-	-
NAGOYA	(I)	C	T	C	T	C	C	T	T	C	T	T	C	C	A	C	T	T	C	C	A	T	A	-	-

THAI RED JUNGLEFOWL # 8 (V)
THAI RED JUNGLEFOWL #11 (V)
1.25% (1.25%)

THAI RED JUNGLEFOWL # 8 (V)
THAI RED JUNGLEFOWL # 3 (VII)
1.75% (4.00%)

THAI RED JUNGLEFOWL #11 (V)
THAI RED JUNGLEFOWL # 3 (VII)
2.25% (4.50%)

THAI RED JUNGLEFOWL #11 (V)
AYAM CEMANI (V)
0.50% (0.50%)

THAI RED JUNGLEFOWL #11 (V)
BARRED PLYMOUTH ROCK (V)
1.25% (1.25%)

THAI RED JUNGLEFOWL # 8 (V)
AYAM PELUNG (VIII)
1.25% (1.25%)

THAI RED JUNGLEFOWL # 3 (VII)
WHITE LEGHORN (I)
3.00% (5.25%)

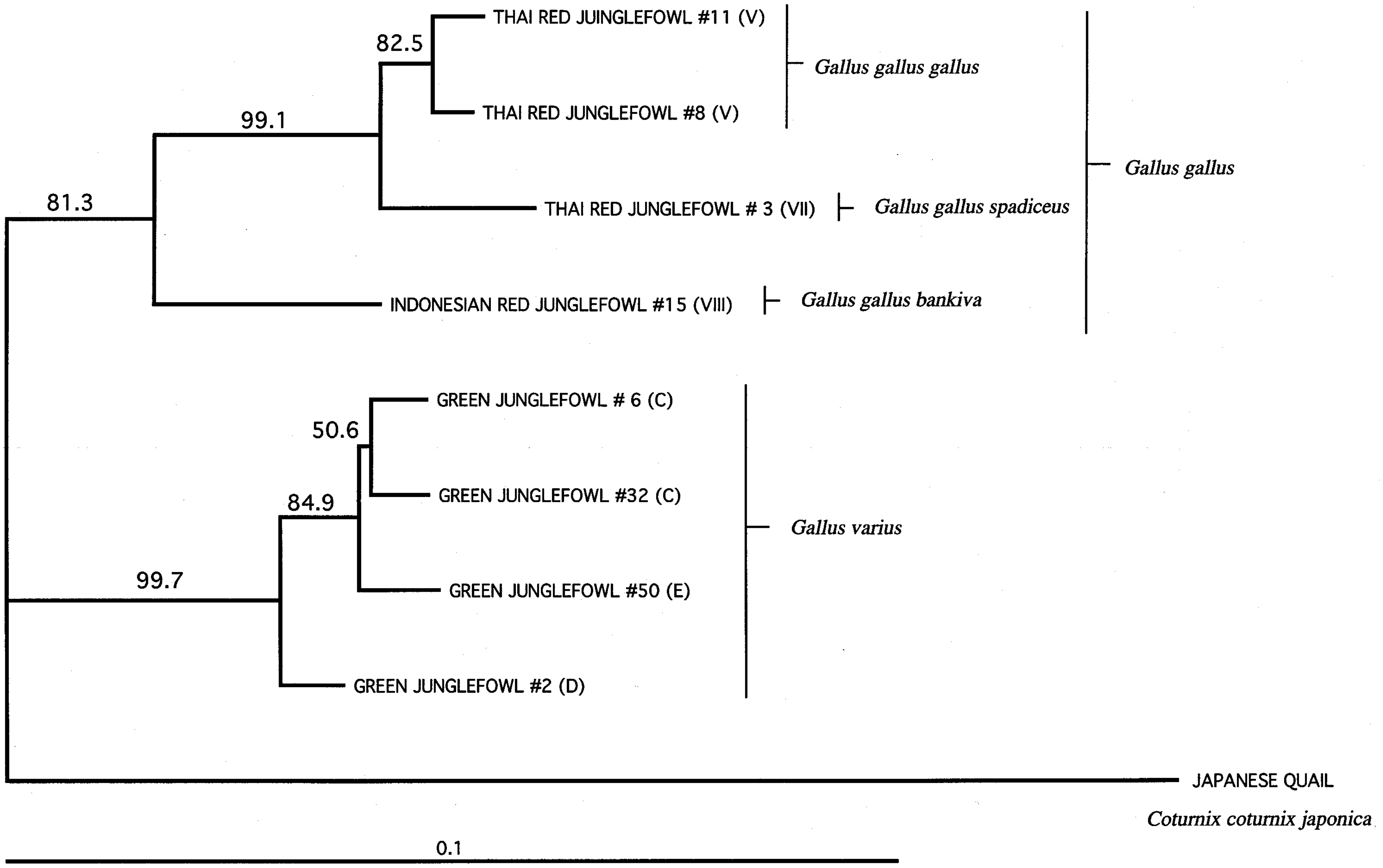
WHITE LEGHORN (I)
NAGOYA (I)
0.50% (0.50%)

AYAM CEMANI (V)
AYAM PELUNG (VIII)
0.50% (0.50%)

AYAM CEMANI (V)
BARRED PLYMOUTH ROCK (V)
0.75% (0.75%)

WHITE LEGHORN (I)
AYAM PELUNG (VIII)
2.75% (2.75%)

Figure 3-3.



82.5
THAI RED JUINGLEFOWL #11 (V)
THAI RED JUNGLEFOWL #8 (V)
Gallus gallus gallus
99.1
81.3
THAI RED JUNGLEFOWL # 3 (VII)
Gallus gallus spadiceus
Gallus gallus
INDONESIAN RED JUNGLEFOWL #15 (VIII)
Gallus gallus bankiva
50.6
GREEN JUNGLEFOWL # 6 (C)
GREEN JUNGLEFOWL #32 (C)
84.9
Gallus varius
99.7
GREEN JUNGLEFOWL #50 (E)
GREEN JUNGLEFOWL #2 (D)
JAPANESE QUAIL
Coturnix coturnix japonica
0.1

Figure 3-4.

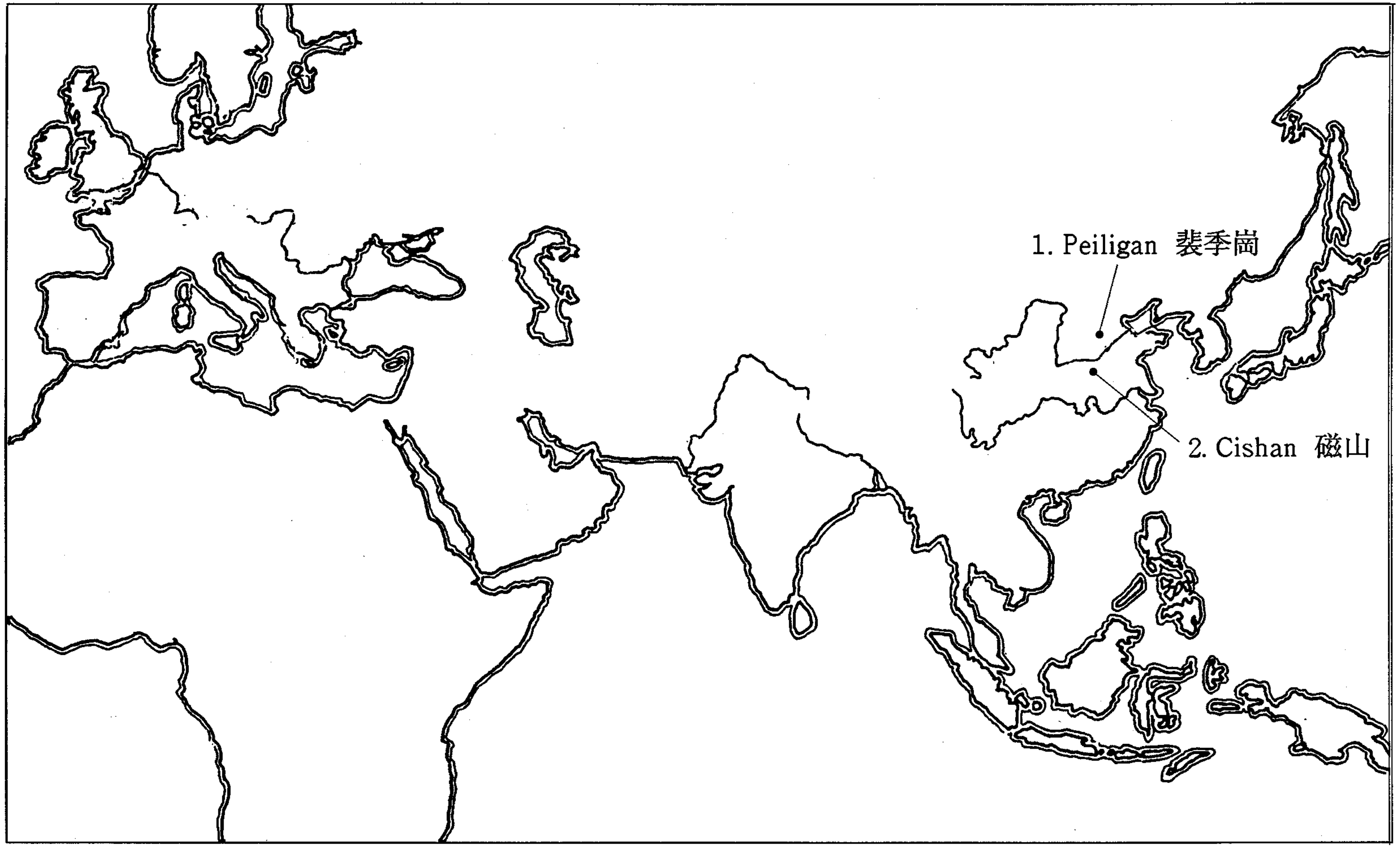


Figure 3-5.

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GG_gallus11    AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
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GG_gallus58    AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
GG_gallus8     AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
GG_gallus10    AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
GG_spadiceus3  AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
GG_spadiceus4  AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
GG_spadiceus5  AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
G_lafayettei1  AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
G_lafayettei2  AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
G_sonneratii   AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
G_varius2      AATTTTA-TT TTTTAACCCA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
G_varius32     AATTTTA-TT TTTTAACCCA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
G_varius50     AATTTTA-TT TTTTAACCCA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
G_varius6      AATTTTA-TT TTTTAACCCA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
Cemani         AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
Ayam63         AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
Ayam71         AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
Pelung         AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
Bantam8        AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
Barred_Plymous AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
Nagoya         AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
White_Leghorn1 AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
White_Leghorn2 AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
White_Leghorn3 AATTTTA-TT TTTTAACCTA ACTCCCCTAC TAAGTGTACC CCCCCTTTCC CCCCCAGGGG
C_coturnix     AAC--ACTTT TTTTAACCTA ACTCCCCTAC TTAGTGTACC CCCCCTTTCC CCCCCAGGGG

               61                                                            120
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GG_bankiva18   GGGTATACTA TGCATAATCG TGCATACATT TATATACCAC ATATATTATG GTACCGGTAA
GG_bankiva19   GGGTATACTA TGCATAATCG TGCATACATT TATATACCAC ATATATTATG GTACCGGTAA
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G_sonneratii   GGGTATACTA TGTATAATCG TGCATACATT TATATACCAC ATATATTATG GTACCGGTAA
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G_varius50     GGGTATACTA TGCATAATCG TGCATACATT TATATACCAC ATATACTATG GTACCGGTAA
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Cemani         GGGTATACTA TGCATAATCG TGCATACATT TATATACCAC ATATATTATG GTACCGGTAA
Ayam63         GGGTATACTA TGCATAATCG TGCATACATT TATATACCAC ATATATTATG GTACCGGTAA
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Barred_Plymous GGGTATACTA TGCATAATCG TGCATACATT TATATACCAC ATATATTATG GTACCGGTAA
Nagoya         GGGTATACTA TGCATAATCG TGCATACATT TATATACCAC ATATATTATG GTACCGGTAA
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Cemani         TATATACTAT ATATGTACTA AACCCATTAT ATGTATACGG GCATTAATCT ATATTCCACA
Ayam63         TATATACTAT ATATGTACTA AACCCATTAT ATGTATACGG GCATTAATCT ATATTCCACA
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Barred_Plymous TATATACTAT ATATGTACTA AACCCATTAT ATGTATACGG GCATTAATCT ATATTCCACA
Nagoya         TATATACTAT ATATGTACTA AACCCATTAT ATGTATACGG GCATTAACCT ATATTCCACA
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Cemani         TTTCTCCCAA TGTCCATTCT ATGCATGATC CAGGACATAC TCATTCACCC TCCCCATAGA
Ayam63         TTTCTCCCAA TGTCCATTCT ATGCATGATC CAGGGCATAC TCATTCACCC TCCCCATAGA
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Pelung         TTTCTCCCAA TGTCCATTCT ATGCATGATC CAGGACATAC TTATTCACCC TCCCCATAGA
Bantam8        TTTCTCCCAA TGTCCATTCT ATGCATGATC CAAGACATAC TCATTCACCC TCCCCATA-A
Barred_Plymous TTTCTCCCAA TGTCCATTCT ATGCATGATC CAGGACACAC TCATTCACCC TCCCCATAGA
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               241                                                           300
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Cemani         CAG----CTC CAAACCACTA CCAAGTCACC TAACTATGAA TGGTTGCAGG ACATAAA-TC
Ayam63         CAG----CTC CAAACCACTA CCAAGTCACC TAACTATGAA TGGTTGCAGG ACATAAA-TC
Ayam71         CAG----CTC CAAACCACTA CCAAGTCACC TAACTATGAA TGGTTGCAGG ACATAAA-TC
Pelung         CAG----CTC CAAACCACTA CCAAGTCACC TAACTATGAA TGGTTGCAGG ACATAAA-TC
Bantam8        CAG----TTC TAAACCACTA TCAAGCCACC TAACTATGAA TGGTTACAGG ACATAAA-TC
Barred_Plymous CAG----CTC CAAACCACTA CCAAGTCACC TAACTATGAA TGGTTACAGG ACATAAA-TC
Nagoya         CAG----TTC CAAACCACTA TCAAGCCACC TAACTATGAA TGGTTACAGG ACATAAA-TC
White_Leghorn1 CAG----TTC CAAACCACTA TCAAGCCACC TAACTATGAA TGGTTACAGG ACATAAA-TC
White_Leghorn2 CAG----TTC CAAACCACTA CCAAGTCACC TAACTATGAA TGGTTACAGG ACATAAA-TC
White_Leghorn3 CAG----CTC TAAACCACTA CCAAGTCACC TAACTATGAA TGGTTACAGG ACATAAA-TC
C_coturnix     ATAG------ ---------- ---------- ---------- ---------- ----------

               301                                                           360
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Pelung         TCACTCTCAT GCTCCTCCCC CAACAAGTCA CC-TAACTAT GAATGGTTAC AGGACATACA
Bantam8        TCACTCTCAT GTTCTCCCCC TAACAAGTCA CC-TAACTAT GAATGGTTAC AGGACATACA
Barred_Plymous TCACTCTCAT GTTCTTCCCC CAACAAGTCA CC-TAACTAT GAATGGTTAC AGGACATACA
Nagoya         TCACTCTCAT GTTCTCCCCC CAACAAGTCA CC-TAACTAT GAATGGTTAC AGGACATACA
White_Leghorn1 TCACTCTCAT GTTCTCCCCC CAACAAGTCA CC-TAACTAT GAATGGTTAC AGGACATACA
White_Leghorn2 TCACTCTCAT GTTCTTCCCC CAACAAGTCA CC-TAACTAT GAATGGTTAC AGGACATACA
White_Leghorn3 TCACTCTCAT GTTCTTCCCC CAACAAGTCA CC-TAACTAT GAATGGTTAC AGGACATACA
C_coturnix     ---------- -ACTTTCCAC TAACAGGACA CCATAACTAT GAATGGTTGC AGGACATAAG
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Figure 4-1.

```
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GG_bankiva18   -TTTAACTAT C-ATGATTCT AACCCATTTG GTTATGCTCG T-GTATCAGA TGGATTTATT
GG_bankiva19   -TTTAACTAT C-ATGATTCT AACCCATTTG GTTATGCTCG T-GTATCAGA TGGATTTATT
GG_gallus11    -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
GG_gallus39    -CTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
GG_gallus41    -CCTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
GG_gallus58    -CTTAACTAC T-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
GG_gallus8     -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
GG_gallus10    -TTTAACTAT T-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
GG_spadiceus3  -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA ----------
GG_spadiceus4  -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
GG_spadiceus5  -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
G_lafayettei1  CTCCAATCCT T-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
G_lafayettei2  CTCCAATCCT T-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
G_sonneratii   CCTAAATCCT T-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
G_varius2      -TTTAACTAC C-ATG-ATCT AACCCATTTG GTTATGCTCG TCGTACCAGA TGGATTTATT
G_varius32     -TCTAACTAC C-ATG-ATCT AACCCATTTG GTTATGCTCG T-GTACCAGA TGGATTTATT
G_varius50     -TCTAACTAC C-ATG-ATCT AACCCATTTG GTTATGCTCG T-GTACAGT- ----------
G_varius6      -TCTAACTAC C-ATG-ATCT AACCCATTTG GTTATGCTCG TCGTACCAGA TGGATTTATT
Cemani         -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
Ayam63         -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
Ayam71         -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG TCGTATCAGA TGGATTTATT
Pelung         -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA ----------
Bantam8        -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
Barred_Plymous -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
Nagoya         -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA CGGATTTATT
White_Leghorn1 -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA TGGATTTATT
White_Leghorn2 -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA ----------
White_Leghorn3 -TTTAACTAC C-ATG-TTCT AACCCATTTG GTTATGCTCG CCGTATCAGA ----------
C_coturnix     -CTTACTAAA TACTT--AGC TCCCCATTTG GTTATGCTAG ACGTACCAGA TGGATTTATT

               421                                                         480
GG_bankiva15   ---------- ---------- ---------- ---------- ---------- ----------
GG_bankiva18   GATCGTTCAC CTCACGAGAG AGCAGCAACC CCTG------ ---------- ----------
GG_bankiva19   GATCGTTCAC CTCACG---- ---------- ---------- ---------- ----------
GG_gallus11    G--------- ---------- ---------- ---------- ---------- ----------
GG_gallus39    GATCGTTCAC CTCACGAGAG ATCAGCAACC CCTGCTCGTA ATG-TACTTC ATGACCAGTC
GG_gallus41    GATCGTTCAC CTCACGAGAG ATCAGCAACC CCTGCTCGTA ATG-TACTTC ATGACCAGTC
GG_gallus58    GATCGTTCAC CTCACGAGAG ATCA------ ---------- ---------- ----------
GG_gallus8     GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCCTGT- ---------- ----------
GG_gallus10    GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCCTGTA ATG-TACTTC ATGACCAGTC
GG_spadiceus3  ---------- ---------- ---------- ---------- ---------- ----------
GG_spadiceus4  GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCTTGTA ATG-TACTTC ATGACCAGTC
GG_spadiceus5  GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCTTGTA ATG-TACTTC ATGACCAGTC
G_lafayettei1  GATCGTTCAC CTCACGAGAG ATCAGCAACC CCTGCCTGTA ATG-TACTTC ATGACCAGTC
G_lafayettei2  GATCG----- ---------- ---------- ---------- ---------- ----------
G_sonneratii   GATCGTTCAC CTCACGAGAG ATCAGCAACC CCTGCCTGTA ATG-TACTTC ATGACCAGTC
G_varius2      GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCCCGTA ATG-TACTT- ----------
G_varius32     GATCG----- ---------- ---------- ---------- ---------- ----------
G_varius50     ---------- ---------- ---------- ---------- ---------- ----------
G_varius6      GATCGTC-AC CTCACGAGAG ATCAGCAACC CCTGCC-GTA ATG-TACTT- ATGACCAGTC
Cemani         GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCCTGTA ATG-TACTTC ATGACCAGTC
Ayam63         GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCT---- ---------- ----------
Ayam71         GATCGTCCAC CTCACGAG-- ---------- ---------- ---------- ----------
Pelung         ---------- ---------- ---------- ---------- ---------- ----------
Bantam8        GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCCTGTA ATG-TACTTC ATGACCAGTC
Barred_Plymous GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCTTGTA ATG-TACTTC ATGACCAGTC
Nagoya         GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCCTGTA ATG-TACTTC ATGACCAGTC
White_Leghorn1 GATCGTCCAC CTCACGAGAG ATCAGCAACC CCTGCCTGTA ATG-TACTTC ATGACCAGTC
White_Leghorn2 ---------- ---------- ---------- ---------- ---------- ----------
White_Leghorn3 ---------- ---------- ---------- ---------- ---------- ----------
C_coturnix     GATCGTACAC CTCACGAGAG ATCACCAACC CCTGTCTGTA ATGCTATTCC GTGACTAGCT

               481                                                         540
GG_bankiva15   ---------- ---------- ---------- ---------- ---------- ----------
GG_bankiva18   ---------- ---------- ---------- ---------- ---------- ----------
GG_bankiva19   ---------- ---------- ---------- ---------- ---------- ----------
GG_gallus11    ---------- ---------- ---------- ---------- ---------- ----------
GG_gallus39    TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTACTTG ---------- ----------
GG_gallus41    TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTACTT- ---------- ----------
GG_gallus58    ---------- ---------- ---------- ---------- ---------- ----------
GG_gallus8     ---------- ---------- ---------- ---------- ---------- ----------
GG_gallus10    TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTACTTG CCTTCCACC- ----------
GG_spadiceus3  ---------- ---------- ---------- ---------- ---------- ----------
GG_spadiceus4  TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTACTTG CCTTCCACC- ----------
GG_spadiceus5  TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTA---- ---------- ----------
G_lafayettei1  TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTACTTG CCTTCCAC-- ----------
G_lafayettei2  ---------- ---------- ---------- ---------- ---------- ----------
G_sonneratii   TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTACTTG CCTTCCACC- ----------
G_varius2      ---------- ---------- ---------- ---------- ---------- ----------
G_varius32     ---------- ---------- ---------- ---------- ---------- ----------
G_varius50     ---------- ---------- ---------- ---------- ---------- ----------
G_varius6      TCAGGCC-AT TCTTTCCCC- TACACCCTTG CCTACTTG-- ---------- ----------
Cemani         TCAGGCCCAT TCTTT----- ---------- ---------- ---------- ----------
Ayam63         ---------- ---------- ---------- ---------- ---------- ----------
Ayam71         ---------- ---------- ---------- ---------- ---------- ----------
Pelung         ---------- ---------- ---------- ---------- ---------- ----------
Bantam8        TCAGGCC--- ---------- ---------- ---------- ---------- ----------
Barred_Plymous TCAGGCCCAT TCTTTCCCCC TACACCC--- ---------- ---------- ----------
Nagoya         TCAGGCCCAT TCTTTCCCCC TACACCC--- ---------- ---------- ----------
White_Leghorn1 TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCTACTTG CCTTC----- ----------
White_Leghorn2 ---------- ---------- ---------- ---------- ---------- ----------
White_Leghorn3 ---------- ---------- ---------- ---------- ---------- ----------
C_coturnix     TCAGGCCCAT TCTTTCCCCC TACACCCCTC GCCCCTCTTG CTCTTTTGCG CCTCTGGTTC
//
```

Figure 4-1. (*continued*)

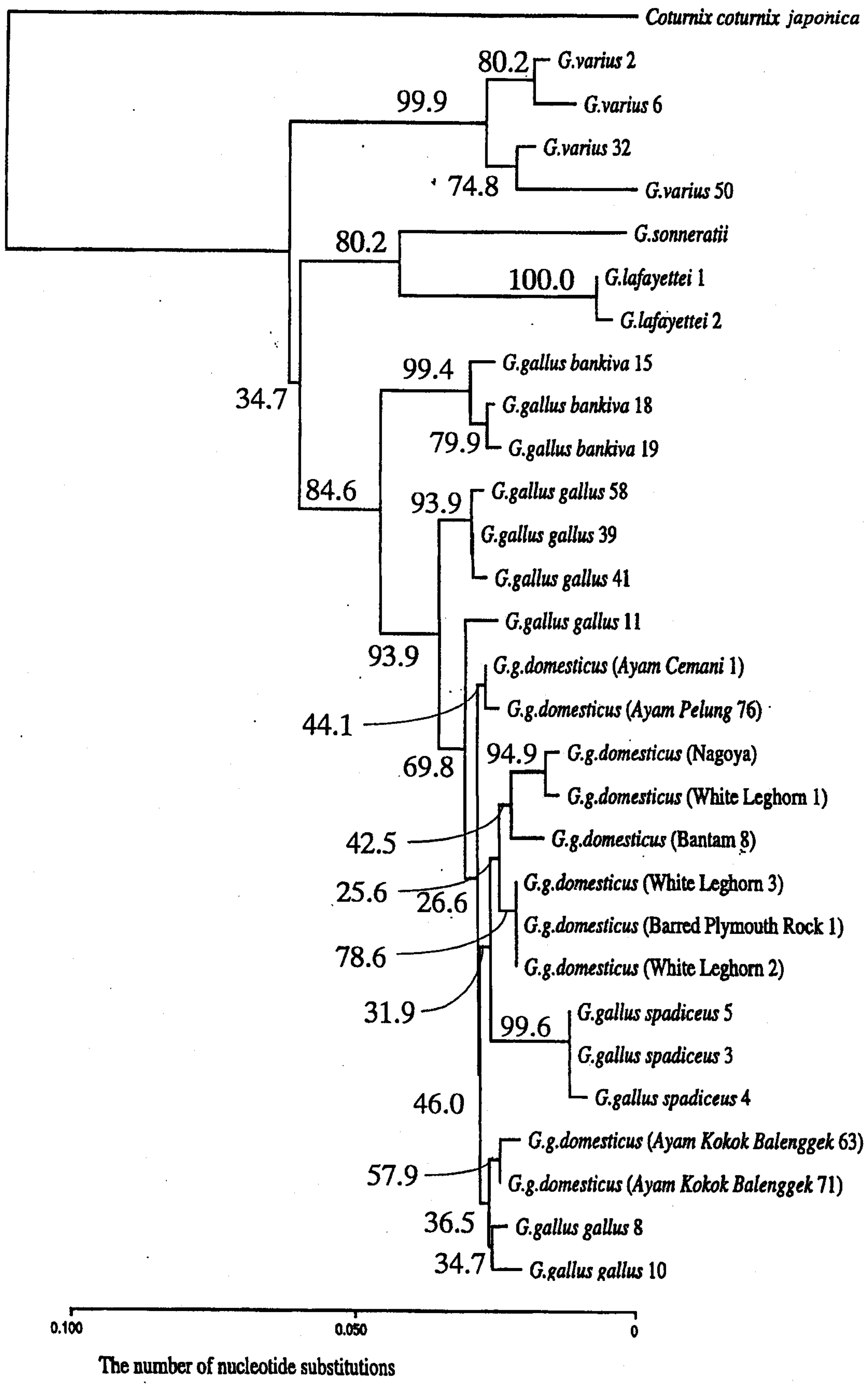
Coturnix coturnix japonica
80.2
G.varius 2
99.9
G.varius 6
G.varius 32
74.8
G.varius 50
80.2
G.sonneratii
100.0
G.lafayettei 1
G.lafayettei 2
34.7
99.4
G.gallus bankiva 15
G.gallus bankiva 18
79.9
G.gallus bankiva 19
84.6
93.9
G.gallus gallus 58
G.gallus gallus 39
G.gallus gallus 41
G.gallus gallus 11
93.9
G.g.domesticus (Ayam Cemani 1)
44.1
G.g.domesticus (Ayam Pelung 76)
69.8
94.9
G.g.domesticus (Nagoya)
G.g.domesticus (White Leghorn 1)
42.5
G.g.domesticus (Bantam 8)
25.6
26.6
G.g.domesticus (White Leghorn 3)
78.6
G.g.domesticus (Barred Plymouth Rock 1)
G.g.domesticus (White Leghorn 2)
31.9
G.gallus spadiceus 5
99.6
G.gallus spadiceus 3
G.gallus spadiceus 4
46.0
G.g.domesticus (Ayam Kokok Balenggek 63)
57.9
G.g.domesticus (Ayam Kokok Balenggek 71)
36.5
G.gallus gallus 8
34.7
G.gallus gallus 10
0.100
0.050
0
The number of nucleotide substitutions

Figure 4-2.

Appendix A

Nucleotide Sequences Determined in this Study

```
LOCUS       CHKMTB01     400 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82897
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:bankiva, isolate:15) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
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                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="bankiva"
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta cattcctcat
      181 ttctcccaat gtccattcca tgcatgatcc aagtcattct tagtcatatt ccccataagc
      241 agctctaacc actaccaaga cacctaacta tgaatggtta caggacataa ctcttactct
      301 catgctcctc ccccaacaag tcacctaact atgaatggtt acaggacata catttaacta
      361 ccatgattct aacccatttg gttatgctcg tgtatcagat
//
```

```
LOCUS       CHKMTB02     442 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82898
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:bankiva, isolate:18) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 442)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
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                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="bankiva"
BASE COUNT      129 a    117 c     58 g    138 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta cattcctcat
      181 ttctcccaat gtccattcca tgcatgatcc aagtcattct agtcatattc cccataagta
      241 gctctaacca ctaccaagac acctaactat gaatggtcac aggacataac tctcactctc
      301 atgttcttcc cccaacaagt cacctaacta tgaatggtta caggacatac atttaactat
      361 catgattcta acccatttgg ttatgctcgt gtatcagatg gatttattga tcgttcacct
      421 cacgagagag cagcaacccc tg
//
```

```
LOCUS       CHKMTB03     424 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82899
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:bankiva, isolate:19) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 424)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 424)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..424
                     /isolate="19"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="bankiva"
BASE COUNT      122 a    109 c     54 g    139 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta cattcctcat
      181 ttctcccaat gtccattcca tgcatgatcc aagtcattct agtcatattc cccataagta
      241 gctctaacca ctaccaagac acctaactat gaatggttac aggacataac tcttactctc
      301 atgttcttcc cccaacaagt cacctaacta tgaatggttg caggacatac atttaactat
      361 catgattcta acccatttgg ttatgctcgt gtatcagatg gatttattga tcgttcacct
      421 cacg
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LOCUS       CHKMTG04     448 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82900
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:gallus, isolate:8) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 448)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
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                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="gallus"
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ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta cattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt gtaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tgcaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga tggatttatt gatcgtcacc
      421 tcacgagaga tcagcaaccc ctgcctgt
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```
LOCUS       CHKMTG05      518 bp ds-DNA            VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82901
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:gallus, isolate:10) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 518)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
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                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="gallus"
BASE COUNT      140 a    155 c     67 g    156 t      0 others
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      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt gcaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tgcaggacat acatttaact
      361 attatgttct aacccatttg gttatgctcg ccgtatcaga tggatttatt gatcgtccac
      421 ctcacgagag atcagcaacc cctgcctgta atgtacttca tgaccagtct caggcccatt
      481 ctttccccct acaccctcg ccctacttgc cttccacc
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```
LOCUS       CHKMTG06      412 bp ds-DNA            VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82902
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:gallus) mitochondrion DNA, clone:11.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 412)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 412)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..412
                     /clone="11"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="gallus"
     repeat_region   245..368
     repeat_unit     245..307
     repeat_unit     308..368
BASE COUNT      120 a    112 c     52 g    128 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt gcaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacccaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg tccgtatcag atggatttat tg
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LOCUS       CHKMTG07     509 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82903
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:gallus, isolate:39) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 509)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 509)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
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                     /sequenced_mol="DNA"
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BASE COUNT      143 a    147 c     64 g    155 t      0 others
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      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aagacatact cattcacctt ccccatagat
      241 agctccaaac cactaccaag acacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tacaggacat atacttaact
      361 accatgttct aacccatttg gttatgctcg tcgtatcaga tggatttatt gatcgttcac
      421 ctcacgagag atcagcaacc cctgctcgta atgtacttca tgaccagtct caggcccatt
      481 ctttccccct acacccctcg ccctacttg
//
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```
LOCUS       CHKMTG08     508 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82904
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:gallus, isolate:41) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 508)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 508)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..508
                     /isolate="41"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="gallus"
BASE COUNT      143 a    148 c     63 g    154 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aagacatact cattcacctt ccccatagat
      241 agctccaaac cactaccaag acacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tacaggacat atacctaact
      361 accatgttct aacccatttg gttatgctcg tcgtatcaga tggatttatt gatcgttcac
      421 ctcacgagag atcagcaacc cctgctcgta atgtacttca tgaccagtct caggcccatt
      481 ctttccccct acacccctcg ccctactt
//
```

```
LOCUS       CHKMTG09      434 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82905
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:gallus, isolate:58) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 434)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 434)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..434
                     /isolate="58"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="gallus"
BASE COUNT      130 a    116 c     54 g    134 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aagacatact cattcacctt ccccatagac
      241 agccccaaac cactaccaag acacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tacaggacat atacttaact
      361 actatgttct aacccatttg gttatgctcg tcgtatcaga tggatttatt gatcgttcac
      421 ctcacgagag atca
//
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```
LOCUS       CHKMTS10      400 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82906
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:spadiceus, isolate:3) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..400
                     /isolate="3"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="spadiceus"
     repeat_region   245..368
     repeat_unit     245..307
     repeat_unit     308..368
BASE COUNT      117 a    109 c     49 g    125 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccctacagac
      241 agctccaaac caccaccaag tcacttaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctt cccctaccaa gtcacctaac tatgaatggt tgcaggacat atatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga
//
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```
LOCUS       CHKMTS11      518 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82907
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:spadiceus, isolate:4) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 518)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..518
                     /isolate="4"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="spadiceus"
BASE COUNT      141 a    154 c     66 g    157 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtaaacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccctacagac
      241 agctccaaac caccaccaag tcacttaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctt cccctaccaa gtcacctaac tatgaatggt tgcaggacat atatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga tggatttatt gatcgtccac
      421 ctcacgagag atcagcaacc cctgcttgta atgtacttca tgaccagtct caggcccatt
      481 ctttccccct acacccctcg ccctacttgc cttccacc
//
```

```
LOCUS       CHKMTS12      505 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82908
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:spadiceus, isolate:5) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 505)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 505)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..505
                     /isolate="5"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="spadiceus"
BASE COUNT      139 a    147 c     65 g    154 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccctacagac
      241 agctccaaac caccaccaag tcacttaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctt cccctaccaa gtcacctaac tatgaatggt tgcaggacat atatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga tggatttatt gatcgtccac
      421 ctcacgagag atcagcaacc cctgcttgta atgtacttca tgaccagtct caggcccatt
      481 ctttccccct acacccctcg cccta
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```
LOCUS       CHKMTL13      578 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Cingalese mitochondrial DNA for D-loop region.
ACCESSION   D82909
KEYWORDS    D-loop region.
SOURCE      Gallus lafayettei (isolate:1) mitochondrion DNA.
  ORGANISM  Gallus lafayettei
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 578)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..578
                     /isolate="1"
                     /mitochondrion
                     /organism="Gallus lafayettei"
                     /sequenced_mol="DNA"
BASE COUNT      158 a    169 c     73 g    178 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta cattccccat
      181 ttctcccaat gtccatctca tgaatggtcc aggtcaatcc tatctatcct acccatacat
      241 aatctttacc actaacaagt cacctaacta tgaatggtta caggacatac atctaacctt
      301 aatgctcttc ctctaacaag ccacctaact atgaatggtt acaggacata catctaacct
      361 taatgctctt cccctgacag gtcacctaac tatgaatggt tacaggacat accctccaat
      421 ccttatgttc taacccattt ggttatgctc gtcgtatcag atggatttat tgatcgttca
      481 cctcacgaga gatcagcaac ccctgcctgt aatgtacttc atgaccagtc tcaggcccat
      541 tctttccccc tacacccctc gccctacttg ccttccac
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LOCUS       CHKMTL14      476 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Cingalese mitochondrial DNA for D-loop region.
ACCESSION   D82910
KEYWORDS    D-loop region.
SOURCE      Gallus lafayettei (isolate:2) mitochondrion DNA.
  ORGANISM  Gallus lafayettei
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 476)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..476
                     /isolate="2"
                     /mitochondrion
                     /organism="Gallus lafayettei"
                     /sequenced_mol="DNA"
BASE COUNT      137 a    127 c     60 g    152 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta cattccccat
      181 ttctcccaat gtccatctca tgaatggtcc aggtcaatcc tatctatcct acccatacat
      241 aacctttacc actaccaagt cacctaacta tgaatggtta caggacatac atttaacctt
      301 aatgctcttc ctctaacaag ccacctaact atgaatggtt acaggacata catttaacct
      361 taatgctcct cccctgacag gtcacctaac tatgaatggt tacaggacat accctccaat
      421 ccttatgttc taacccattt ggttatgctc gtcgtatcag atggatttat tgatcg
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```

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LOCUS       CHKMTS15      580 bp ds-DNA              VRT       17-JUN-1996
DEFINITION  Grey Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82911
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:sonnerati, isolate:1) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 580)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 580)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..580
                     /isolate="1"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /sub_species="sonnerati"
BASE COUNT      153 a    170 c     78 g    179 t      0 others
ORIGIN
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       61 ggtatactat gtataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaaccta tattccccat
      181 ttctccccat gtccatctca tgaatggtcc aagtcatcct attcacctca cccatacatg
      241 gcttatatcc actaccaggc cacctaacta tgaatggttg caggacatac acttaacttt
      301 aatgctcttc ctcccacagg tcacctaatc atgaatgatc ataggtcata cggtttaatt
      361 ccaatgctcg tccccttaca agtcacctaa ctatgaatgg tcacaggaca tgaacctaaa
      421 tccttatgtt ctaacccatt tggttatgct cgtcgtatca gatggattta ttgatcgttc
      481 acctcacgag agatcagcaa cccctgcctg taatgtactt catgaccagt ctcaggccca
      541 ttctttcccc ctacacccct cgccctactt gccttccacc
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LOCUS       CHKMTV16      457 bp ds-DNA              VRT       17-JUN-1996
DEFINITION  Gallus varius mitochondrial DNA for D-loop region.
ACCESSION   D82912
KEYWORDS    D-loop region.
SOURCE      Gallus varius mitochondrion DNA, clone:2.
  ORGANISM  Gallus varius
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 457)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 457)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..457
                     /clone="2"
                     /mitochondrion
                     /organism="Gallus varius"
                     /sequenced_mol="DNA"
     repeat_region   244..367
     repeat_unit     244..306
     repeat_unit     307..367
BASE COUNT      134 a    125 c     59 g    139 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacgga cattaaccta cattccccat
      181 ttctccccat gtacattcca tgaatgatcc aagtcattac atcgtcctac cccatatcta
      241 actctatacc actaacaggt cacttaacta tgaatggtta caggacatac ctctaatact
      301 agtgctctac ccctaacagg tcacctaact atgaatggtt acaggacata catttaacta
      361 ccatgatcta acccatttgg ttatgctcgt cgtaccagat ggatttattg atcgtccacc
      421 tcacgagaga tcagcaaccc ctgcccgtaa tgtactt
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```

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LOCUS       CHKMTV17      502 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Green Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82913
KEYWORDS    D-loop region.
SOURCE      Gallus varius (isolate:6) mitochondrion DNA.
  ORGANISM  Gallus varius
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 502)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..502
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                     /mitochondrion
                     /organism="Gallus varius"
                     /sequenced_mol="DNA"
BASE COUNT      142 a    143 c     66 g    151 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacgga cattaaccta cattccccat
      181 ttctccccat gtacattcca tgaatgatcc aagtcattac gtcgtccata ccctacatcc
      241 aactctatac cactaacagg tcacttaact atgaatggtt acaggacata cctctaatac
      301 tagtgctcta cccctaacag gtcacctaac tatgaatggt tacaggacat acatctaact
      361 accatgatct aacccatttg gttatgctcg tcgtaccaga tggatttatt gatcgtcacc
      421 tcacgagaga tcagcaaccc ctgccgtaat gtacttatga ccagtctcag gccattcttt
      481 cccctacacc cttgcctact tg
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```
LOCUS       CHKMTV18      474 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Green Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82914
KEYWORDS    D-loop region.
SOURCE      Gallus varius (isolate:32) mitochondrion DNA.
  ORGANISM  Gallus varius
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 474)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 474)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..474
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                     /mitochondrion
                     /organism="Gallus varius"
                     /sequenced_mol="DNA"
     repeat_region   245..368
     repeat_unit     245..307
     repeat_unit     308..368
BASE COUNT      142 a    126 c     61 g    145 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacgga cattaaccta cattccccat
      181 ttctccccat gtacattcca tgaatgatcc aagtcattac atcgtcctac cctatatcca
      241 actctatacc actaacaggt cacttaacta tgaatggtta caggacatac ttctaatacc
      301 agtgctctac ccctaacagg tcacctaact atgaatggtt acaggacata cttctaatac
      361 cagtgctcta cccctaacag gtcacctaac tatgaatggt tacaggacat acatctaact
      421 accatgatct aacccatttg gttatgctcg tgtaccagat ggatttattg atcg
//
```

```
LOCUS       CHKMTV19      520 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Green Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82915
KEYWORDS    D-loop region.
SOURCE      Gallus varius mitochondrion DNA, clone:50.
  ORGANISM  Gallus varius
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 520)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 519)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..519
                     /clone="50"
                     /mitochondrion
                     /organism="Gallus varius"
                     /sequenced_mol="DNA"
     repeat_region   244..488
     repeat_unit     244..306
     repeat_unit     307..367
     repeat_unit     368..427
     repeat_unit     428..488
BASE COUNT      154 a    143 c     68 g    155 t      0 others
ORIGIN
        1 aattttattt tttaacccaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatactatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacgga cattaatcta cattccccat
      181 ttctccccat gtacattcca tgaatgatcc aagtcattac gtcgtcctac cctatatcca
      241 actctttacc actaacaggt cacttaacta tgaatggtta caggacatac ctctaatatt
      301 agtgctctac ccccaacagg tcacctaact atgaatggtt acaggacata cctctaatgt
      361 tagtgctcta cccccaacag gtcacctaac tatgaatggt tacaggacat acctctaata
      421 ttagtgctcc tacccccaac aggtcaccta accatgaatg gttacaggac atacatctaa
      481 ctaccatgat ctaacccatt tggttatgct cgtgtacagt
//
```

```
LOCUS       CHKMTD20      483 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82916
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:Ayam Cemani,
            isolate:1) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 483)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..483
                     /isolate="1"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="Ayam Cemani"
                     /sub_species="domesticus"
BASE COUNT      137 a    135 c     64 g    147 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt gcaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga tggatttatt gatcgtccac
      421 ctcacgagag atcagcaacc cctgcctgta atgtacttca tgaccagtct caggccattc
      481 ttt
//
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```
LOCUS       CHKMTD21       446 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82917
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:Ayamkokok Balenggek,
            isolate:63) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 446)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 446)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..446
                     /isolate="63"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="Ayamkokok Balenggek"
                     /sub_species="domesticus"
BASE COUNT      127 a    124 c     60 g    135 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc agggcatact cattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt gcaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tgcaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg tcgtatcaga tggatttatt gatcgtccac
      421 ctcacgagag atcagcaacc cctgct
//
```

```
LOCUS       CHKMTD22       428 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82918
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:Ayamkokok Balenggek,
            isolate:71) mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 428)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 428)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..428
                     /isolate="71"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="Ayamkokok Balenggek"
                     /sub_species="domesticus"
BASE COUNT      123 a    117 c     56 g    132 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact cattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt gcaggacata aatctcactc
      301 tcatgctctt cccccaacaa gtcacctaac tatgaatggt tgcaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg tcgtatcaga tggatttatt gatcgtccac
      421 ctcacgag
//
```

```
LOCUS       CHKMTD23      400 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82919
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:Pelung)
            mitochondrion DNA, clone:1.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..400
                     /clone="1"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="Pelung"
                     /sub_species="domesticus"
BASE COUNT      118 a    111 c     49 g    122 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatact tattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt gcaggacata aatctcactc
      301 tcatgctcct cccccaacaa gtcacctaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga
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```

```
LOCUS       CHKMTD24      502 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Chicken mitochondrial DNA for D-loop region.
ACCESSION   D82920
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:Barred Plymouth
            Rock) mitochondrion DNA, clone:1.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 502)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..502
                     /clone="1"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="Barred Plymouth Rock"
                     /sub_species="domesticus"
     repeat_region   245..368
     repeat_unit     245..307
     repeat_unit     308..368
BASE COUNT      140 a    144 c     65 g    153 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacacact cattcaccct ccccatagac
      241 agctccaaac cactaccaag tcacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctt cccccaacaa gtcacctaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga tggatttatt gatcgtcacc
      421 tcacgagaga tcagcaaccc tgcttgtatg tacttatgac cagtctcagg ccatctttcc
      481 cctacaccct cgcctacttg ct
//
```

```
LOCUS       CHKMTD25      491 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82921
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:Nagoya)
            mitochondrion DNA, clone:1.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 491)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 442)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..491
                     /clone="1"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="Nagoya"
                     /sub_species="domesticus"
     repeat_region   245..368
     repeat_unit     245..307
     repeat_unit     308..368
BASE COUNT      140 a    141 c     63 g    147 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaaccta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacatacc catttaccct ccccatagac
      241 agttccaaac cactatcaag ccacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctc cccccaacaa gtcacctaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga cggatttatt gatcgtccac
      421 ctcacgagag atcagcaacc cctgcctgta atgtacttat gaccagtcta ggcattcttt
      481 cccctacacc c
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```

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LOCUS       CHKMTD26      476 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82922
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:Bantam, isolate:8-3)
            mitochondrion DNA.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 476)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 476)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..476
                     /isolate="8-3"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="Bantam"
                     /sub_species="domesticus"
BASE COUNT      138 a    131 c     62 g    145 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aagacatact cattcaccct ccccatagac
      241 agttctaaac cactatcaag ccacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctc cccctaacaa gtcacctaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga tggatttatt gatcgtccac
      421 ctcacgagag atcagcaacc cctgcctgta atgtacttca tgaccagtct caggcc
//
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```
LOCUS       CHKMTD27     400 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82923
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:White leghorn)
            mitochondrion DNA, clone:2.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..400
                     /clone="2"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="White leghorn"
                     /sub_species="domesticus"
BASE COUNT      119 a    110 c     48 g    123 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacacact cattcaccct ccccatagac
      241 agttccaaac cactaccaag tcacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctt cccccaacaa gtcacctaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga
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```

```
LOCUS       QULMTJ28     465 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Quail mitochondrial DNA for D-loop region.
ACCESSION   D82924
KEYWORDS    D-loop region.
SOURCE      Coturnix coturnix (sub_species:japonica) mitochondrion DNA.
  ORGANISM  Coturnix coturnix
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 465)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 465)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..465
                     /mitochondrion
                     /organism="Coturnix coturnix"
                     /sequenced_mol="DNA"
                     /sub_species="japonica"
     repeat_unit     241..301
BASE COUNT      121 a    134 c     67 g    143 t      0 others
ORIGIN
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       61 gtatactatg cataatcgtg catacattta tattccacat atactatggt accggtaata
      121 tatattatat acgtactaaa cccattatat gtatacgggc attacatatt gtccccattt
      181 ctccccatgt acattagtgc atgctccaag acataaacca tacgttcacc tagtaataga
      241 ctttccacta acaggacacc ataactatga atggttgcag gacataagct tactaaatac
      301 ttagctcccc atttggttat gctagacgta ccagatggat ttattgatcg tacacctcac
      361 gagagatcac caacccctgt ctgtaatgct attccgtgac tagcttcagg cccattcttt
      421 ccccctacac ccctcgcccc tcttgctctt ttgcgcctct ggttc
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LOCUS       CHKMTD29       400 bp ds-DNA             VRT       17-JUN-1996
DEFINITION  Red Junglefowl mitochondrial DNA for D-loop region.
ACCESSION   D82925
KEYWORDS    D-loop region.
SOURCE      Gallus gallus (sub_species:domesticus, strain:White leghorn)
            mitochondrion DNA, clone:3.
  ORGANISM  Gallus gallus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JAN-1996) to the DDBJ/EMBL/GenBank databases.
            Akishinonomiya Fumihito, Yamashina Institute for Ornithology; 115
            Tsutsumine-aza, Abiko-shi, Chiba 270-11, Japan
            (E-mail:nkojima@lab.nig.ac.jp)
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 400)
  AUTHORS   Fumihito,A.
  JOURNAL   Unpublished (1996)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
     source          1..400
                     /clone="3"
                     /mitochondrion
                     /organism="Gallus gallus"
                     /sequenced_mol="DNA"
                     /strain="White leghorn"
                     /sub_species="domesticus"
BASE COUNT      119 a    110 c     48 g    123 t      0 others
ORIGIN
        1 aattttattt tttaacctaa ctcccctact aagtgtaccc cccctttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta tattccacat
      181 ttctcccaat gtccattcta tgcatgatcc aggacacact cattcaccct ccccatagac
      241 agctctaaac cactaccaag tcacctaact atgaatggtt acaggacata aatctcactc
      301 tcatgttctt cccccaacaa gtcacctaac tatgaatggt tacaggacat acatttaact
      361 accatgttct aacccatttg gttatgctcg ccgtatcaga
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LOCUS       AGUMTK         423 bp ds-DNA             ORG       26-FEB-1996
DEFINITION  Great argus pheasant mitochondrial gene, D-loop region.
ACCESSION   D66898
KEYWORDS    D-loop; hypervariable region.
SOURCE      Argusianus argus adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Argusianus argus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 423)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 423)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
            Tetsuo Miyake
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            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /mitochondrion
                     /organism="Argusianus argus"
                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..423
BASE COUNT      121 a    127 c     59 g    116 t      0 others
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       61 ggtatactat gtataattgt acatacattt atataccaca tacattatgg tcacagtaat
      121 agatatgtat acgtactaaa cccattatat gtagacggac attacaccta gcccacattt
      181 atcccaaccc catcccatgc atgctcctag acattaagtc caccctaacc taccacgctg
      241 ctccagaacc ctcaagtcac caaactatga atggtcacag gacataatat tcaattactg
      301 ctacacccca tttggttatg ctagtcgtac cagatggatt tattgatcgt acacctcacg
      361 agagatcagc aacccctgcc gtaatgtact tcatgaccag gttcaggccc attctttccc
      421 ctt
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LOCUS       AUKMTC        444 bp ds-DNA             ORG       26-FEB-1996
DEFINITION  Chukar partridge mitochondrial gene, D-loop region.
ACCESSION   D66890
KEYWORDS    D-loop; hypervariable region.
SOURCE      Alectoris chukar adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Alectoris chukar
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 444)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 444)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
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            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
                     /mitochondrion
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                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..444
BASE COUNT      117 a    140 c     60 g    127 t      0 others
ORIGIN
        1 aacacttttt ttaaccaaac tcccctacct agtgtacccc ccctttcccc cccagggggg
       61 gtacactatg cataatcgtg catatattta tatgccccat atatatgata gcggtaatat
      121 atatgtatac gtactaaacc cattatatgt acacggacat aacaacatta gccccatttc
      181 tcccaacccc atatcatgta tatctacagg tcatacacat ggcttccaac ctatcacttt
      241 cttctccccc cccaaggcac ctaatctatg aatggtcaca ggacatactc ctacatttat
      301 ggtactccac atctggttat gccagtcgta tcagatggat ttattgatcg tacacctcac
      361 gagagatcac caacccctgc ctgtaatgta ctccatgact aggttcaggc ccattctttc
      421 cccctacacc cctcgcccct cttg
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LOCUS       BBAMTB        451 bp ds-DNA             ORG       26-FEB-1996
DEFINITION  Chinese bamboo partridge mitochondrial gene, D-loop region.
ACCESSION   D66889
KEYWORDS    D-loop; hypervariable region.
SOURCE      Bambusicola thoracica adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Bambusicola thoracica
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 451)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 451)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
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            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
                     /mitochondrion
                     /organism="Bambusicola thoracica"
                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..451
BASE COUNT      122 a    131 c     62 g    136 t      0 others
ORIGIN
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       61 aggtatacta tgtataatcg tgcatacatt tatataccac atatattatg gtaccggtaa
      121 tatatactat atacgtacta aacccattat acgtatacag acattactct atatcccaca
      181 tttctcccca tgtacaatct atgcatgctc tagggcataa agcctcatcc tacaccggaa
      241 ctctgctcaa ttcactaaca agtcacctaa ctatgaatgg ttacgggaca taaacttaat
      301 atacatgctc tacctcattt ggttatgctc ggcgtaccag atggatttat tgatcgtaca
      361 cctcacgaga gaccagcaac ccctgcctgt aatgtacttc atgactaggc tcaggcccat
      421 tctttccccc tacacccctc gcccttcttg c
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LOCUS       CH2MTH        475 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  Golden pheasant mitochondrial gene, D-loop region.
ACCESSION   D66895
KEYWORDS    D-loop; hypervariable region.
SOURCE      Chrysolophus pictus adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Chrysolophus pictus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 475)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
            Tetsuo Miyake
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            Takatagun, Hiroshima 739-11
            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
     source          1..475
                     /dev_stage="adult"
                     /mitochondrion
                     /organism="Chrysolophus pictus"
                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..475
BASE COUNT      124 a    143 c     70 g    138 t      0 others
ORIGIN
        1 aacaaacttt tttaactcaa ctcccctatt gaatgtaccc ccccttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatactatgg taccggtact
      121 atatattata atcgtactaa acccattata tgtatacgga cattacacca cagccacatt
      181 tctccccatg tacatatcca tgcaatgctc ccaaactatc caagctccct caccaaacaa
      241 tgctctacaa cttccaggtc cccatattca tgaatggtta caggacatac atgtaatact
      301 aggtatttcc ccatttggtt atgctcgacg taccagatgg atttattgat cgtacacctc
      361 acgagagatc agcaacccct gcctgtaatg tactctatga ctaggttcag ggccattctt
      421 tccccctaca cccctcggcc ctcttgctct tttgcgcctc tggttctcgg tcagg
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LOCUS       CHKMTA        502 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  Green junglefowl mitochondrial gene, D-loop region.
ACCESSION   D64163
KEYWORDS    D-loop; hypervariable region.
SOURCE      Gallus varius adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Gallus varius
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 502)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 502)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (15-Sep-1995) to DDBJ by:
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            Takatagun, Hiroshima 739-11
            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4531
FEATURES             Location/Qualifiers
     source          1..502
                     /dev_stage="adult"
                     /mitochondrion
                     /organism="Gallus varius"
                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..502
BASE COUNT      142 a    143 c     66 g    151 t      0 others
ORIGIN
        1 aattttattt tttaacccaa ctcccctact aagtgtaccc ccccttccc ccccaggggg
       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacgga cattaaccta cattccccat
      181 ttctccccat gtacattcca tgaatgatcc aagtcattac gtcgtccata ccctacatcc
      241 aactctatac cactaacagg tcacttaact atgaatggtt acaggacata cctctaatac
      301 tagtgctcta cccctaacag gtcacctaac tatgaatggt tacaggacat acatctaact
      361 accatgatct aacccatttg gttatgctcg tcgtaccaga tggatttatt gatcgtcacc
      421 tcacgagaga tcagcaaccc ctgccgtaat gtacttatga ccagtctcag gccattcttt
      481 cccctacacc cttgcctact tg
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LOCUS       CHKMTE       580 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  Grey junglefowl mitochondrial gene, D-loop region.
ACCESSION   D66892
KEYWORDS    D-loop; hypervariable region.
SOURCE      Gallus sonneratii adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Gallus sonneratii
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 580)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 580)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
            Tetsuo Miyake
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            Phone:  0826-45-2331
            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /mitochondrion
                     /organism="Gallus sonneratii"
                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..580
BASE COUNT      153 a    170 c     78 g    179 t      0 others
ORIGIN
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       61 ggtatactat gtataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaaccta tattccccat
      181 ttctccccat gtccatctca tgaatggtcc aagtcatcct attcacctca cccatacatg
      241 gcttatatcc actaccaggc cacctaacta tgaatggttg caggacatac acttaacttt
      301 aatgctcttc ctcccacagg tcacctaatc atgaatgatc ataggtcata cggtttaatt
      361 ccaatgctcg tccccttaca agtcacctaa ctatgaatgg tcacaggaca tgaacctaaa
      421 tccttatgtt ctaacccatt tggttatgct cgtcgtatca gatggattta ttgatcgttc
      481 acctcacgag agatcagcaa cccctgcctg taatgtactt catgaccagt ctcaggccca
      541 ttctttcccc ctacacccct cgccctactt gccttccacc
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LOCUS       CHKMTF       578 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  Sri Lanka junglefowl mitochondrial gene, D-loop region.
ACCESSION   D66893
KEYWORDS    D-loop; hypervariable region.
SOURCE      Gallus lafayettei adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Gallus lafayettei
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 578)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 578)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
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            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..578
BASE COUNT      158 a    169 c     73 g    178 t      0 others
ORIGIN
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atatactata tatgtactaa acccattata tgtatacggg cattaatcta cattccccat
      181 ttctcccaat gtccatctca tgaatggtcc aggtcaatcc tatctatcct acccatacat
      241 aatctttacc actaacaagt cacctaacta tgaatggtta caggacatac atctaacctt
      301 aatgctcttc ctctaacaag ccacctaact atgaatggtt acaggacata catctaacct
      361 taatgctctt cccctgacag gtcacctaac tatgaatggt tacaggacat accctccaat
      421 ccttatgttc taacccattt ggttatgctc gtcgtatcag atggatttat tgatcgttca
      481 cctcacgaga gatcagcaac ccctgcctgt aatgtacttc atgaccagtc tcaggcccat
      541 tctttccccc tacacccctc gccctacttg ccttccac
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LOCUS       LOUMTJ       442 bp ds-DNA             ORG       26-FEB-1996
DEFINITION  Silver lophura mitochondrial gene, D-loop region.
ACCESSION   D66897
KEYWORDS    D-loop; hypervariable region.
SOURCE      Lophura nycthemera adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Lophura nycthemera
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 442)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
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            Takatagun, Hiroshima 739-11
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            Phone:  0826-45-2331
            Fax:    0826-45-4351
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                     /organism="Lophura nycthemera"
                     /sequenced_mol="DNA"
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     D-loop          1..442
BASE COUNT      129 a    132 c     61 g    120 t      0 others
ORIGIN
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       61 ggtatactat gtataatcgt gcatacattt atataccaca tatactatgg taccggtact
      121 atatattata tacgtactaa acccattata tgtagacgga cataacacca tatccccatt
      181 catcccaatg tactatcacc gtaatgctct aacacataag acctcacacc taccccacat
      241 aacaggtccg ggacccacaa gccaccataa catgaatggt tacaggacat actattaaat
      301 accatgttct atccacattt ggttatgctc gacgtaccag atggatttat tgatcgtaca
      361 cctcacgaga gatcagcaac ccctgcccgt aatgtacttc atgactaggt tcaggcccat
      421 tctttccccc tacacccctc gc
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LOCUS       PBTMTL       461 bp ds-DNA             ORG       26-FEB-1996
DEFINITION  Burmese peacock-pheasant mitochondrial gene, D-loop region.
ACCESSION   D66899
KEYWORDS    D-loop; hypervariable region.
SOURCE      Polyplectron bicalcaratum adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Polyplectron bicalcaratum
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 461)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 461)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
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            Phone:  0826-45-2331
            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /mitochondrion
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                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..461
BASE COUNT      122 a    138 c     67 g    134 t      0 others
ORIGIN
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       61 ggtatactat gtataatcgt gcatacattt atataccaca tatattatgg taccggtaat
      121 atctattgta tacgtactaa acccattata tgtagacgga cataacacct tatccccatt
      181 tctcccaatg tacatccatg catgccacaa ggactaactc actacaactc ccctgccacg
      241 gttatctaca accctcaagt cccctaaact atgaatggtt acaggacata acttcaatac
      301 tgtatctacc ccatttggtt atgcaagtcg tatcagatgg atttattgat cggacacctc
      361 acgagagatc agcaacccct gccgtaatgt acggtatgac taggttcagg cccattcttt
      421 ccccctacac ccctcgccct ccttgctctt ttgcgcctct g
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LOCUS       PHSMTG        455 bp ds-DNA            ORG        26-FEB-1996
DEFINITION  Green pheasant mitochondrial gene, D-loop region.
ACCESSION   D66894
KEYWORDS    D-loop; hypervariable region.
SOURCE      Phasianus versicolor adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Phasianus versicolor
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 455)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 455)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
            Tetsuo Miyake
            Dept. of Institute for Biotechnology Research
            Wakunaga Pharmaceutical Co.,Ltd.
            1624 Shimokotachi, Kodachou
            Takatagun, Hiroshima 739-11
            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /dev_stage="adult"
                     /mitochondrion
                     /organism="Phasianus versicolor"
                     /sequenced_mol="DNA"
                     /tissue_type="blood"
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      121 ctatatatta taatcgtact aaacccatta tatgtagacg gacattacac cttgacccca
      181 tttctcccaa tgtacaacct atgcaactcc ccaagacatt aatgctctta ccccagtaaa
      241 tgatctacaa cttccaggtc accataccat gaatggttac aggacataca tgcaatacta
      301 ggtattaccc catttggtta tgctcgacgt accagatgga tttattgatc gtacacctca
      361 cgagagatca ccaacccctg cctataatgt actccatgac tagcttcagg cccattcttt
      421 ccccctacac ccctcgcccc tcttgctctt ttgcg
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LOCUS       PVQMTB        439 bp ds-DNA            ORG        26-FEB-1996
DEFINITION  Green peafowl mitochondrial gene, D-loop region.
ACCESSION   D64164
KEYWORDS    D-loop; hypervariable region.
SOURCE      Pavo muticus adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Pavo muticus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 439)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 439)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (15-Sep-1995) to DDBJ by:
            Tetsuo Miyake
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            Takatagun, Hiroshima 739-11
            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4531
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                     /sequenced_mol="DNA"
                     /tissue_type="blood"
     D-loop          1..439
BASE COUNT      121 a    142 c     55 g    121 t      0 others
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       61 gtatactatg cataatcgtg catacattta tataccacat acattatggt cacagtaata
      121 catactatat acgtactaaa cccattatat gtagacggac attacactat cttccccatt
      181 tatccccacg ttcaaccaat gcatactcct agacataaca cctatactta cccattccct
      241 gctcccacaa cccacaagcc acctaactat gaatggtcac aggacataac gttcatatta
      301 cagctctccc ccatttggtt atgctcgacg tatcagatgg atttattgat cgtacacctc
      361 acgagagatc agcaacccct gcctgtaatg tacttcatga ctagcttcag gcccattctt
      421 tccccctaca cccctcgcc
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LOCUS       PVQMTM       443 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  Common peafowl mitochondrial gene, D-loop region.
ACCESSION   D66900
KEYWORDS    D-loop; hypervariable region.
SOURCE      Pavo cristatus adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Pavo cristatus
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
  STANDARD  full staff_review
REFERENCE   1  (bases 1 to 443)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT
FEATURES             Location/Qualifiers
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                     /sequenced_mol="DNA"
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     D-loop          1..443
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       61 gtatactatg cataatcgtg catacattta tataccacat atattatggt cacggtaata
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      181 tatccccacg ttcaatcaat gcatgttcct agacataaca ctcataccta cctatccctt
      241 tctctctcag acccacaagt cacctaacta tgaatggtta caggacataa tcttcatatt
      301 acagctcttc cccatttggt tatgctcgac gtaccagatg gatttattga tcgtacacct
      361 cacgagagat cagcaacccc tgcccgtaat gtactccatg actaggttca ggcccattct
      421 ttccccctac acccctcgcc ctt
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LOCUS       PXDMTD       483 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  European grey partridge mitochondrial gene, D-loop region.
ACCESSION   D66891
KEYWORDS    D-loop; hypervariable region.
SOURCE      Perdix perdix adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Perdix perdix
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 483)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 483)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
            Tetsuo Miyake
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            Takatagun, Hiroshima 739-11
            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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                     /mitochondrion
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BASE COUNT      124 a    148 c     71 g    140 t      0 others
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       61 ggtatgctat gtacagcgtg catatctttg tgttccccat acattatggt aacagtacta
      121 tatattatat accgtactag gcccattata tgtaaacgga cattacacta tcagccccat
      181 ctctcctcac gtgcatatta accattctct aagactatac ttgctacctc accaacactg
      241 cctacaaagc ccacaaggca ccataactat taatggttac aggacataat acttaatatt
      301 ctatcacctc cacatttggt tatgctcgac gtaccagatg gatttattga tcggacacct
      361 cacgagagat cagcaacccc tgcccgtaat gtacttcatg actagcttca ggcccattct
      421 ttccccctac acccctcgcc ctacttgctc ttttgcgcct ctggttcctc gggcaggaca
      481 tcc
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LOCUS       QULMTA        459 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  Blue-breasted quail mitochondrial gene, D-loop region.
ACCESSION   D66888
KEYWORDS    D-loop; hypervariable region.
SOURCE      Coturnix sinesis adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Coturnix sinesis
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 459)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 459)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
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            Takatagun, Hiroshima 739-11
            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4351
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       61 gtatactatg tataatcgtg catacattta tattccacat atattatggt accggtaata
      121 gatattatat acgtactaaa cccattatat gtatacggac attaaagatt tgccccattt
      181 ctcccaatgt acattaatgc atgctcctag acattaaact ctctctacca gcccacgatt
      241 ctaacccaaa caaggcacca tagacatgaa tggttacagg acatacctct aatacataat
      301 gtcattccac atttggttat gctcgtcgta tcagatggat ttattgatcg gacacctcac
      361 gagagatcag caacccctgc tcgtaatgtt tatcatgact agtttcaggc ccattctttc
      421 cccctacacc cctcgccctc cttcgtcttt tgcgcctct
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LOCUS       SIYMTI        440 bp ds-DNA            ORG       26-FEB-1996
DEFINITION  Mrs. Hume's pheasant mitochondrial gene, D-loop region.
ACCESSION   D66896
KEYWORDS    D-loop; hypervariable region.
SOURCE      Syrmaticus humiae adult blood mitochondrion DNA.
  ORGANISM  Mitochondrion Syrmaticus humiae
            Eukaryota; Animalia; Chordata; Vertebrata; Aves; Neornithes;
            Neognathae; Galliformes; Phasianidae.
REFERENCE   1  (bases 1 to 440)
  AUTHORS   Miyake,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1995) to the DDBJ/EMBL/GenBank databases. Tetsuo
            Miyake, Wakunaga Pharmaceutical Co., Ltd., Institute for
            Biotechnology Research, 1624 Shimokotachi, Koda-cho, Takata-gun,
            Hiroshima 739-11, Japan
  STANDARD  full staff_review
REFERENCE   2  (bases 1 to 440)
  AUTHORS   Akishinonomiya,F., Miyake,T., Takada,M., Ohno,S. and Kondo,N.
  TITLE     The genetic link between the Chinese bamboo partridge (Bambusicola
            thracica) and the chicken and junglefowls of the genus Gallus.
  JOURNAL   Proc. Natl. Acid. Sci. U.S.A. 92, 11053-11056 (1995)
  STANDARD  full staff_review
COMMENT     Submitted (14-Sep-1995) to DDBJ by:
            Tetsuo Miyake
            Dept. of Institute for Biotechnology Research
            Wakunaga Pharmaceutical Co.,Ltd.
            1624 Shimokotachi, Kodachou
            Takatagun, Hiroshima 739-11
            Japan
            Phone:  0826-45-2331
            Fax:    0826-45-4351
FEATURES             Location/Qualifiers
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BASE COUNT      126 a    130 c     57 g    127 t      0 others
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       61 ggtatactat gcataatcgt gcatacattt atataccaca tatactatgg taccggtact
      121 atatattata atcgtactaa acccattata tgtagacgga cattaaacta ataccctcat
      181 ttctcccaat gtacagtcta tgcaatgctc ctagacttac cctccaacct ccccaagtaa
      241 ctagctccag agccctcaag tcaccataac tatgaatggt tacaggacat actatctaat
      301 acaatattct tcctcatttg gttatgctcg acgtaccaga tggatttatt aatcgtacac
      361 ctcacgagag atcaccaacc cctgtctgta atgtattccg tgaccagact caggcccatt
      421 cttttcccct acacccctcg
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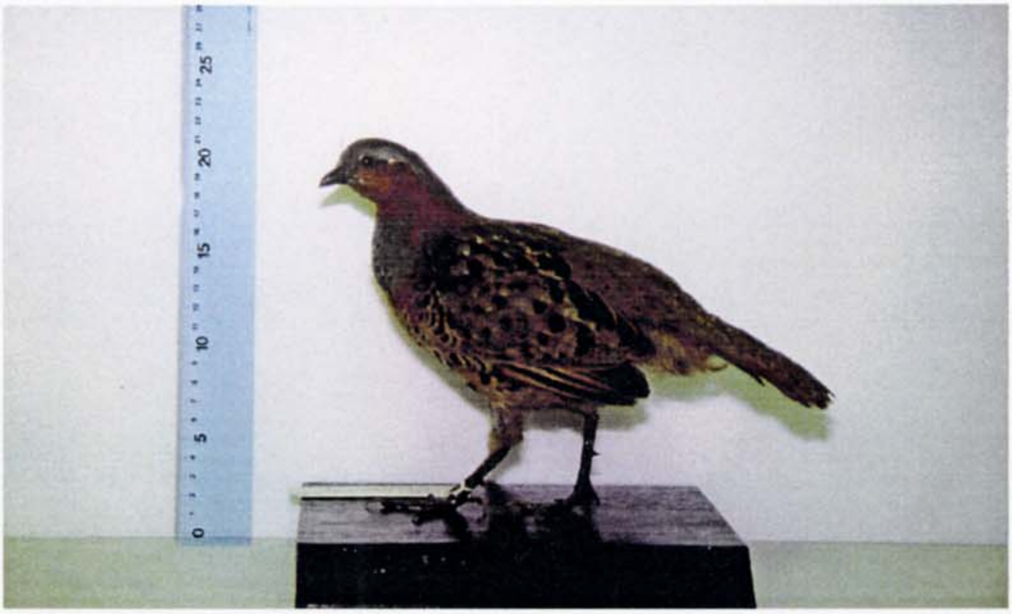
Appendix B

Photographs of the Phasianid Birds that are the Same Species from which the Blood Samples are Taken

Coturnix coturnix japonica

Coturnix or Excalfactoria chinensis



Bambusicola thoracica

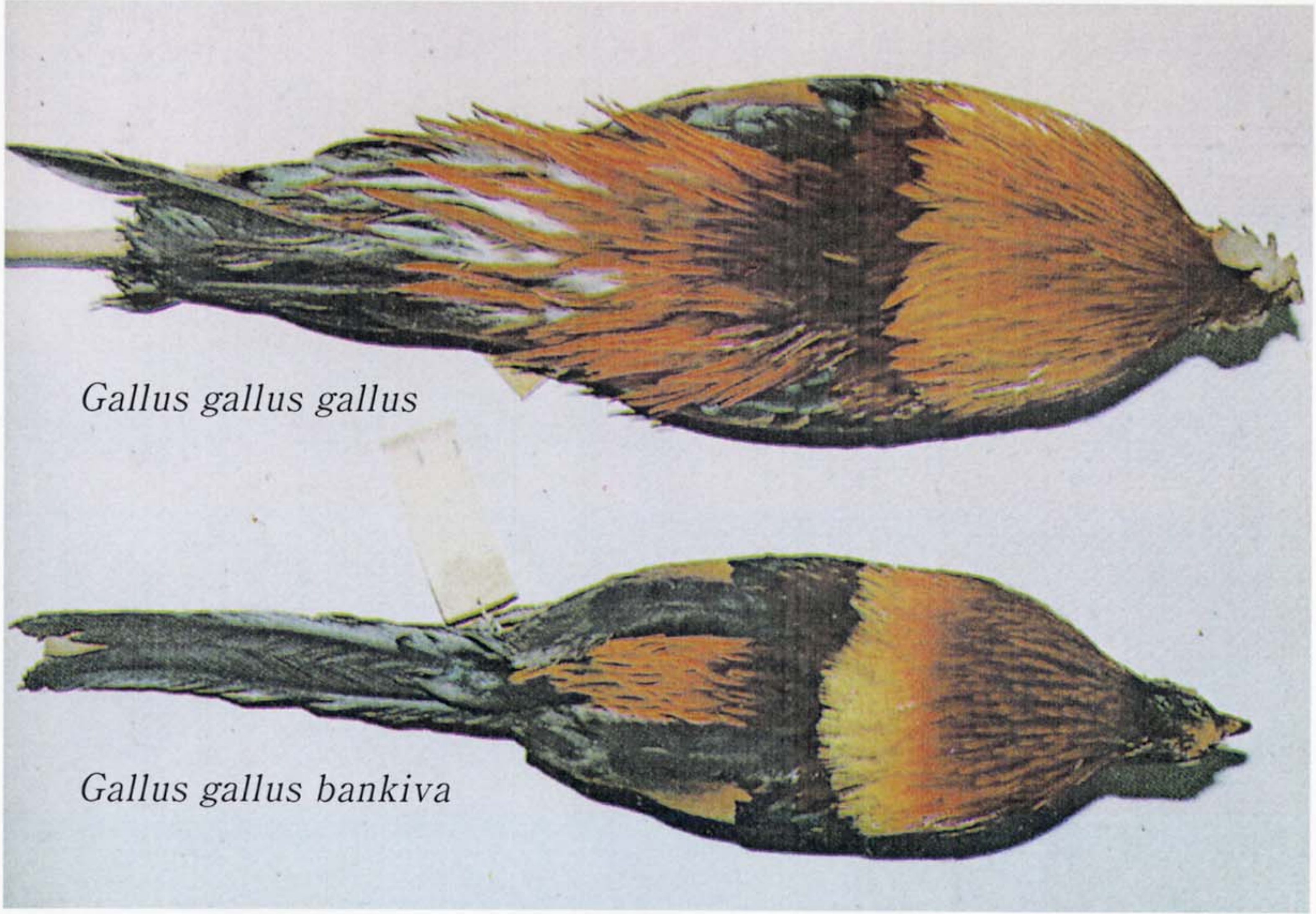
Alectoris graeca

Perdix perdix perdix

Gallus varius

Gallus gallus

Gallus gallus bankiva



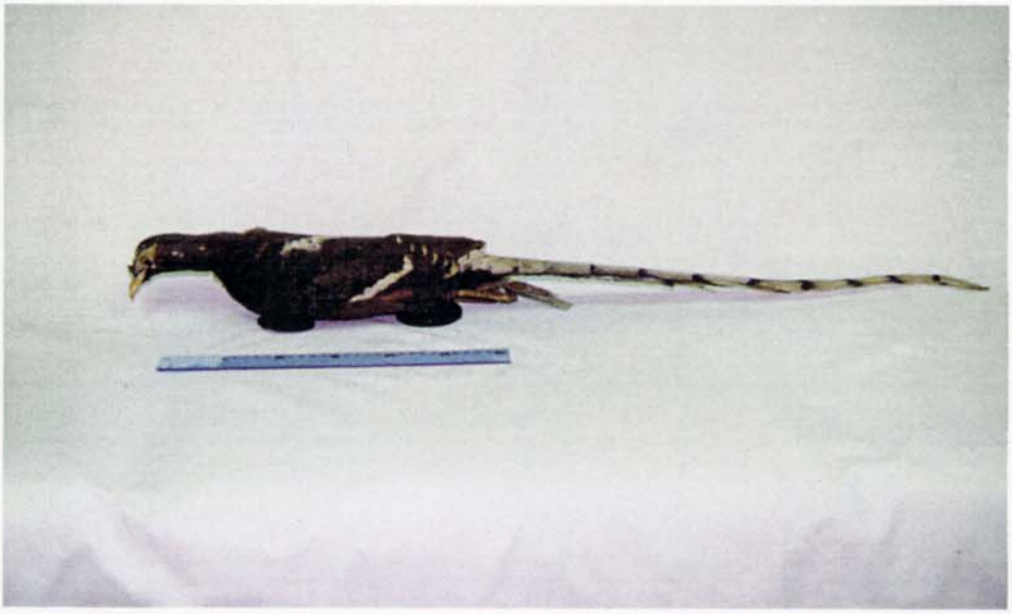
Morphological comparison between *Gallus gallus gallus* and *Gallus gallus bankiva*

Gallus sonnerati

Gallus lafayettei

Phasianus versicolor

Chrysolophus pictus



Syrmaticus humiae

Lophura nycthemera

Pavo muticus

Pavo muticus

Pavo cristatus

Polyplectron bicalcaratum

Argusianus argus

Argusianus argus