

Supplementary Material

1 Supplementary Data

1.1 Supplementary Data S1

Materials and Methods

Study area

Chiang Rai is Thailand's northernmost province and forms part of the Golden Triangle region bordering Laos and Myanmar (19° 00'–20° 30' N, 99° 15'–100° 45' E). Occurrence data of the Chee Fah and Fah Luang chickens were collected from smallholder poultry and backyard chicken farms and analyzed to construct a land suitability model. Sampling occurrence data covered 18 villages in three districts, Mae Fa Luang (20° 16' 2" N 99° 48' 5" E), Wiang Kaen (20° 6' 44" N, 100° 30' 49" E), and Wiang Chiang Rung (20° 0' 47" N 100° 3' 25" E). In the study area, Chee Fah and Fah Luang chickens (Figure S1) are raised for poultry production by local communities rather than for sociocultural reasons (Figure S2). Fishnet polygons of 30 m² were created within the boundaries of 18 villages for predictive modeling of the Chee Fah and Fah Luang chickens, with a random sample point of 30% from the total polygons using ArcGIS 10.4.1 [1].

Environmental data

The environmental variables that affected the Chee Fah and Fah Luang chickens were elevation, distance to water, normalized difference vegetation index (NDVI), tree canopy cover, and forest canopy height. Elevation data at 30 m resolution were obtained from the Department of National Parks, Wildlife and Plant Conservation of Thailand, Ministry of Natural Resources and Environment (Figure S3a). The distance to water was calculated as the Euclidean distance between the main rivers (Figure S3b). Data for the inland water layers were obtained from the Land Development Department of the Ministry of Agriculture and Cooperatives, Thailand. The NDVI estimated vegetation activity, measured by Landsat 8 satellite images from January to March 2022, was provided by the U.S. Geological Survey from the Earth Explorer website (Figure S3c). Tree canopy cover, representing the estimated maximum tree canopy cover per pixel at 1–100% for 2010 in integer values (1–100), was obtained from Global Land Analysis and Discovery [2] (Figure S3d). Global Landsat analysis-ready data were used to extrapolate the Global Ecosystem Dynamics Investigation footprint-level forest canopy height measurements [3] (Figure S3e), and ArcGIS was used to interpolate the environmental factors at the same spatial resolution of 30 m in raster format.

Species distribution modeling

The MaxEnt algorithm was used with the available software package, MaxEnt ver. 3.4.4, to perform breed distribution modeling of the Chee Fah and Fah Luang chickens [4,5]. MaxEnt combines environmental predictors and location data as inputs [6] and uses location-only data as appropriate for breed with small locations [7–9]. We selected the logistic output with suitability data ranging from 0 to 1, representing the occurrence probability of the Chee Fah and Fah Luang chickens, with default settings for the convergence threshold and maximum number of iterations (500) (Phillips and Dudík, 2008). Regularization data were selected automatically using MaxEnt software to reduce model overfitting [8]. The optimal MaxEnt model was selected using the 10th percentile presence probability and a 10-fold cross-validation method was used to generate a binary map. Response curves of the predictor variables were developed, and Jackknife importance was tested in the final optimal model [10]. To decrease the predictive uncertainty, we used the ensemble forecasting approach following Araújo and New [11] and applied the basic mathematical function of mean ensembles to calculate the final logistic outputs [12]. Model validation and predictive performance were used to evaluate the area under the curve (AUC) of receiver operating characteristics [13]. AUC data were threshold-independent measures of model accuracy that illustrated discrimination ability [13], where an AUC value of 0 indicated a model with no better discrimination than chance, an AUC value of 1 indicated perfect discrimination, and an AUC value greater than 0.8 indicated excellent discrimination. Averaged prediction maps of the final depicted presence probability of the breed were produced, with continuous values ranging from 0 to 1. This presence probability was classified into five equal-sized categorical (SC) classes following Li et al. [14]: SC-5 = very high suitability ($p > 0.8$), SC-4 = high suitability ($0.6 > p \leq 0.8$), SC-3 = moderate suitability ($0.4 > p \leq 0.6$), SC-2 = least suitability ($0.2 \geq p \leq 0.4$), and SC-1 = no suitability ($p < 0.2$). Finally, the area under each of the classified categories was calculated using map algebra in ArcGIS.

Comparison of environmental factors between local chicken farms in Mae Hong Son and Chiang Rai Provinces

Data from 466 Chee Fah and Fah Luang chicken farms in Mae Hong Son and 918 in Chiang Rai were selected for the study (Figure S4a–S4f). The elevation of Mae Hong Son ranged between 234–2,005 m and Chiang Rai ranged between 26–2,007 m, with detailed characteristics of the selected sites shown in Figure S4a and S4d. Annual mean temperature

(°C) and annual precipitation (mm) data (averaged for the year 1950–2000) from WorldClim2 [15] are shown in Figure S4b, S4e, S4c, and S4f. The elevation, annual mean temperature, and annual precipitation of local chicken farms in Mae Hong Son and Chiang Rai were extracted and processed using ArcGIS extract values for the point function. Datasets of elevation, annual mean temperature, and annual precipitation were compared between Mae Hong Son and Chiang Rai using paired *t*-tests.

Mitochondrial DNA D-loop sequence analysis

Multiple sequence alignments were performed for 39 sequences in the mitochondrial DNA (mtDNA) D-loop dataset of the Chee Fah and Fah Luang chickens using the default parameters of the Molecular Evolutionary Genetics Analysis 11 (MEGA11) software [16]. Ambiguous sites, sequences containing gaps and sequence primers were carefully discarded from the dataset. Estimates of the haplotype (*h*) and nucleotide (π) diversity, number of haplotypes (*H*), the estimator theta (*S*), overall haplotype and average number of nucleotide differences (*k*) were calculated using DnaSP version 6.12.03 [17]. To investigate haplotype grouping and population dynamics, a statistical parsimony network from consensus sequences was built in PopART version 1.7 based on the Templeton, Crandall and Sing (TCS) algorithm [18]. Arlequin version 3.5.2.2 was used to calculate the genetic differentiation coefficient (*G_{ST}*), Wright's *F* statistic for subpopulations within the total population (*F_{ST}*) and Φ_{ST} values from sequence and haplotype data [19]. The *F_{ST}* (based on differences in haplotype frequencies) and Φ_{ST} (the relationship between haplotypes based on molecular genetic distance) values were calculated between populations using 1,000 permutations [20,21]. DnaSP version 6.12.03 was used to examine the average number of nucleotide substitutions for each site between populations (*D_{xy}*) and the net nucleotide substitutions for each site between populations (*D_a*).

MtDNA D-loop sequences from this study were combined with data of the Chee Fah and Fah Luang chickens, data derived from the reference dataset of the Siam Chicken Bioresource Project [22,23, Wongloet et al., submitted data] and additional sequences deposited in the National Center for Biotechnology Information (NCBI) database (<https://www.ncbi.nlm.nih.gov/>). In total, 978 (496 sequences from the reference dataset of the Siam Chicken Bioresource Project, 443 sequences from the NCBI database and 39 sequences from this study) mtDNA D-loop sequences were aligned and prepared as mentioned above.

The dataset was trimmed to 398 bp to construct phylogenetic relationships and pairwise distances between the Chee Fah and Fah Luang chickens, red junglefowl and other domestic chicken breeds. The best fit nucleotide substitution model was estimated using ModelFinder [24] and a phylogenetic tree was reconstructed based on maximum likelihood, with ultrafast 10,000 bootstrap replicates [25] implemented in IQ-TREE v1.6.12 [26] and visualized using Interactive Tree of Life (iTOL) v5 online (<https://itol.embl.de/>, [27]). Genetic pairwise distances between the Chee Fah and Fah Luang chickens and other breeds were calculated using the default parameters for between-group genetic distance calculations implemented in MEGA11 software [16].

Analysis of genetic diversity and population structure of Chee Fah and Fah Luang chickens based on microsatellite DNA markers

Genetic diversity and population structure analyses based on microsatellite markers were previously described [22,23]. Genetic diversity parameters including allelic frequency, number of alleles (N_a), number of effective alleles (N_{ea}), observed heterozygosity (H_o), expected heterozygosity (H_e), linkage equilibrium and Wright's F-statistic for subpopulations within the total population (F_{ST}) were calculated using Arlequin version 3.5.2.2 [19]. To account for limited population size, deviations from the Hardy-Weinberg equilibrium were assessed at each locus by implementing the Markov chain Monte Carlo (MCMC) approximation of Fisher's exact test in the "genepop" function in the package "stats" of R version 4.1.2 [28–30]. Significant differences and equal variances of H_o and H_e between the Chee Fah and Fah Luang populations were assessed by Welch's t-test (unequal variance between samples) using the "t.test" function and Bartlett's homogeneity of variance test using the "bartlett.test" function in "stats" of R version 4.1.2 [30,31]. FSTAT version 2.9.4 was used to calculate allelic richness (AR) [32]. The MicroChecker program was used to locate null allelic markers [33] and Excel Microsatellite Toolkit add-ins were utilized to determine the polymorphic information content (PIC) for each locus [34]. For each locus within populations, Shannon's information index (I) and fixation index (F) were determined using GenAlEx version 6.5 [35]. To account for the possibility of sibling-sibling or parent-offspring pairs within populations, the Chee Fah and Fah Luang chickens were assessed by relatedness values (r) by calculating relatedness between all female-female, male-male and male-female pairs based on population allelic frequencies using GenAlEx version 6.5 [35]. The LynchRt estimator [36], as implemented in the program COANCESTRY [37], was used to calculate

individual and overall F_{IS} with 95% confidence intervals. Both estimations (r values and F_{IS}) assumed that average values did not differ significantly from random assortments of unrelated individuals.

The infinite allele model (IAM) based on corrected p -values of F_{ST} , as implemented in Arlequin version 3.5.2.2. and the stepwise mutation model (SMM) using R_{ST} in FSTAT version 2.9.3 [32] were determined to assess pairwise genetic distances among the population. To account for null alleles on the estimation of genetic differentiation, ENA (excluding null alleles) corrections using the FreeNA program [38] were implemented to obtain pairwise F_{ST} ENA values.

To elucidate the group structure, an analysis of molecular variance (AMOVA) was performed using Arlequin 3.5.2.2. Unlike F_{ST} , this algorithm identifies subgroup hierarchical structure and does not require a priori assumption of the Hardy-Weinberg equilibrium. Nei's genetic distances between groups were then examined using GenAlEx version 6.5 [39]. Principal coordinate analysis (PCoA) was performed using GenAlEx version 6.5 [35] to assess the overall relationship among individuals in the population. Analysis of principal components (DAPC) was performed using the package ADEGENET 2.0 [40] in R 4.1.2 [30]. DAPC makes no assumptions about population models [40] and defines synthetic variables where genetic variation is maximized between clusters of individuals (K) and minimized within clusters. The model-based clustering method implemented in STRUCTURE version 2.3.4 was used to determine population structure [41]. The run length was set to 100,000 MCMC replicates after a burn-in period of 100,000 generations using correlated allelic frequencies under a straight admixture model. The number of clusters (K) varied from 1 to 25, with 25 replicates for each value of K . The most probable number of bunches was dictated by plotting the log likelihood of the information ($\ln \Pr (X|K)$) [41] over the scope of tested K esteems before choosing the K esteem value at which $\ln \Pr (X|K)$ settled. The ΔK strategy was also applied using Structure Harvester [42]. To investigate the possibility of selective sweep within the two populations of the Chee Fah and Fah Luang chickens, the individuals/population expected heterozygosity (H_e), observed heterozygosity (H_o) and inbreeding coefficient (F_{IS}) values based on genotype data were plotted for each microsatellite locus (28 loci in total). The sweep or purifying selection signature is reflected by high F_{IS} and low H_e , whereas neutral or balanced selection is shown by low F_{IS} and high H_e .

To investigate the origin of the Chee Fah and Fah Luang chickens, we performed PCoA, DAPC and model-based clustering methods based on ΔK value using genotypic data of red

junglefowl and Thai domestic chicken breeds/ecotypes retrieved from “The Siam Chicken Bioresource Project” together with the data of the Chee Fah and Fah Luang chickens [22,23] as mentioned above. To date a possibility of selective sweep of the Chee Fah and Fah Luang, red junglefowl and other domestic chickens within the Siam Chicken Bioresource Project, the same methods were performed as mentioned previously.

References

1. Morehouse, S.; The arc/info geographic information system. *Comput. Geosci.* **1992**, *18*, 435–441. doi: 10.1016/0098-3004(92)90073-Z.
2. Hansen, M.C.; Potapov, P.V.; Moore, R.; Hancher, M.; Turubanova, S.A.; Tyukavina, A.; Thau, D.; Stehman, S.V.; Goetz, S.J.; Loveland, T.R.; et al. High-resolution global maps of 21st-century forest cover change. *Science* **2013**, *342*, 850–853. doi: 10.1126/science.1239552.
3. Potapov, P.; Hansen, M.C.; Kommareddy, I.; Kommareddy, A.; Turubanova, S.; Pickens, A.; Adusei, B.; Tyukavina, A.; Ying, Q. Landsat analysis ready data for global land cover and land cover change mapping. *Remote Sens.* **2020**, *12*, 246. doi: 10.3390/rs12030426
4. Phillips, S.J.; Anderson, R.P.; Schapire, R.E. Maximum entropy modeling of species geographic distributions. *Ecol. Model.* **2006**, *190*, 231–259. doi: 10.1016/j.ecolmodel.2005.03.026.
5. Phillips, S.J.; Dudík, M. Modeling of species distributions with Maxent: new extensions and a comprehensive evaluation. *Ecography* **2008**, *31*, 161–175. doi: 10.1111/j.2007.0906-7590.05203.
6. Elith, J.; Phillips, S.J.; Hastie, T.; Dudík, M.; Chee, Y.E.; Yates, C.J. A statistical explanation of MaxEnt for ecologists. *Divers. Distrib.* **2011**, *17*, 43–57. doi: 10.1111/j.1472-4642.2010.00725.x.
7. Elith, J.; Graham, C.H.; Anderson, R.P.; Dudík, M.; Ferrier, S.; Guisan, A.; Hijmans, R.J.; Huettmann, F.; Leathwick, J.R.; Lehmann, A.; et al. Novel methods improve prediction of species’ distributions from occurrence data. *Ecography* **2006**, *29*, 129–151. doi: 10.1111/j.2006.0906-7590.04596.x.
8. Pearson, R.G.; Raxworthy, C.J.; Nakamura, M.; Peterson, A.T. Predicting species distributions from small numbers of occurrence records: a test case using cryptic geckos in Madagascar. *J. Biogeogr.* **2006**, *34*, 102–117. doi: 10.1111/j.1365-2699.2006.01594.x.

9. Wisz, M.S.; Hijmans, R.J.; Li, J.; Peterson, A.T.; Graham, C.H.; Guisan, A. Effects of sample size on the performance of species distribution models. *Divers. Distrib.* **2008**, *14*, 763–773. doi: 10.1111/j.1472-4642.2008.00482.x.
10. Baldwin, R.A. Use of maximum entropy modeling in wildlife research. *Entropy* **2009**, *11*, 854–866. doi: 10.3390/e11040854.
11. Araujo, M.B.; New, M. Ensemble forecasting of species distributions. *Trends Ecol. Evol.* **2007**, *22*, 42–47. doi: 10.1016/j.tree.2006.09.010.
12. Marmion, M.; Parviainen, M.; Luoto, M.; Heikkinen, R.K.; Thuiller, W. Evaluation of consensus methods in predictive species distribution modelling. *Divers. Distrib.* **2009**, *15*, 59–69. doi: 10.1111/j.1472-4642.2008.00491.x.
13. Fielding, A.H.; Bell, J.F. A review of methods for the assessment of prediction errors in conservation presence/absence models. *Environ. Conserv.* **1997**, *24*, 38–49. doi: 10.1017/S0376892997000088.
14. Li, C.; Wang, J.; Wang, L.; Hu, L.; Gong, P. Comparison of classification algorithms and training sample sizes in urban land classification with Landsat thematic mapper imagery. *Remote Sens.* **2014**, *6*, 964–983. doi: 10.3390/rs6020964.
15. Fick, S.E.; Hijmans, R.J. WorldClim 2: new 1-km spatial resolution climate surfaces for global land areas. *Int. J. Climatol.* **2017**, *37*, 4302–4315. doi: 10.1002/joc.5086.
16. Tamura, K.; Stecher, G.; Kumar, S. Molecular evolutionary genetics analysis version 11. *Mol. Biol. Evol.* **2021**, *38*, 3022–302. doi: 10.1093/molbev/msab120.
17. Rozas, J.; Ferrer-Mata, A.; Sanchez-DelBarrio, J.C.; Guirao-Rico, S.; Librado, P.; Ramos-Onsins, S.E.; Sanchez-Gracia, A. DnaSP 6: DNA sequence polymorphism analysis of large data sets. *Mol. Biol. Evol.* **2017**, *34*, 3299–3302. doi: 10.1093/molbev/msx248.
18. Clement, M.; Snell, Q.; Walker, P.; Posada, D.; Crandall, K. TCS: estimating gene genealogies. 16th International Parallel and Distributed Processing Symposium (IPDPS 2002), Fort Lauderdale, FL, USA, 15-19 April 2002.
19. Excoffier, L.; Lischer, H.E. Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Mol. Ecol. Resour.* **2010**, *10*, 564–567. doi: 10.1111/j.1755-0998.2010.02847.x.
20. Weir, B.S.; Cockerham, C.C. Estimating F-statistics for the analysis of population structure. *Evolution* **1984**, *38*, 1358–1370. doi: 10.2307/2408641.
21. Excoffier, L.; Smouse, P.E.; Quattro, J. Analysis of molecular variance inferred from metric distances among DNA haplotypes: application to human mitochondrial DNA restriction data. *Genetics* **1992**, *131*, 479–491. doi: 10.1093/genetics/131.2.479.

22. Hata, A.; Nunome, M.; Suwanasopee, T.; Duengkae, P.; Chaiwatana, S.; Chamchumroon, W.; Suzuki, T.; Koonawootrittriron, S.; Matsuda, Y.; Srikulnath, K. Origin and evolutionary history of domestic chickens inferred from a large population study of Thai red junglefowl and indigenous chickens. *Sci. Rep.* **2021**, *11*, 2035. doi: 10.1038/s41598-021-81589-7.
23. Singchat, W.; Chaiyes, A.; Wongloet, W.; Ariyaraphong, N.; Jaisamut, K.; Panthum, T.; Ahmad, S.F.; Chaleekarn, W.; Suksavate, W.; Inpota, M.; et al. Red junglefowl resource management guide: Bioresource reintroduction for sustainable food security in Thailand. *Sustainability* **2022**, *14*, 7895. doi: 10.3390/su14137895.
24. Kalyaanamoorthy, S.; Minh, B.Q.; Wong, T.K.F.; von Haeseler, A.; Jermini, L.S. ModelFinder: fast model selection for accurate phylogenetic estimates. *Nat Methods*. **2017**, *14*, 587–589. doi: 10.1038/nmeth.4285.
25. Hoang, D.T.; Chernomor, O.; Von Haeseler, A.; Minh, B.Q.; Vinh, L.S. UFBoot2: Improving the ultrafast bootstrap approximation. *Mol. Biol. Evol.* **2017**, *35*, 518–522. doi: 10.1093/molbev/msx281.
26. Trifinopoulos, J.; Nguyen, L.T.; von Haeseler, A.; Minh, B.Q. W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic. Acids. Res.* **2016**, *44*, W232–235. doi: 10.1093/nar/gkw256.
27. Letunik, I.; Bork, P. Interactive Tree Of Life (iTOL) v5: an online tool for phylogenetic tree display and annotation. *Nucleic Acids Res.* **2021**, *49*, W293–W296. doi: 10.1093/nar/gkab301.
28. Guo, S.W.; Thompson, E. A Monte Carlo method for combined segregation and linkage analysis. *Am. J. Hum. Genet.* **1992**, *51*, 1111–1126.
29. Raymond, M.; Rousset, F. An exact test for population differentiation. *Evolution* **1995**, *49*, 1280–1283.
30. R Core Team. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria, **2022**.
31. Welch, B.L. The generalization of 'STUDENT'S' problem when several different population variances are involved. *Biometrika* **1947**, *34*, 28–35. doi: 10.1093/biomet/34.1-2.28.
32. Goudet, J. FSTAT (version 1.2): a computer program to calculate F-statistics. *J. Hered.* **1995**, *86*, 485–486. doi: 10.1093/oxfordjournals.jhered.a111627.

33. Van Oosterhout, C.; Hutchinson, W.F.; Wills, D.P.; Shipley, P. MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data. *Mol. Ecol. Notes*. **2004**, *4*, 535–538. doi: 10.1111/j.1471-8286.2004.00684.x.
34. Park, S.D.E. The Excel microsatellite toolkit (version 3.1). Animal Genomics Laboratory, University College Dublin, Ireland, 2001.
35. Peakall, R.; Smouse, P.E. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research--an update. *Bioinformatics* **2012**, *28*, 2537–2539. doi: 10.1093/bioinformatics/bts460.
36. Lynch, M.; Ritland, K. Estimation of pairwise relatedness with molecular markers. *Genetics* **1999**, *152*, 1753–1766. doi: 10.1093/genetics/152.4.1753.
37. Wang, J. COANCESTRY: a program for simulating, estimating and analysing relatedness and inbreeding coefficients. *Mol. Ecol. Resour.* **2011**, *11*, 141–145. doi: 10.1111/j.1755-0998.2010.02885.x.
38. Chapuis, M.P.; Estoup, A. Microsatellite null alleles and estimation of population differentiation. *Mol. Biol. Evol.* **2007**, *24*, 621–631. doi: 10.1093/molbev/msl191.
39. Nei, M. Genetic distance between populations. *Am. Nat.* **1972**, *106*, 283–292.
40. Jombart, T. adegenet: a R package for the multivariate analysis of genetic markers. *Bioinformatics* **2008**, *24*, 1403–1405. doi: 10.1093/bioinformatics/btn129.
41. Pritchard, J.K.; Stephens, M.; Donnelly, P. Inference of population structure using multilocus genotype data. *Genetics* **2000**, *155*, 945–959. doi: 10.1093/genetics/155.2.945.
42. Earl, D.A.; von Holdt, B.M. STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conserv Genet Resour* **2011**, *4*, 359–361. doi: 10.1007/s12686-011-9548-7.

2 Supplementary Figures and Tables

2.1 Supplementary Figures

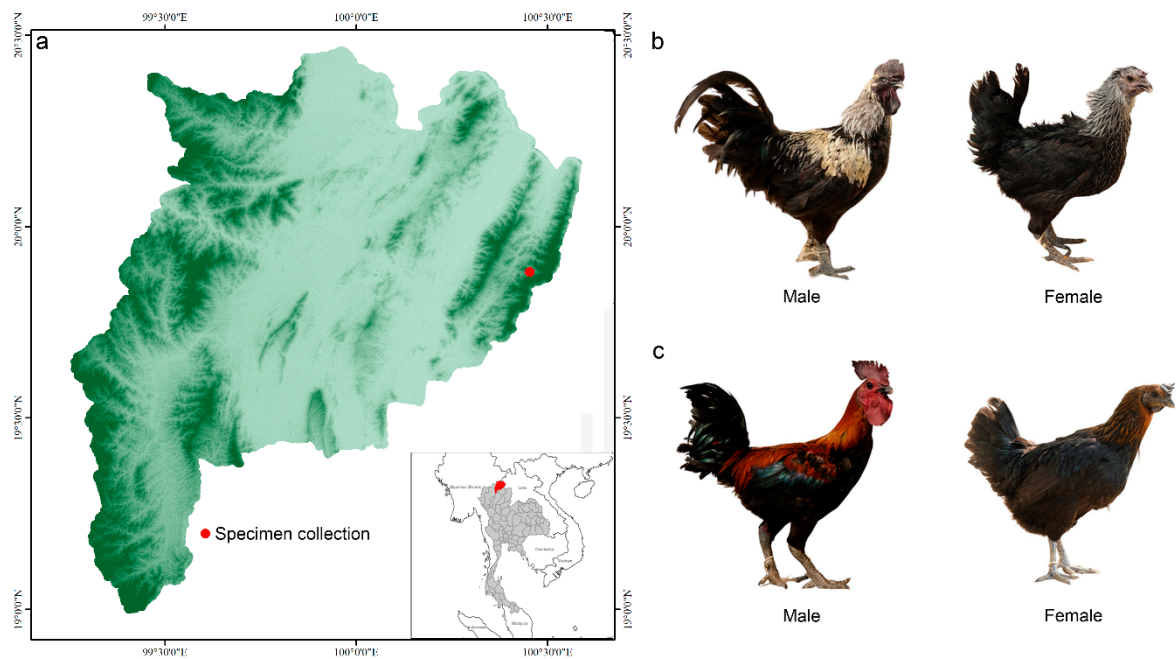


Figure S1. Specimen origin (a) and phenotypic characteristics of male and female Chee Fah (b) and Fah Luang (c) Northern Thailand domestic chicken breeds.

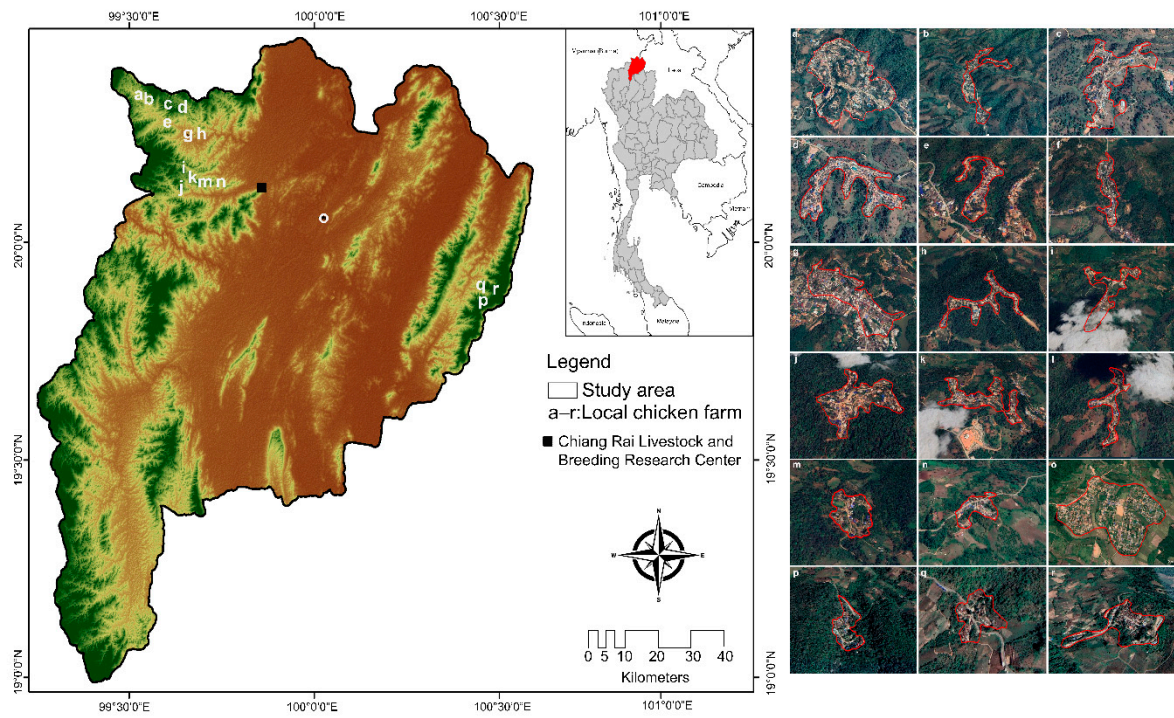


Figure S2. Study area and occurrence data of the Chee Fah and Fah Luang chickens.

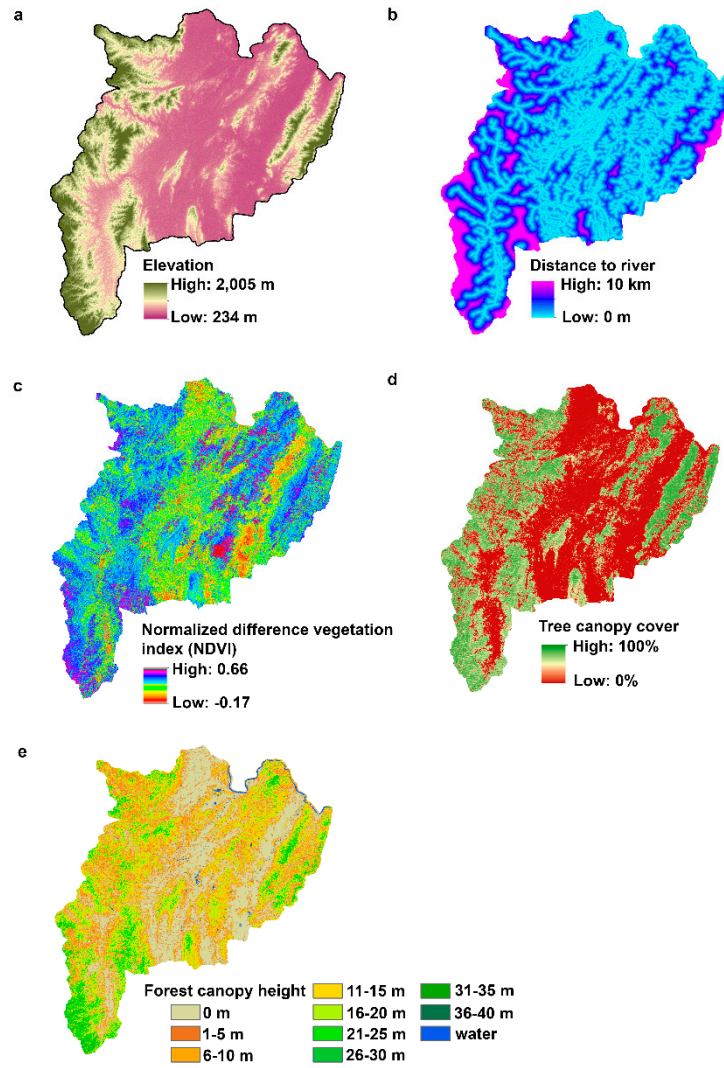


Figure S3. Environmental variables used to assess the species distribution model of the Chee Fah and Fah Luang chickens: (a) elevation, (b) distance to water, (c) normalized difference vegetation index (NDVI), (d) tree canopy cover and (e) forest canopy height.

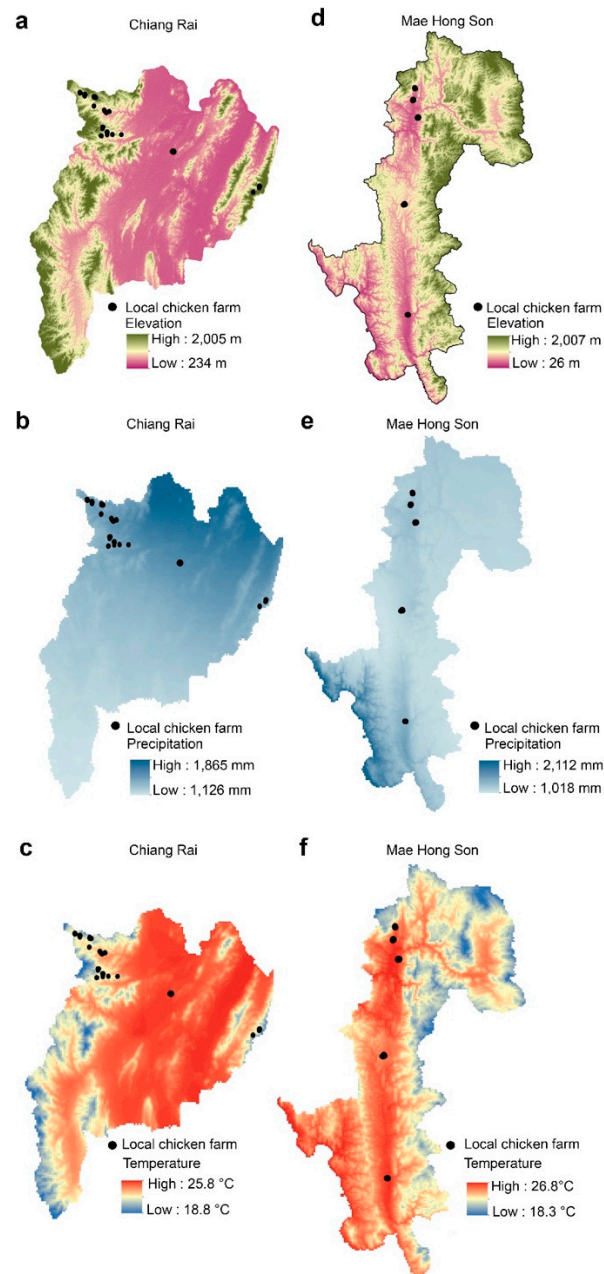


Figure S4. Elevation (a,d), annual mean temperature (b,e) and annual precipitation (c,f) map with 466 local chicken farm stations from Mae Hong Son province and 918 local chicken farm stations from Chiang Rai province.

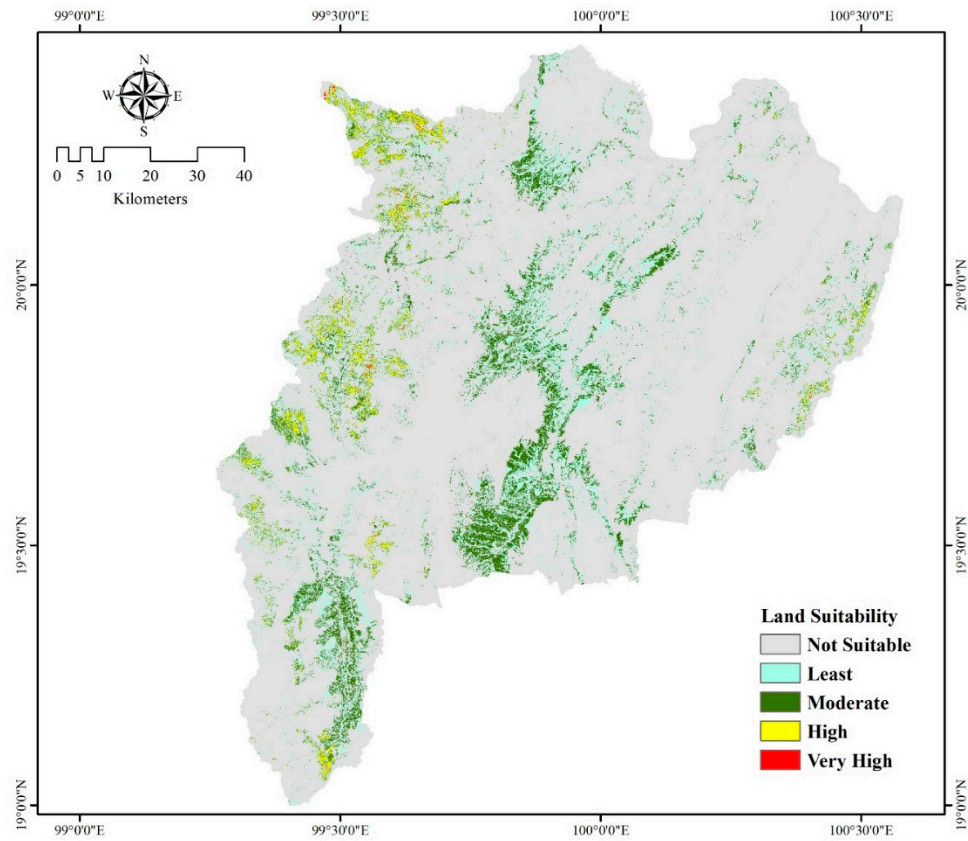


Figure S5. Potential land suitability modeling of the Chee Fah and Fah Luang chickens in Thailand.

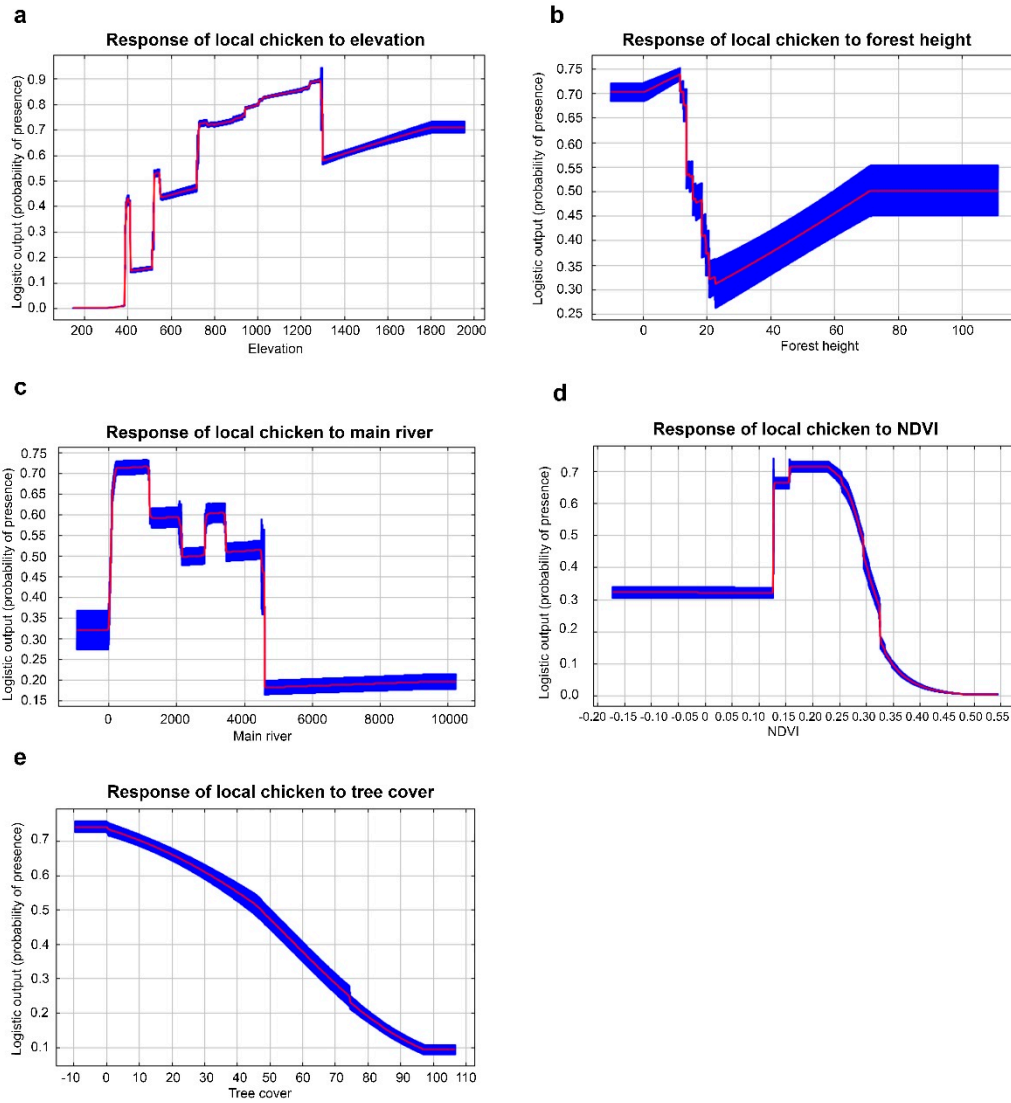


Figure S6. Maximum entropy modeling response area curves of the predictor variables influencing the Chee Fah and Fah Luang chicken distribution: (a) elevation, (b) forest canopy height, (c) main river, (d) normalized difference vegetation index (NDVI) and (e) tree cover.

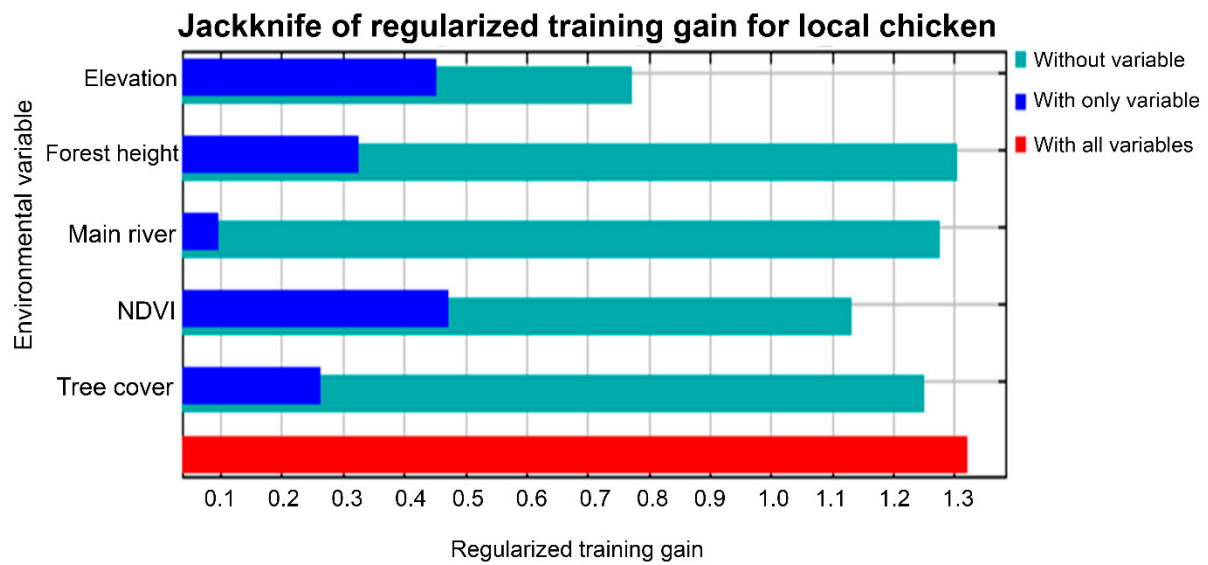


Figure S7. The Jackknife method used in maximum entropy modeling and environmental factors affecting the potential distribution of the Chee Fah and Fah Luang chickens.

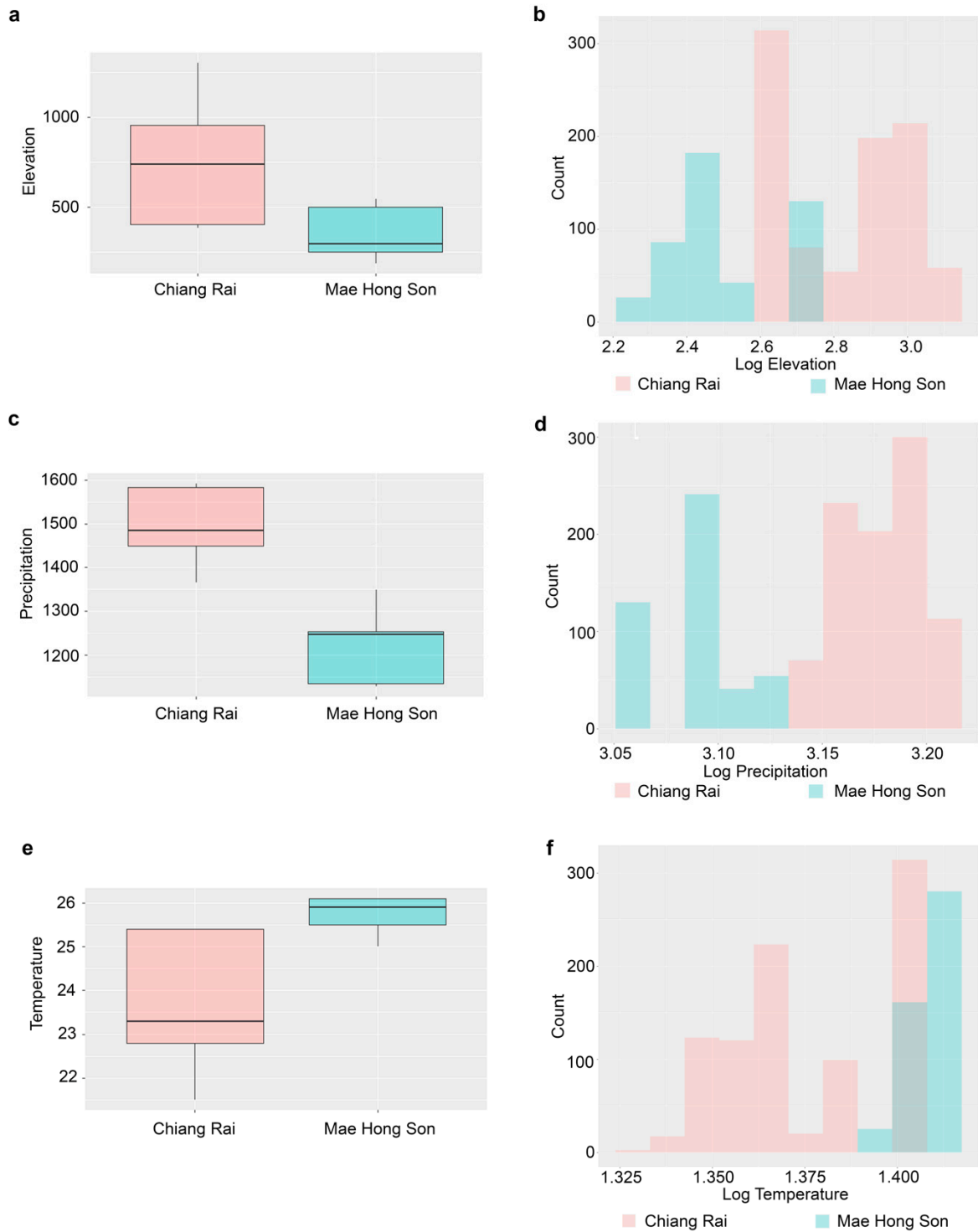


Figure S8. Environmental factor characteristics including (a) mean and (b) histogram of elevation, (c) mean and (d) histogram of annual precipitation and (e) mean and (f) histogram of annual temperature compared between Chiang Rai and Mae Hong Son provinces.

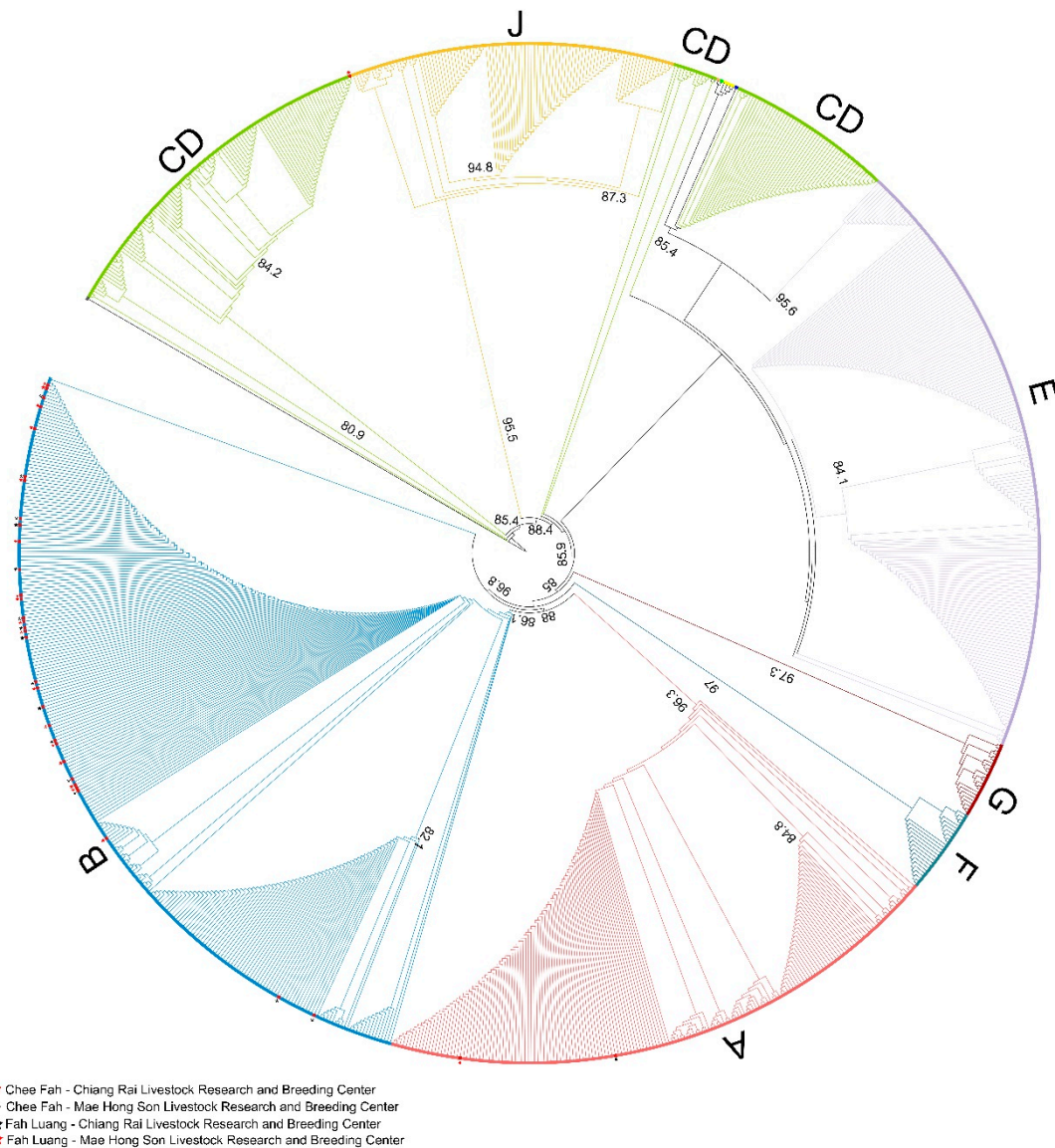


Figure S9. Phylogenetic relationships between Chee Fah and Fah Luang, domestic breeds and red junglefowl based on the maximum likelihood approach with 10,000 ultrafast bootstrap replicates. The red dot represents samples from this study. The number above the node denote bootstrap value. The letter and color indicate assigned haplogroups. Haplogroups nomenclature are based on Miao et al. [1].

1. Miao, Y.W.; Peng, M.S.; Wu, G.S.; Ouyang, Y.N.; Yang, Z.Y.; Yu, N.; Liang, J.P.; Pianchou, G.; Beja-Pereira, A.; Mitra, B.; et al. Chicken domestication: an updated perspective based on mitochondrial genomes. *Heredity* **2013**, *110*, 277–282. doi: 10.1038/hdy.2012.83.

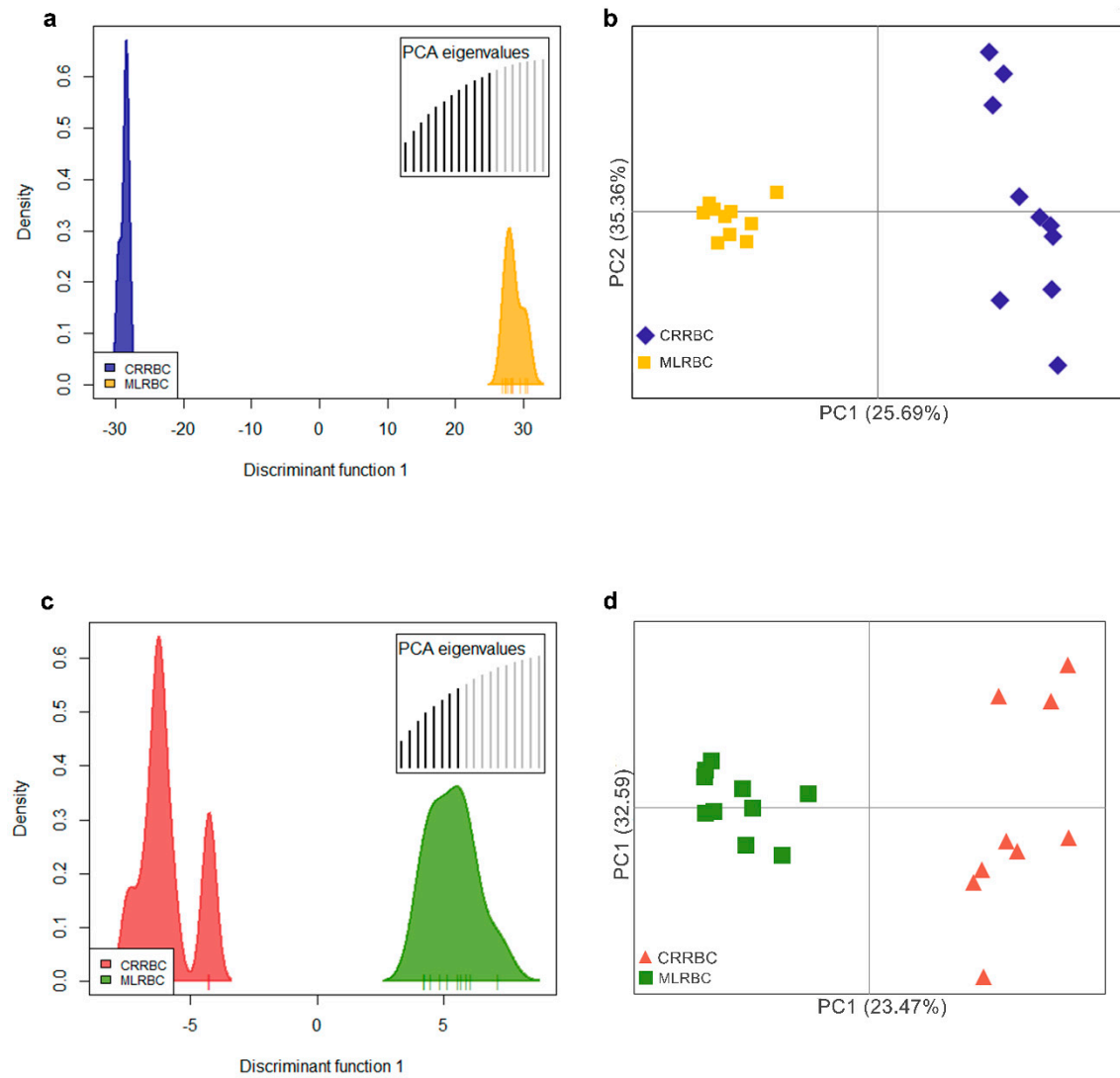


Figure S10. Discriminant Analysis of Principal Components (DAPC) and Principal Coordinate Analysis (PCoA) results of (a, b) Chee Fah and (c, d) Fah Luang breeds from two populations (Mae Hong Son Livestock Research and Breeding Center: MLRBC and Chiang Rai Livestock Research and Breeding Center: CRRBC). Assigned genetic clusters are represented by different colors while dots represent different individuals.

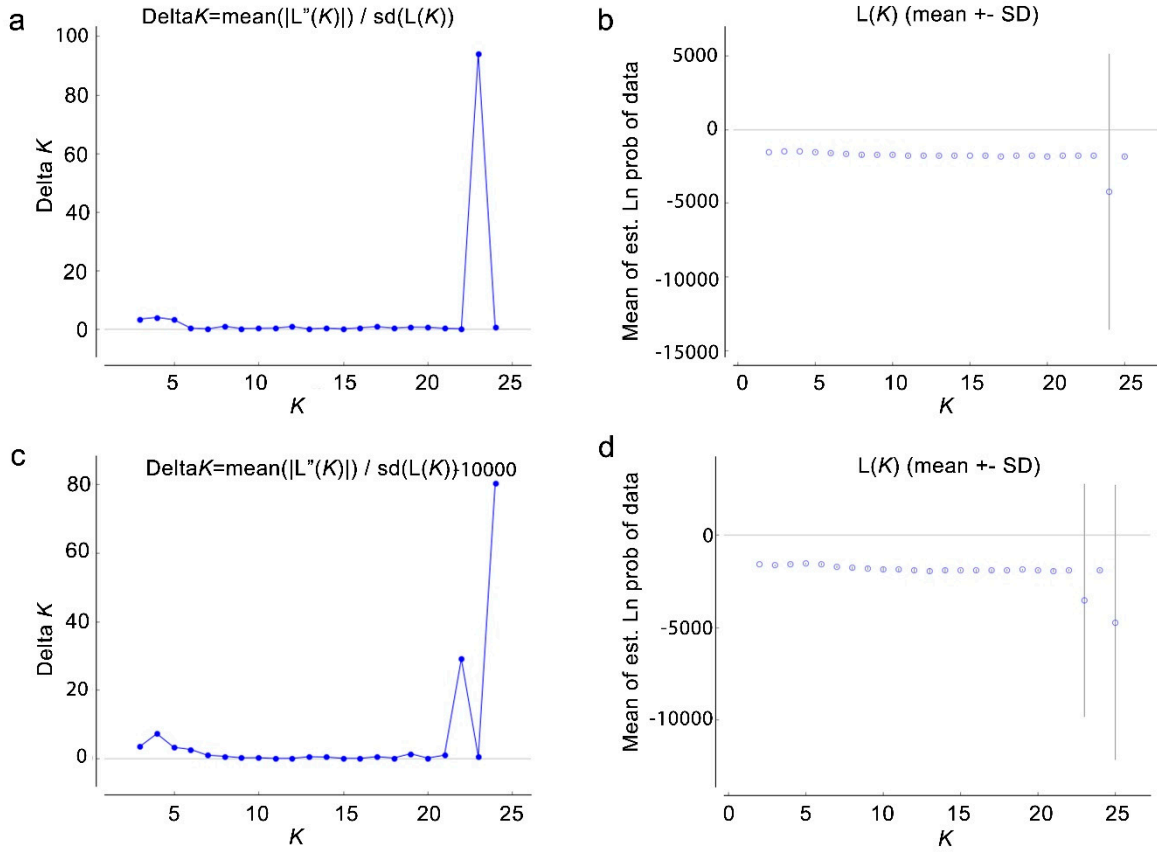


Figure S11. Different population structure patterns of the Chee Fah (n= 20) and Fah Luang chickens (n =19) generated by model-based Bayesian clustering algorithms implemented in STRUCTURE. (a) Plot of Evanno's ΔK of Chee Fah chickens, (b) plot of Evanno's ΔK of the Fah Luang chickens, (c) plot of $\ln P(K)$ of the Chee Fah chickens, and (d) Plot of $\ln P(K)$ of the Fah Luang chickens.

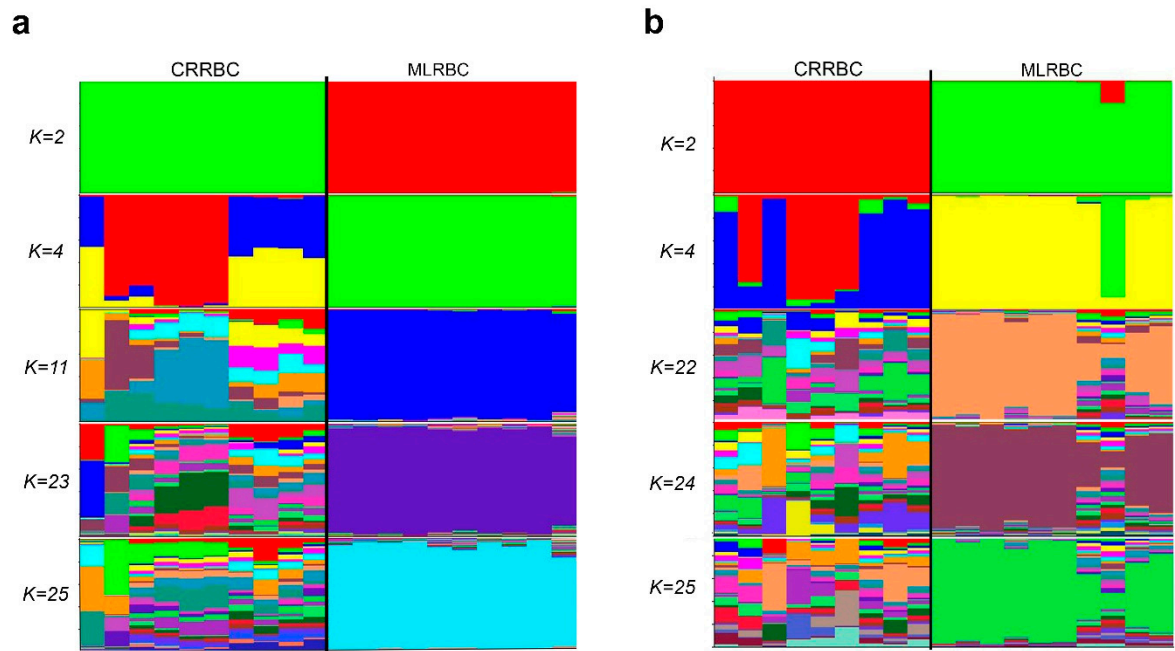


Figure S12. Population structure of (a) the Chee Fah (n=20) and (b) Fah Luang (n=19) chicken individuals from two populations (Mae Hong Son Livestock Research and Breeding Center: MLRBC and Chiang Rai Livestock Research and Breeding Center: CRRBC). Each vertical bar on the x-axis represents an individual, while the y-axis represents the proportion of membership (posterior probability) in each genetic cluster. Black vertical lines indicating the boundaries. Detailed information on all indigenous chicken individuals is presented in Table S1.

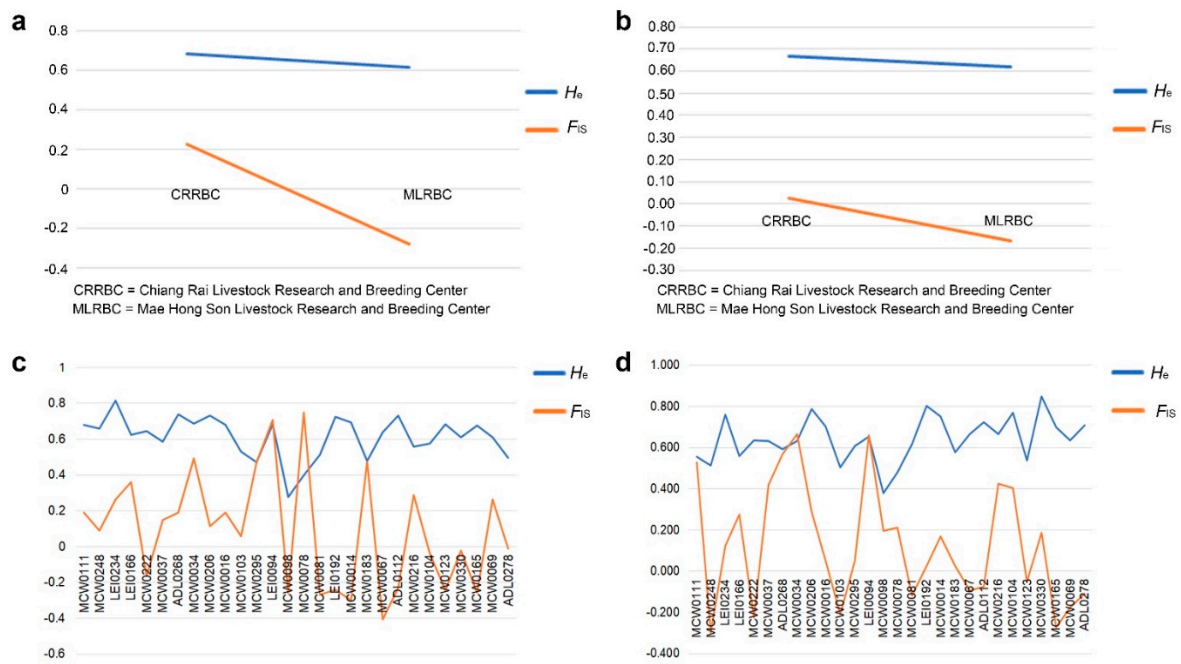


Figure S13. Mapping of expected heterozygosity (H_e) against inbreeding coefficients (F_{IS}) along the length of the physical map. (a) Chee Fah chicken populations, (b) Fah Luang chicken populations, (c) microsatellite loci of the Chee Fah chickens and (d) microsatellite loci of the Fah Luang chickens.

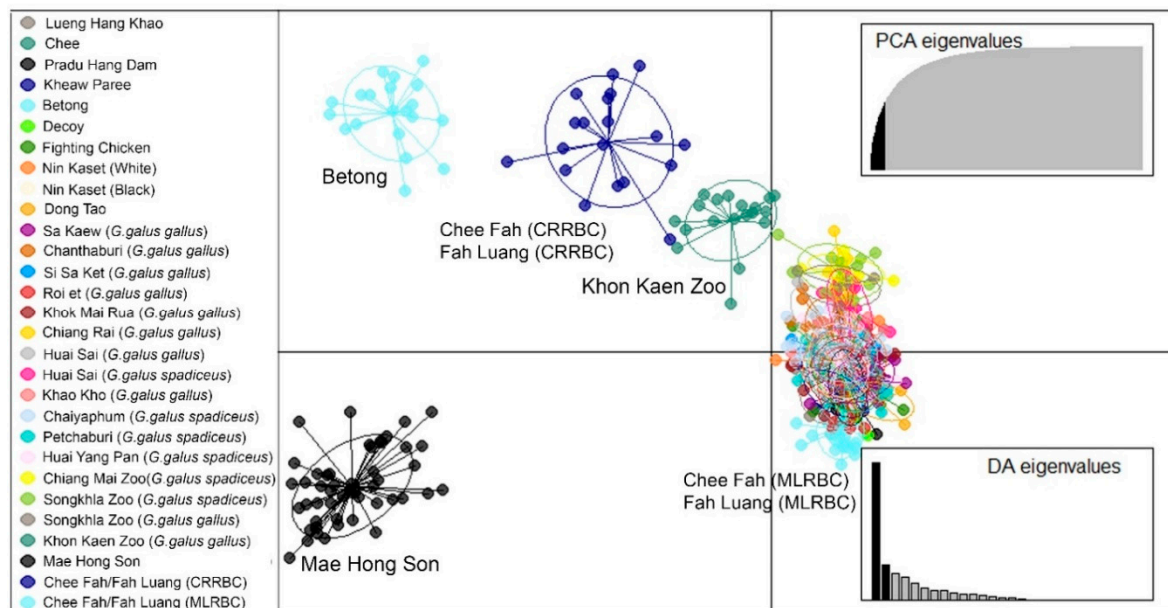


Figure S14. Discriminant Analysis of Principal Components (DAPC) of Chee Fah and Fah Luang Chickens from Chiang Rai Livestock Research and Breeding Center (CRRBC) and Mae Hong Son Livestock Research and Breeding Center (MLRBC) with red junglefowl and domestic breeds. Scatter plots based on DAPC output for assigned genetic clusters are indicated by different colors. Dots represent different individuals.

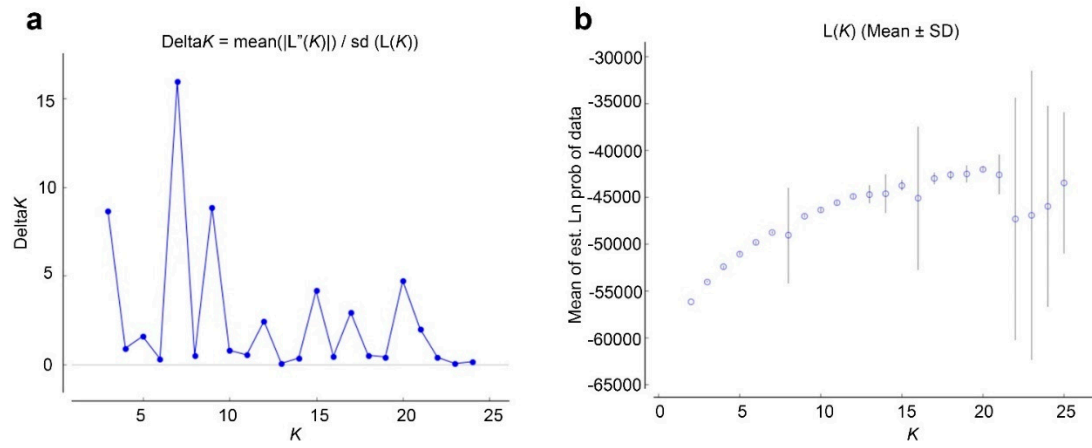
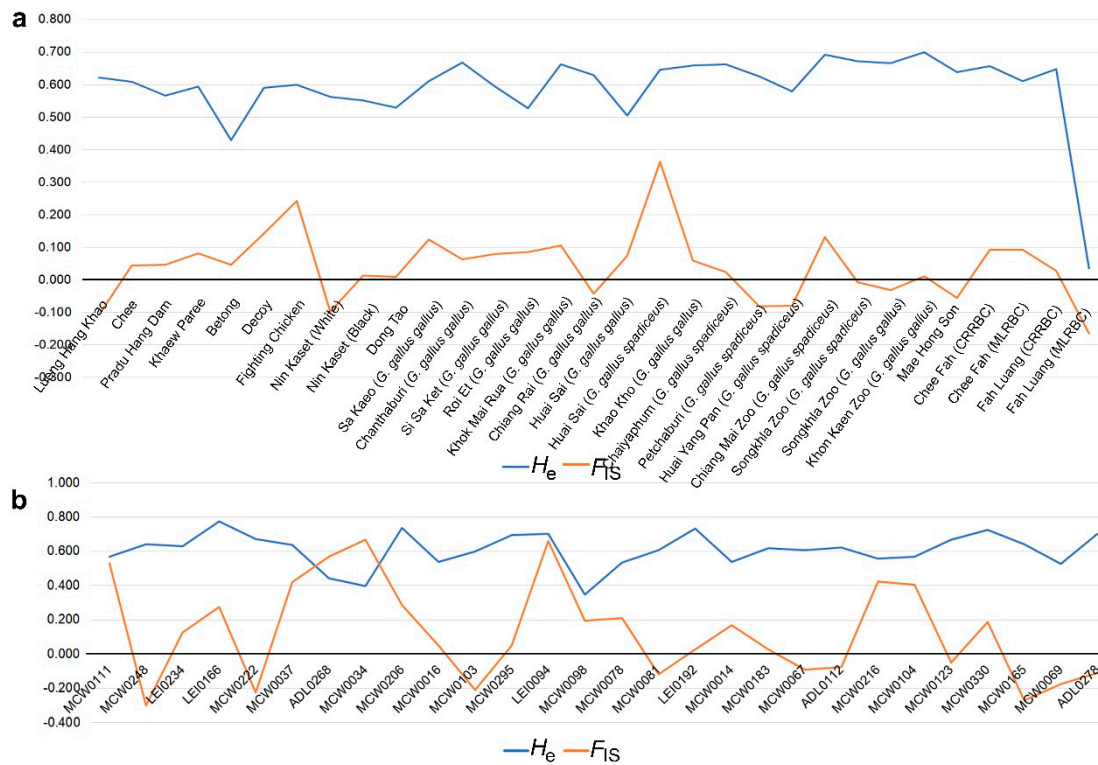


Figure S15. Different population structure patterns of Chee Fah ($n = 20$), Fah Luang ($n = 19$), red junglefowl and domestic chicken breeds, generated by model-based Bayesian clustering algorithms implemented in STRUCTURE. (a) Plot of Evanno's ΔK and (b) Plot of $\ln P(K)$.



CRRBC = Chiang Rai Livestock Research and Breeding Center, Chiang Rai
MLRBC = Mae Hong Son Livestock Research and Breeding Center, Mae Hong Son

Figure S16. Mapping of expected heterozygosity (H_e) against inbreeding coefficients (F_{IS}) along the length of the physical map. (a) Chee Fah and Fah Luang chicken breeds, red junglefowl and domestic chicken breeds and (b) microsatellite loci.

2.2 Supplementary Tables

Table S1 Representative specimens of two populations of Chee Fah and Fah Luang chicken breeds in Thailand. All mtDNA D-loop sequences were deposited in the DNA Data Bank of Japan (DDBJ).

No.	Abbreviation/ Code	Sex	Locality	Mitochondrial D-loop DDBJ accession number	Haplogroup
1	CF1	Male	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740535	B
2	CF2	Male	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740540	B
3	CF3	Male	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740530	B
4	CF4	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740544	B
5	CF5	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740537	B
6	CF6	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740541	B
7	CF7	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740538	B
8	CF8	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740543	B
9	CF9	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740529	B
10	CF10	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740545	B
11	CFM1	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740526	B
12	CFM2	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740527	B
13	CFM3	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740531	B
14	CFM4	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740542	B
15	CFM5	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740536	B
16	CFFM1	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740528	B
17	CFFM2	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740533	B
18	CFFM3	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740534	B

No.	Abbreviation/ Code	Sex	Locality	Mitochondrial D-loop DDBJ accession number	Haplogroup
19	CFFM4	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740532	B
20	CFFM5	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740539	B
21	FL1	Male	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740563	A
22	FL2	Male	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740550	B
23	FL3	Male	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740559	B
24	FL5	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740564	B
25	FL6	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740552	B
26	FL7	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740551	A
27	FL8	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740555	B
28	FL9	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740553	B
29	FL10	Female	Chiang Rai Livestock Research and Breeding Center, CRRBC	LC740554	B
30	FLM1	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740546	B
31	FLM2	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740549	B
32	FLM3	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740547	B
33	FLM4	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740556	B
34	FLM5	Male	Maehongson Livestock Research and Breeding Center, MLRBC	LC740548	B
35	FLFM1	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740561	B
36	FLFM2	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740557	B
37	FLFM3	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740562	CD
38	FLFM4	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740558	A
39	FLFM5	Female	Maehongson Livestock Research and Breeding Center, MLRBC	LC740560	B

Table S2 Microsatellite primers and sequences of Chee Fah and Fah Luang chicken specimens.

Primer	Chromosome	Annealing temperate (°C)	Fluorescence	Primer sequence 5' to 3'		Size (bp)
				Forward	Reverse	
ADL0268	1	58	Hex	CTCCACCCCTCTCAGAACTA	CAACTTCCCATCTACCTACT	106–127
MCW0111	1	58	Hex	GCTCCATGTGAAGTGGTTTA	GCTCCATGTGAAGTGGTTTA	94–120
MCW0247	1	58	Fam	GTTGTTCAAAAGAAGATGCATG	TTGCATTAAGTGGGCACTTTC	208–222
LEI0234	2	58	Hex	ATGCATCAGATTGGTATTCAA	CGTGGCTGTGAACAAATATG	218–373
MCW0034	2	58	Hex	ATCTTGAAACCTCACAAAGC	TCTTCCAACCTATTTTATAGT	211–241
MCW0206	2	58	Fam	CTTGACAGTGATGCATTAAATG	ACATCTAGAATTGACTGTTTAC	217–247
LEI0166	3	58	Hex	CTCCTGCCCTTAGCTACGCA	TATCCCCTGGCTGGGAGTTT	338–365
MCW0222	3	58	Hex	GCAGTTACATTGAAATGATTCC	TTCTCAAAACACCTAGAAGAC	218–230
MCW0016	3	58	Fam	ATGGCGCAGAAGGCAAAGCGATAT	TGGCTTCTGAAGCAGTTGCTATGG	126–177
MCW0037	3	58	Fam	ACCGGTGCCATCAATTACCTATTA	GAAAGCTCACATGACACTGCGAAA	149–154
MCW0103	3	58	Fam	AACTGCGTTGAGAGTGAATGC	TTTCCTAACTGGATGCTTCTG	263–270
MCW0295	4	58	Fam	ATCACTACAGAACCCCTCTC	TATGTATGCACGCAGATATCC	82–111
LEI0094	4	58	Hex	GATCTCACCAGTATGAGCTGC	TCTCACACTGTAACACAGTGC	243–281
MCW0078	5	58	Hex	CCACACGAGAGAGAGAAGGTCT	TAGCATATGAGTGTACTGAGCTTC	144–154
MCW0098	4	58	Hex	GGCTGCTTTGTGCTCTTCTCG	CGATGGTCGTAATTCTCACGT	247–257
MCW0081	5	58	Fam	GTTGCTGAGAGCCTGGTGCAG	CCTGTATGTGGAATTACTTCTC	107–146
LEI0192	6	58	Hex	TGCCAGAGCTTCAGTCTGT	GTCATTACTGTTATGTTTATTGC	251–490
MCW0014	6	58	Hex	TATTGGCTCTAGGAAGTGC	GAAATGAAGGTAAGACTAGC	169–202
MCW0183	7	58	Hex	ATCCCAGTGTCGAGTATCCGA	TGAGATTTACTGGAGCCTGCC	293–361
ADL0278	8	58	Hex	CCAGCAGTCTACCTTCCTAT	TGTCATCCAAGAACAGTGTG	118–136
MCW0067	10	58	Fam	GCACTACTGTGTGCTGCAGTTT	GAGATGTAGTTGCCACATTCGGAC	170–182
ADL0112	10	58	Hex	GGCTTAAGCTGACCCATTAT	ATCTCAAATGTAATGCGTGC	132–142
MCW0216	13	58	Hex	GGGTTTTACAGGATGGGACG	AGTTTCACTCCCAGGGCTCG	135–170
MCW0104	13	58	Hex	TAGCACAACCTCAAGCTGTGAG	AGACTTGCACAGCTGTGACC	194–249
MCW0123	14	58	Hex	CCACTAGAAAAGAACATCCTC	GGCTGATGTAAGAAGGGATGA	84–106
MCW0330	17	58	Hex	TGGACCTCATCAGTCTGACAG	AATGTTCTCATAGAGTTCCTGC	259–291
MCW0165	23	58	Hex	CAGACATGCATGCCCAGATGA	GATCCAGTCCTGCAGGCTGC	111–115
MCW0069	26	58	Hex	GCACTCGAGAAAACCTTCCTGCG	ATTGCTTCAGCAAGCATGGGAGGA	155–178

HEX = HEXTM Dye Phosphoramidite, FAM = 6-FAM (6-Carboxyfluorescein)

Table S3 Comparison of environmental factors at local chicken farms in Chiang Rai and Mae Hong Son provinces.

Variable	t-test	<i>p</i>-value
Elevation	34.74	$<2.2 \times 10^{-16}$
Annual Precipitation	74.09	$<2.2 \times 10^{-16}$
Annual Temperature	-42.9	$<2.2 \times 10^{-16}$

Table S4 Genetic differentiation between two populations of Chee Fah and Fah Luang chicken for mitochondrial DNA D-loop sequence. Genetic differentiation coefficient (G_{ST}), Wright's F -statistics for subpopulations within the total population (F_{ST}), Φ_{ST} from sequence data and haplotype data, average number of nucleotide substitutions per site between populations (D_{xy}) and net nucleotide substitutions per site between populations (D_a). Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Breed	Population 1	Population 2	F_{ST}	G_{ST}	Φ_{ST}	D_{xy}	D_a
Chee Fah	MLRBC ¹	CRRBC ²	0.044*	0.023	0.044	0.006	0.0003
Fah Luang	MLRBC ¹	CRRBC ²	0.014*	0.008	0.014	0.007	0.0008

* $p < 0.05$

¹CRRBC = Chiang Rai Livestock Research and Breeding Center, Chiang Rai

²MLRBC = Mae Hong Son Livestock Research and Breeding Center, Mae Hong Son

Table S5 Pairwise differentiation of linkage disequilibrium of Chee Fah chicken individuals at Chiang Rai Livestock Research and Breeding Center (CRRBC) based on 28 microsatellite loci. Numbers indicate *p*-values with 110 permutations. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Locus	MCW0 111	MCW0 247	LEI0 234	LEI0 166	MCW0 222	MCW0 037	ADL0 268	MCW0 034	MCW0 206	MCW0 016	MCW0 103	MCW0 295	LEI0 094	MCW0 098	MCW0 078	MCW0 081	LEI0 192	MCW0 014	MCW0 183	MCW0 067	ADL0 112	MCW0 216	MCW0 104	MCW0 123	MCW0 330	MCW0 165	MCW0 069	ADL0 278	
MCW0 111	0.000																												
MCW0 247	0.273	0.000																											
LEI023 4	0.303	0.180	0.000																										
LEI016 6	0.208	0.930	1.000	0.000																									
MCW0 222	0.230	0.191	0.220	0.561	0.000																								
MCW0 037	0.478	0.257	1.000	0.800	0.435	0.000																							
ADL02 68	0.314	0.668	1.000	0.533	0.553	0.042	0.000																						
MCW0 034	0.105	0.056	1.000	0.683	0.212	0.691	0.709	0.000																					
MCW0 206	0.807	1.000	1.000	0.449	0.912	1.000	0.450	1.000	0.000																				
MCW0 016	0.016	0.784	0.158	0.191	0.201	0.263	0.673	0.435	0.634	0.000																			
MCW0 103	0.745	0.472	0.444	0.682	1.000	0.855	0.686	0.450	1.000	1.000	0.000																		
MCW0 295	0.134	0.255	0.768	0.883	0.379	0.003	0.067	0.227	1.000	0.060	0.828	0.000																	
LEI009 4	0.830	1.000	1.000	0.358	0.833	0.218	0.169	1.000	1.000	0.590	0.412	0.341	0.000																
MCW0 098	0.564	0.599	0.008	1.000	1.000	0.719	0.802	1.000	0.363	0.321	0.311	0.249	0.910	0.000															
MCW0 078	0.227	1.000	0.810	0.549	0.377	0.596	0.550	0.236	0.912	0.199	0.675	0.376	0.300	1.000	0.000														
MCW0 081	1.000	0.452	1.000	0.516	0.389	0.875	0.945	1.000	0.291	0.917	0.278	1.000	1.000	1.000	0.797	0.000													
LEI019 2	0.489	0.393	1.000	0.270	0.626	1.000	1.000	1.000	1.000	1.000	0.393	1.000	1.000	1.000	1.000	1.000	0.000												
MCW0 014	1.000	0.844	0.798	0.966	1.000	1.000	0.372	1.000	1.000	0.835	0.596	1.000	0.582	0.781	0.735	0.928	1.000	0.000											
MCW0 183	1.000	1.000	0.534	1.000	0.444	0.383	1.000	1.000	1.000	0.528	0.526	0.712	1.000	0.524	1.000	0.574	1.000	0.443	0.000										
MCW0 067	0.905	1.000	1.000	0.386	0.661	0.354	0.053	1.000	0.241	0.790	1.000	0.456	0.531	0.363	0.658	0.682	1.000	0.293	1.000	0.000									
ADL01 12	0.418	0.860	0.031	0.471	0.395	0.514	0.793	0.870	0.626	0.031	0.438	0.119	0.924	0.039	0.386	0.286	1.000	1.000	0.279	0.158	0.000								
MCW0 216	0.344	0.059	0.772	0.588	0.378	1.000	1.000	0.054	1.000	0.829	1.000	1.000	1.000	0.865	1.000	0.574	0.249	0.809	0.715	1.000	0.751	0.000							
MCW0 104	0.503	1.000	0.672	0.637	0.772	0.716	0.547	0.668	1.000	0.264	0.255	0.235	0.156	0.704	0.238	0.930	1.000	0.647	1.000	0.856	0.286	0.818	0.000						
MCW0 123	0.047	0.236	0.812	0.025	0.385	0.267	0.421	0.779	0.485	0.248	0.530	0.465	0.639	0.273	0.364	0.661	0.293	0.916	1.000	0.505	0.398	0.716	0.829	0.000					
MCW0 330	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.000			
MCW0 165	0.417	0.861	0.030	0.473	0.406	0.499	0.790	0.863	0.619	0.035	0.461	0.096	0.927	0.034	0.402	0.292	1.000	1.000	0.279	0.146	0.001	0.749	0.269	0.415	N/A	0.000			
MCW0 069	0.054	0.065	0.040	0.910	0.136	1.000	0.890	0.531	1.000	0.214	0.576	0.952	0.783	0.166	0.702	0.773	0.156	0.965	0.467	1.000	0.485	0.266	0.837	0.322	N/A	0.446	0.000		
ADL02 78	0.275	0.046	0.338	0.698	0.220	0.162	0.711	1.000	1.000	0.159	0.934	0.202	0.544	0.148	0.797	0.529	1.000	0.690	0.164	0.445	0.183	0.776	1.000	0.019	N/A	0.169	0.501	0.000	

Table S6 Pairwise differentiation of linkage disequilibrium of Chee Fah chicken individuals at Mae Hong Son Livestock Research and Breeding Center (MLRBC) based on 28 microsatellite loci. Numbers indicate p -values with 110 permutations. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Locus	MCW0 111	MCW0 247	LEI0 234	LEI0 166	MCW0 222	MCW0 037	ADL0 268	MCW0 034	MCW0 206	MCW0 016	MCW0 103	MCW0 295	LEI0 094	MCW0 098	MCW0 078	MCW0 081	LEI0 192	MCW0 014	MCW0 183	MCW0 067	ADL0 112	MCW0 216	MCW0 104	MCW0 123	MCW0 330	MCW0 165	MCW0 069	ADL0 278
MCW0 111	0.000																											
MCW0 247	0.389	0.000																										
LEI023 4	0.302	0.067	0.000																									
LEI016 6	0.707	0.238	0.876	0.000																								
MCW0 222	1.000	0.209	1.000	0.921	0.000																							
MCW0 037	1.000	0.013	0.461	0.916	0.119	0.000																						
ADL02 68	0.369	0.771	0.488	0.508	0.562	1.000	0.000																					
MCW0 034	0.326	0.772	0.937	0.324	1.000	1.000	0.277	0.000																				
MCW0 206	0.303	0.070	0.000	0.878	1.000	0.482	0.480	0.931	0.000																			
MCW0 016	1.000	0.231	0.404	0.094	1.000	0.485	1.000	0.927	0.418	0.000																		
MCW0 103	0.370	1.000	0.953	0.621	0.763	1.000	0.765	0.758	0.954	0.522	0.000																	
MCW0 295	0.149	0.730	1.000	0.113	1.000	1.000	0.261	0.720	1.000	1.000	0.162	0.000																
LEI009 4	0.587	0.070	0.733	0.286	0.826	0.320	0.806	0.600	0.727	0.752	0.705	0.054	0.000															
MCW0 098	0.326	0.116	0.442	1.000	1.000	0.220	1.000	1.000	0.443	0.651	1.000	1.000	0.551	0.000														
MCW0 078	0.542	1.000	0.155	0.508	0.773	1.000	0.066	0.120	0.153	1.000	0.816	0.384	0.622	1.000	0.000													
MCW0 081	1.000	1.000	1.000	1.000	1.000	0.454	1.000	0.624	1.000	1.000	0.622	1.000	0.683	1.000	1.000	0.000												
LEI019 2	1.000	0.729	1.000	0.563	0.251	1.000	1.000	0.701	1.000	1.000	1.000	1.000	0.433	0.557	0.394	1.000	0.000											
MCW0 014	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.394	1.000	1.000	0.743	1.000	0.106	1.000	0.000										
MCW0 183	1.000	1.000	1.000	0.533	0.342	1.000	1.000	1.000	1.000	1.000	0.669	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.000									
MCW0 067	0.063	0.657	1.000	0.393	1.000	1.000	0.724	0.804	1.000	0.621	0.112	0.393	0.233	0.341	1.000	0.628	1.000	0.233	0.278	0.000								
ADL01 12	1.000	0.734	1.000	0.114	0.273	1.000	1.000	0.711	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.103	1.000	0.000							
MCW0 216	1.000	0.899	0.298	0.686	1.000	1.000	1.000	0.908	0.291	1.000	0.383	0.168	0.145	1.000	0.105	1.000	1.000	1.000	1.000	0.524	1.000	0.000						
MCW0 104	1.000	1.000	1.000	0.428	0.200	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	N/A	0.057	1.000	0.089	1.000	0.000					
MCW0 123	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.277	1.000	1.000	0.275	0.276	1.000	1.000	0.509	1.000	1.000	N/A	1.000	1.000	1.000	0.296	1.000	0.000				
MCW0 330	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.429	1.000	1.000	0.784	1.000	0.124	1.000	0.022	1.000	0.188	1.000	1.000	N/A	N/A	0.000			
MCW0 165	1.000	0.906	1.000	1.000	0.726	0.728	0.735	0.253	1.000	0.619	0.114	1.000	0.510	1.000	0.904	0.138	1.000	0.224	1.000	0.165	1.000	0.503	1.000	0.512	0.198	0.000		
MCW0 069	1.000	0.896	1.000	0.705	0.386	1.000	0.361	0.900	1.000	1.000	0.395	1.000	1.000	1.000	0.571	1.000	1.000	1.000	1.000	0.481	1.000	0.241	1.000	1.000	1.000	0.069	0.000	
ADL02 78	1.000	0.424	1.000	0.654	0.348	1.000	1.000	0.810	1.000	1.000	1.000	1.000	0.653	0.428	1.000	1.000	0.083	N/A	1.000	1.000	0.184	1.000	1.000	1.000	N/A	1.000	1.000	0.000

Table S7 Pairwise differentiation of linkage disequilibrium of Fah Luang chicken individuals at Chiang Rai Livestock Research and Breeding Center (CRRBC) based on 28 microsatellite loci. Numbers indicate p -values with 110 permutations. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1

Locus	MCW0 111	MCW0 247	LEI0 234	LEI0 166	MCW0 222	MCW0 037	ADL0 268	MCW0 034	MCW0 206	MCW0 016	MCW0 103	MCW0 295	LEI0 094	MCW0 098	MCW0 078	MCW0 081	LEI0 192	MCW0 014	MCW0 183	MCW0 067	ADL0 112	MCW0 216	MCW0 104	MCW0 123	MCW0 330	MCW0 165	MCW0 069	ADL0 278
MCW0 111	0.000																											
MCW0 247	0.390	0.000																										
LEI023 4	0.302	0.067	0.000																									
LEI016 6	0.707	0.238	0.876	0.000																								
MCW0 222	1.000	0.209	1.000	0.921	0.000																							
MCW0 037	1.000	0.013	0.461	0.916	0.119	0.000																						
ADL02 68	0.369	0.772	0.488	0.508	0.562	1.000	0.000																					
MCW0 034	0.326	0.772	0.937	0.324	1.000	1.000	0.277	0.000																				
MCW0 206	0.303	0.070	0.000	0.878	1.000	0.482	0.480	0.931	0.000																			
MCW0 016	1.000	0.231	0.404	0.094	1.000	0.485	1.000	0.927	0.418	0.000																		
MCW0 103	0.370	1.000	0.953	0.621	0.763	1.000	0.765	0.758	0.954	0.523	0.000																	
MCW0 295	0.149	0.730	1.000	0.113	1.000	1.000	0.261	0.720	1.000	1.000	0.162	0.000																
LEI009 4	0.587	0.070	0.733	0.286	0.826	0.320	0.806	0.601	0.727	0.752	0.705	0.054	0.000															
MCW0 098	0.324	0.116	0.442	1.000	1.000	0.220	1.000	1.000	0.443	0.651	1.000	1.000	0.551	0.000														
MCW0 078	0.542	1.000	0.155	0.508	0.773	1.000	0.066	0.120	0.153	1.000	0.816	0.384	0.622	1.000	0.000													
MCW0 081	1.000	1.000	1.000	1.000	1.000	0.454	1.000	0.624	1.000	1.000	0.622	1.000	0.683	1.000	1.000	0.000												
LEI019 2	1.000	0.729	1.000	0.563	0.251	1.000	1.000	0.701	1.000	1.000	1.000	1.000	0.433	0.558	0.394	1.000	0.000											
MCW0 014	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.394	1.000	1.000	0.743	1.000	0.107	1.000	0.000										
MCW0 183	1.000	1.000	1.000	0.533	0.342	1.000	1.000	1.000	1.000	1.000	0.670	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.000									
MCW0 067	0.063	0.657	1.000	0.393	1.000	1.000	0.724	0.804	1.000	0.621	0.112	0.393	0.233	0.341	1.000	0.628	1.000	0.233	0.278	0.000								
ADL01 12	1.000	0.734	1.000	0.114	0.273	1.000	1.000	0.711	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.103	1.000	0.000							
MCW0 216	1.000	0.900	0.298	0.687	1.000	1.000	1.000	0.908	0.291	1.000	0.383	0.168	0.145	1.000	0.105	1.000	1.000	1.000	1.000	0.524	1.000	0.000						
MCW0 104	1.000	1.000	1.000	0.428	0.200	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	N/A	0.058	1.000	0.090	1.000	0.000					
MCW0 123	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.277	1.000	1.000	0.275	0.276	1.000	1.000	0.509	1.000	1.000	N/A	1.000	1.000	1.000	0.296	1.000	0.000				
MCW0 330	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.430	1.000	1.000	0.784	1.000	0.124	1.000	0.022	1.000	0.189	1.000	1.000	N/A	N/A	0.000			
MCW0 165	0.897	1.000	0.705	0.386	1.000	0.362	0.901	1.000	1.000	0.395	1.000	1.000	1.000	0.571	1.000	1.000	1.000	1.000	0.481	1.000	0.242	1.000	1.000	1.000	0.070	0.000		
MCW0 069	1.000	0.906	1.000	1.000	0.726	0.728	0.735	0.253	1.000	0.619	0.114	1.000	0.510	1.000	0.904	0.138	1.000	0.224	1.000	0.165	1.000	0.503	1.000	0.512	0.199	1.000	0.000	
ADL02 78	1.000	0.424	1.000	0.654	0.348	1.000	1.000	0.810	1.000	1.000	1.000	1.000	0.653	0.428	1.000	1.000	0.083	N/A	1.000	1.000	0.184	1.000	1.000	1.000	N/A	1.000	1.000	0.000

Table S8 Pairwise differentiation of linkage disequilibrium of Fah Luang chicken individuals at Mae Hong Son Livestock Research and Breeding Center (MLRBC) based on 28 microsatellite loci. Numbers indicate *p*-values with 110 permutations. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Locus	MCW0 111	MCW0 247	LEI0 234	LEI0 166	MCW0 222	MCW0 037	ADL0 268	MCW0 034	MCW0 206	MCW0 016	MCW0 103	MCW0 295	LEI0 094	MCW0 098	MCW0 078	MCW0 081	LEI0 192	MCW0 014	MCW0 183	MCW0 067	ADL0 112	MCW0 216	MCW0 104	MCW0 123	MCW0 330	MCW0 165	MCW0 069	ADL0 278
MCW0 111	0.000																											
MCW0 247	0.273	0.000																										
LEI023 4	0.303	0.180	0.000																									
LEI016 6	0.208	0.930	1.000	0.000																								
MCW0 222	0.230	0.191	0.220	0.561	0.000																							
MCW0 037	0.478	0.257	1.000	0.800	0.435	0.000																						
ADL02 68	0.314	0.668	1.000	0.533	0.553	0.042	0.000																					
MCW0 034	0.105	0.056	1.000	0.683	0.212	0.691	0.709	0.000																				
MCW0 206	0.807	1.000	1.000	0.449	0.912	1.000	0.450	1.000	0.000																			
MCW0 016	0.016	0.784	0.158	0.191	0.201	0.263	0.673	0.435	0.634	0.000																		
MCW0 103	0.745	0.472	0.444	0.682	1.000	0.855	0.686	0.450	1.000	1.000	0.000																	
MCW0 295	0.134	0.255	0.768	0.883	0.379	0.003	0.067	0.227	1.000	0.060	0.828	0.000																
LEI009 4	0.830	1.000	1.000	0.358	0.833	0.218	0.169	1.000	1.000	0.590	0.412	0.341	0.000															
MCW0 098	0.564	0.599	0.008	1.000	1.000	0.719	0.802	1.000	0.363	0.321	0.311	0.249	0.910	0.000														
MCW0 078	0.227	1.000	0.810	0.549	0.377	0.596	0.550	0.236	0.912	0.199	0.675	0.376	0.300	1.000	0.000													
MCW0 081	1.000	0.452	1.000	0.516	0.389	0.875	0.945	1.000	0.291	0.917	0.278	1.000	1.000	1.000	0.797	0.000												
LEI019 2	0.489	0.393	1.000	0.270	0.626	1.000	1.000	1.000	1.000	1.000	0.393	1.000	1.000	1.000	1.000	1.000	0.000											
MCW0 014	1.000	0.844	0.798	0.966	1.000	1.000	0.372	1.000	1.000	0.835	0.596	1.000	0.582	0.781	0.735	0.928	1.000	0.000										
MCW0 183	1.000	1.000	0.534	1.000	0.444	0.383	1.000	1.000	1.000	0.528	0.526	0.712	1.000	0.524	1.000	0.574	1.000	0.443	0.000									
MCW0 067	0.905	1.000	1.000	0.386	0.661	0.354	0.053	1.000	0.241	0.790	1.000	0.456	0.531	0.363	0.658	0.682	1.000	0.293	1.000	0.000								
ADL01 12	0.418	0.860	0.031	0.471	0.395	0.514	0.793	0.870	0.626	0.031	0.438	0.119	0.924	0.039	0.386	0.286	1.000	1.000	0.279	0.158	0.000							
MCW0 216	0.344	0.059	0.772	0.588	0.378	1.000	1.000	0.054	1.000	0.829	1.000	1.000	1.000	0.865	1.000	0.574	0.249	0.809	0.715	1.000	0.751	0.000						
MCW0 104	0.503	1.000	0.672	0.637	0.772	0.716	0.547	0.668	1.000	0.264	0.255	0.235	0.156	0.704	0.238	0.930	1.000	0.647	1.000	0.856	0.286	0.818	0.000					
MCW0 123	0.047	0.236	0.812	0.025	0.385	0.267	0.421	0.779	0.485	0.248	0.530	0.465	0.639	0.273	0.364	0.661	0.293	0.916	1.000	0.505	0.398	0.716	0.829	0.000				
MCW0 330	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A	0.000			
MCW0 165	0.417	0.861	0.030	0.473	0.406	0.499	0.790	0.863	0.619	0.035	0.461	0.096	0.927	0.034	0.402	0.292	1.000	1.000	0.279	0.146	0.001	0.749	0.269	0.415	N/A	0.000		
MCW0 069	0.054	0.065	0.040	0.910	0.136	1.000	0.890	0.531	1.000	0.214	0.576	0.952	0.783	0.166	0.702	0.773	0.156	0.965	0.467	1.000	0.485	0.266	0.837	0.322	N/A	0.446	0.000	
ADL02 78	0.275	0.046	0.338	0.698	0.220	0.162	0.711	1.000	1.000	0.159	0.934	0.202	0.544	0.148	0.797	0.529	1.000	0.690	0.164	0.445	0.183	0.776	1.000	0.019	N/A	0.169	0.000	0.000

Table S9 Genetic diversity of 39 individuals of Chee Fah and Fah Luang chicken breeds based on 28 microsatellite loci. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Breeds	Populations	Locus	N	N_a^1	AR^2	N_{ea}^3	I^4	H_o^5	H_e^6	PIC^7	F^8
Chee Fah	CRRBC ¹	MCW0111	10	6.000	5.800	4.000	1.557	0.200	0.750	0.553	0.733
		MCW0247	10	4.000	3.995	3.333	1.280	0.200	0.700	0.645	0.714
		LEI0234	10	7.000	6.884	5.556	1.818	0.200	0.820	0.730	0.756
		LEI0166	10	4.000	3.800	2.410	1.013	0.200	0.585	0.501	0.658
		MCW0222	10	7.000	6.500	3.077	1.442	0.500	0.675	0.612	0.259
		MCW0037	10	3.000	2.900	2.151	0.845	0.200	0.535	0.436	0.626
		ADL0268	10	7.000	6.884	5.405	1.808	0.400	0.815	0.791	0.509
		MCW0034	10	7.000	6.595	3.226	1.498	0.200	0.690	0.658	0.710
		MCW0206	10	4.000	4.000	3.774	1.354	0.300	0.735	0.685	0.592
		MCW0016	10	5.000	4.889	3.175	1.331	0.100	0.685	0.635	0.854
		MCW0103	10	2.000	2.000	1.923	0.673	0.000	0.480	0.365	1.000
		MCW0295	10	7.000	6.695	4.167	1.653	0.300	0.760	0.618	0.605
		LEI0094	10	4.000	3.989	2.778	1.168	0.000	0.640	0.365	1.000
		MCW0098	10	2.000	1.995	1.220	0.325	0.200	0.180	0.164	-0.111
		MCW0078	10	6.000	5.984	5.000	1.696	0.200	0.800	0.745	0.750
		MCW0081	10	6.000	5.700	3.390	1.440	0.900	0.705	0.663	-0.277
		LEI0192	10	6.000	5.895	4.545	1.639	0.800	0.780	0.749	-0.026
		MCW0014	10	5.000	4.800	3.390	1.349	0.800	0.705	0.653	-0.135
		MCW0183	10	4.000	3.895	2.597	1.094	0.300	0.615	0.544	0.512
		MCW0067	10	4.000	3.995	2.899	1.208	1.000	0.655	0.442	-0.527
		ADL0112	10	8.000	7.600	5.556	1.861	0.800	0.820	0.796	0.024
		MCW0216	10	7.000	6.689	3.333	1.541	0.800	0.700	0.673	-0.143
		MCW0104	10	9.000	8.495	5.263	1.916	1.000	0.810	0.790	-0.235

Breeds	Populations	Locus	N	N_a^1	AR^2	N_{ea}^3	I^4	H_o^5	H_e^6	PIC^7	F^8
		MCW0123	10	6.000	5.795	3.846	1.527	0.800	0.740	0.703	-0.081
		MCW0330	9	7.000	7.000	3.375	1.561	0.444	0.704	0.679	0.368
		MCW0165	10	4.000	3.900	3.175	1.224	0.700	0.685	0.623	-0.022
		MCW0069	10	7.000	6.600	4.082	1.612	0.400	0.755	0.719	0.470
		ADL0278	10	3.000	3.000	2.062	0.886	0.400	0.515	0.460	0.223
		Mean	9.964	5.393	5.224	3.525	1.369	0.441	0.680	0.607	0.350
		SE	0.036	0.346	1.718	0.214	0.071	0.058	0.025	0.151	0.081
	MLRBC ²	MCW0111	10	4.000	3.900	2.564	1.110	0.900	0.610	0.554	-0.475
		MCW0247	10	3.000	3.000	2.632	1.030	1.000	0.620	0.548	-0.613
		LEI0234	10	7.000	6.789	5.263	1.775	1.000	0.810	0.784	-0.235
		LEI0166	10	4.000	3.900	2.985	1.192	0.600	0.665	0.603	0.098
		MCW0222	10	4.000	3.895	2.597	1.094	1.000	0.615	0.389	-0.626
		MCW0037	10	3.000	3.000	2.778	1.055	0.800	0.640	0.563	-0.250
		ADL0268	10	4.000	4.000	2.985	1.238	0.800	0.665	0.618	-0.203
		MCW0034	10	5.000	4.889	3.175	1.331	0.500	0.685	0.635	0.270
		MCW0206	10	4.000	4.000	3.704	1.345	1.000	0.730	0.680	-0.370
		MCW0016	10	4.000	3.995	3.077	1.235	1.000	0.675	0.619	-0.481
		MCW0103	10	3.000	2.995	2.381	0.943	1.000	0.580	0.492	-0.724
		MCW0295	10	3.000	2.800	1.227	0.394	0.200	0.185	0.177	-0.081
		LEI0094	10	5.000	4.895	3.636	1.415	0.400	0.725	0.681	0.448
		MCW0098	10	2.000	2.000	1.600	0.562	0.500	0.375	0.305	-0.333
		MCW0078	10	1.000	1.000	1.000	0.000	0.000	0.000	0.000	#N/A
		MCW0081	10	2.000	2.000	1.471	0.500	0.400	0.320	0.269	-0.250
		LEI0192	9	5.000	5.000	3.057	1.330	1.000	0.673	0.631	-0.486
		MCW0014	10	5.000	4.800	3.125	1.305	1.000	0.680	0.627	-0.471
		MCW0183	10	3.000	2.989	1.515	0.639	0.200	0.340	0.314	0.412

Breeds	Populations	Locus	N	N_a^1	AR^2	N_{ea}^3	I^4	H_o^5	H_e^6	PIC^7	F^8
		MCW0067	10	4.000	3.995	2.667	1.166	0.800	0.625	0.578	-0.280
		ADL0112	10	4.000	3.900	2.817	1.165	1.000	0.645	0.587	-0.550
		MCW0216	10	2.000	2.000	1.724	0.611	0.000	0.420	0.332	1.000
		MCW0104	10	4.000	3.795	1.527	0.708	0.200	0.345	0.326	0.420
		MCW0123	10	4.000	3.995	2.667	1.166	0.900	0.625	0.578	-0.440
		MCW0330	10	3.000	2.900	2.062	0.824	0.800	0.515	0.424	-0.553
		MCW0165	10	5.000	4.800	2.985	1.290	1.000	0.665	0.618	-0.504
		MCW0069	10	4.000	3.800	1.869	0.871	0.500	0.465	0.420	-0.075
		ADL0278	10	4.000	3.895	1.905	0.914	0.600	0.475	0.440	-0.263
		Mean	9.964	3.750	3.676	3.030	1.188	0.562	0.614	0.493	0.076
		SE	0.036	0.228	1.163	0.151	0.055	0.046	0.023	0.177	0.067
Fah Luang	CRRBC ¹	MCW0111	9	5.000	4.773	4.263	1.505	0.222	0.765	0.726	0.710
		MCW0247	9	4.000	3.516	1.604	0.761	0.333	0.377	0.354	0.115
		LEI0234	9	6.000	5.511	4.050	1.565	0.333	0.753	0.718	0.557
		LEI0166	9	3.000	2.778	2.219	0.868	0.111	0.549	0.448	0.798
		MCW0222	9	4.000	3.956	3.176	1.259	0.556	0.685	0.607	0.189
		MCW0037	9	4.000	3.777	2.842	1.176	0.333	0.648	0.592	0.486
		ADL0268	9	4.000	3.994	3.600	1.334	0.111	0.722	0.674	0.846
		MCW0034	9	6.000	5.072	2.132	1.157	0.222	0.531	0.368	0.581
		MCW0206	9	6.000	5.511	4.263	1.586	0.222	0.765	0.762	0.710
		MCW0016	9	6.000	5.333	4.050	1.538	0.333	0.753	0.550	0.557
		MCW0103	9	2.000	2.000	1.528	0.530	0.222	0.346	0.286	0.357
		MCW0295	9	5.000	4.768	4.050	1.480	0.556	0.753	0.712	0.262
		LEI0094	9	4.000	3.922	3.000	1.215	0.000	0.667	0.372	1.000
		MCW0098	9	2.000	1.778	1.117	0.215	0.111	0.105	0.099	-0.059
		MCW0078	9	5.000	4.777	4.378	1.519	0.556	0.772	0.733	0.280

Breeds	Populations	Locus	N	N_a^1	AR^2	N_{ea}^3	I^4	H_o^5	H_e^6	PIC^7	F^8
		MCW0081	9	4.000	3.777	2.842	1.176	0.778	0.648	0.592	-0.200
		LEI0192	9	8.000	7.062	5.226	1.850	0.667	0.809	0.786	0.176
		MCW0014	8	7.000	6.725	5.333	1.804	0.250	0.813	0.748	0.692
		MCW0183	8	6.000	5.742	4.571	1.630	0.625	0.781	0.748	0.200
		MCW0067	9	5.000	4.333	2.314	1.117	0.556	0.568	0.450	0.022
		ADL0112	9	8.000	7.032	5.063	1.831	0.556	0.802	0.779	0.308
		MCW0216	9	5.000	4.738	3.951	1.461	0.667	0.747	0.704	0.107
		MCW0104	7	8.000	8.000	5.765	1.909	0.714	0.827	0.806	0.136
		MCW0123	7	4.000	4.000	2.130	0.991	0.429	0.531	0.483	0.192
		MCW0330	9	8.000	7.249	6.231	1.937	0.778	0.840	0.820	0.074
		MCW0165	9	6.000	5.333	4.050	1.538	0.778	0.753	0.637	-0.033
		MCW0069	9	5.000	4.951	4.500	1.553	0.889	0.778	0.742	-0.143
		ADL0278	7	3.000	3.000	2.800	1.061	0.571	0.643	0.567	0.111
		Mean	8.714	4.982	4.765	3.324	1.275	0.558	0.643	0.602	0.115
		SE	0.124	0.226	1.535	0.177	0.054	0.040	0.022	0.183	0.056
MLRBC ²		MCW0111	10	4.000	3.795	1.527	0.708	0.300	0.345	0.326	0.130
		MCW0247	10	4.000	3.900	2.857	1.161	1.000	0.650	0.584	-0.538
		LEI0234	10	7.000	6.789	4.348	1.696	1.000	0.770	0.744	-0.299
		LEI0166	10	4.000	3.800	2.326	0.996	0.700	0.570	0.492	-0.228
		MCW0222	10	4.000	3.800	2.410	1.013	1.000	0.585	0.347	-0.709
		MCW0037	10	3.000	3.000	2.597	1.010	0.400	0.615	0.534	0.350
		ADL0268	10	4.000	3.800	1.869	0.871	0.400	0.465	0.420	0.140
		MCW0034	10	5.000	4.989	3.774	1.458	0.200	0.735	0.695	0.728
		MCW0206	10	7.000	6.789	5.263	1.775	0.900	0.810	0.784	-0.111
		MCW0016	10	4.000	3.900	2.857	1.161	1.000	0.650	0.584	-0.538
		MCW0103	10	4.000	3.900	2.985	1.192	1.000	0.665	0.603	-0.504

Breeds	Populations	Locus	N	N_a ¹	AR ²	N_{ea} ³	I ⁴	H_o ⁵	H_e ⁶	PIC ⁷	F ⁸
		MCW0295	10	4.000	3.800	1.869	0.871	0.600	0.465	0.420	-0.290
		LEI0094	9	6.000	6.000	2.793	1.351	0.444	0.642	0.610	0.308
		MCW0098	10	4.000	3.995	2.899	1.208	0.500	0.655	0.603	0.237
		MCW0078	10	3.000	2.800	1.227	0.394	0.200	0.185	0.177	-0.081
		MCW0081	10	3.000	3.000	2.410	0.975	0.600	0.585	0.513	-0.026
		LEI0192	10	7.000	6.789	5.000	1.752	0.900	0.800	0.773	-0.125
		MCW0014	9	5.000	5.000	3.240	1.336	1.000	0.691	0.642	-0.446
		MCW0183	10	2.000	2.000	1.600	0.562	0.500	0.375	0.305	-0.333
		MCW0067	10	5.000	4.900	4.255	1.501	0.900	0.765	0.713	-0.176
		ADL0112	10	5.000	4.795	2.817	1.238	1.000	0.645	0.590	-0.550
		MCW0216	10	3.000	2.995	2.410	0.949	0.100	0.585	0.495	0.829
		MCW0104	10	8.000	7.584	3.448	1.636	0.200	0.710	0.689	0.718
		MCW0123	10	4.000	3.800	2.198	0.967	0.700	0.545	0.476	-0.284
		MCW0330	10	9.000	8.684	6.897	2.056	0.600	0.855	0.839	0.298
		MCW0165	10	5.000	4.795	2.817	1.238	1.000	0.645	0.590	-0.550
		MCW0069	10	6.000	5.595	1.961	1.079	0.600	0.490	0.470	-0.224
		ADL0278	10	7.000	6.695	4.444	1.678	1.000	0.775	0.744	-0.290
		Mean	9.929	4.857	4.703	3.039	1.208	0.669	0.617	0.563	-0.092
		SE	0.050	0.320	1.619	0.241	0.073	0.058	0.029	0.160	0.078

¹Number of alleles (N_a); ²allelic richness (AR); ³number of effective alleles (N_{ea}); ⁴Shannon's information index (I); ⁵observed heterozygosity (H_o); ⁶expected heterozygosity (H_e); ⁷polymorphic information content (PIC); ⁸fixation index (F)

¹CRRBC = Chiang Rai Livestock Research and Breeding Center, Chiang Rai

²MLRBC = Mae Hong Son Livestock Research and Breeding Center, Mae Hong Son

Table S10 Comparison of genetic diversity parameters between Chee Fah and Fah Luang chickens populations based on 28 microsatellite loci. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Observed	Breeds	Population 1	Population 2	df	SE	t-test	p-value
heterozygosity (H_o)	Chee Fah	CRRBC ¹	MLRBC ²	-0.241	0.027	-8.824	$p<0.01$
	Fah Luang	CRRBC ¹	MLRBC ²	-0.0223	-0.002	-9.328	$p<0.01$
heterozygosity (H_e)	Chee Fah	CRRBC ¹	MLRBC ²	0.131	0.013	9.631	$p<0.01$
	Fah Luang	CRRBC ¹	MLRBC ²	0.052	0.0141	3.697	$p<0.01$

H_o = Observed heterozygosity, H_e = Expected heterozygosity

¹CRRBC = Chiang Rai Livestock Research and Breeding Center, Chiang Rai

²MLRBC = Mae Hong Son Livestock Research and Breeding Center, Mae Hong Son

Table S11 Observed and expected heterozygosity of Chee Fah and Fah Luang chickens based on 28 microsatellite loci and genetic bottlenecks for all individuals. Data were calculated using Bottleneck version 1.2.02 (Piry et al., 1999). Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Breeds	Locality	H_o	H_e	p -value
Chee Fah	CRRBC ¹	0.441±0.058	0.680±0.025	$p < 0.05$
	MLRBC ²	0.682±0.064	0.549±0.035	$p < 0.05$
Fah Luang	CRRBC ¹	0.446±0.046	0.669±0.032	$p < 0.05$
	MLRBC ²	0.669±0.058	0.617±0.029	$p < 0.05$

H_o = Observed heterozygosity, H_e = Expected heterozygosity

¹CRRBC = Chiang Rai Livestock Research and Breeding Center, Chiang Rai

²MLRBC = Mae Hong Son Livestock Research and Breeding Center, Mae Hong Son

1. Piry, S.; Luikart, G.; Cornuet, J.M. BOTTLENECK: a program for detecting recent effective population size reductions from allele data frequencies. *J. Hered.* **1999**, *90*, 502–503. doi: 10.1093/jhered/90.4.502

Table S12 Inbreeding coefficients and relatedness of Chee Fah and Fah Luang chicken breeds at the Chiang Rai Livestock Research and Breeding Center (CRRBC, Chiang Rai) and Mae Hong Son Livestock Research and Breeding Center (MLRBC, Mae Hong Son). Estimates were calculated using COANCESTRY version 1.0.1.9 (Wang, 2011) and GenAlEx version 6.5 (Peakall and Smouse, 2012). Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Breeds	Population	N ¹	F_{IS} ²	Relatedness (r)
Chee Fah	CRRBC ¹	10	0.352	-0.068
	MLRBC ²	10	-0.242	-0.047
Fah Luang	CRRBC ¹	9	0.334	-0.078
	MLRBC ²	10	-0.085	-0.055

¹Sample size (N); ²inbreeding coefficient (F_{IS})

¹CRRBC = Chiang Rai Livestock Research and Breeding Center, Chiang Rai

²MLRBC = Mae Hong Son Livestock Research and Breeding Center, Mae Hong Son

1. Peakall, R. Smouse, P.E. GenAlEx 6.5: genetic analysis in Excel. Population genetic software for teaching and research—an update. *Bioinformatics* **2012**, *28*, 2537–2539. doi: 0.1093/bioinformatics/bts460
2. Wang, J. COANCESTRY: a program for simulating, estimating and analysing relatedness and inbreeding coefficients. *Mol. Ecol. Resour.* 2011, *11*, 141–145. doi: 10.1111/j.1755-0998.2010.02885.x

Table S13 Pairwise genetic differentiation (F_{ST}), pairwise F_{ST}^{ENA} values with ENA correction for null alleles and R_{ST} values using FSTAT version 2.9.3 (Goudet, 1995) of Chee Fah and Fah Luang chickens between populations based on 28 microsatellite loci. Numbers indicate p -values, with 110 permutations. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Breeds	Population 1	Population 2	F_{ST}	F_{ST}^{ENA}	R_{ST}
Chee Fah	CRRBC ¹	MLRBC ²	0.112*	0.219	0.3737
Fah Luang	CRRBC ¹	MLRBC ²	0.128*	0.195	0.5232

* p -value < 0.05

¹CRRBC = Chiang Rai Livestock Research and Breeding Center, Chiang Rai

²MLRBC = Mae Hong Son Livestock Research and Breeding Center, Mae Hong Son

1. Goudet, J. FSTAT (version 1.2): a computer program to calculate F-statistics. *J. Hered.* **1995**, 86, 485–486. doi: 10.1093/oxfordjournals.jhered.a111627

Table S14 Pairwise genetic relatedness (r) for Chee Fah and Fah Luang Chickens in Chiang Rai and Mae Hong Son Livestock Research and Breeding Center (CRRBC) and Mae Hong Son Livestock Research and Breeding Center (MLRBC) populations. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1

Chee Fah Chicken						Fah Luang Chicken					
CRRBC			MLRBC			CRRBC			MLRBC		
Specimen 1	Specimen 2	r	Specimen 1	Specimen 2	r	Specimen 1	Specimen 2	r	Specimen 1	Specimen 2	r
CF1	CF2	-0.032	CFM1	CFM2	-0.122	FL1	FL2	-0.003	FLM1	FLM2	0.006
CF1	CF3	-0.037	CFM1	CFM3	-0.050	FL1	FL3	-0.067	FLM1	FLM3	0.016
CF2	CF3	-0.013	CFM2	CFM3	-0.046	FL2	FL3	-0.094	FLM2	FLM3	-0.014
CF1	CF4	-0.144	CFM1	CFM4	-0.112	FL1	FL5	-0.143	FLM1	FLM4	-0.079
CF2	CF4	-0.051	CFM2	CFM4	0.049	FL2	FL5	-0.138	FLM2	FLM4	-0.042
CF3	CF4	-0.019	CFM3	CFM4	0.061	FL3	FL5	-0.078	FLM3	FLM4	-0.036
CF1	CF5	-0.060	CFM1	CFM5	0.078	FL1	FL6	-0.172	FLM1	FLM5	-0.010
CF2	CF5	-0.066	CFM2	CFM5	-0.122	FL2	FL6	-0.052	FLM2	FLM5	-0.017
CF3	CF5	-0.019	CFM3	CFM5	0.039	FL3	FL6	-0.039	FLM3	FLM5	-0.003
CF4	CF5	0.035	CFM4	CFM5	-0.084	FL5	FL6	0.011	FLM4	FLM5	-0.064
CF1	CF6	-0.133	CFM1	CFM6	-0.140	FL1	FL7	-0.142	FLM1	FLM6	-0.012
CF2	CF6	-0.093	CFM2	CFM6	0.046	FL2	FL7	-0.040	FLM2	FLM6	0.001
CF3	CF6	-0.109	CFM3	CFM6	-0.070	FL3	FL7	-0.103	FLM3	FLM6	-0.011
CF4	CF6	-0.023	CFM4	CFM6	-0.074	FL5	FL7	-0.080	FLM4	FLM6	-0.034
CF5	CF6	-0.007	CFM5	CFM6	-0.116	FL6	FL7	-0.040	FLM5	FLM6	-0.037
CF1	CF7	-0.099	CFM1	CFM7	-0.048	FL1	FL8	-0.008	FLM1	FLM7	-0.098
CF2	CF7	-0.088	CFM2	CFM7	-0.016	FL2	FL8	-0.154	FLM2	FLM7	-0.136
CF3	CF7	-0.017	CFM3	CFM7	-0.079	FL3	FL8	-0.019	FLM3	FLM7	-0.087
CF4	CF7	-0.070	CFM4	CFM7	-0.066	FL5	FL8	-0.067	FLM4	FLM7	-0.009
CF5	CF7	-0.112	CFM5	CFM7	-0.063	FL6	FL8	-0.127	FLM5	FLM7	-0.044
CF6	CF7	-0.113	CFM6	CFM7	-0.062	FL7	FL8	-0.081	FLM6	FLM7	-0.077
CF1	CF8	-0.015	CFM1	CFM8	-0.024	FL1	FL9	-0.073	FLM1	FLM8	-0.099
CF2	CF8	-0.066	CFM2	CFM8	-0.050	FL2	FL9	-0.121	FLM2	FLM8	-0.107
CF3	CF8	-0.053	CFM3	CFM8	-0.081	FL3	FL9	0.001	FLM3	FLM8	-0.128
CF4	CF8	-0.110	CFM4	CFM8	-0.056	FL5	FL9	-0.118	FLM4	FLM8	-0.080
CF5	CF8	-0.110	CFM5	CFM8	-0.040	FL6	FL9	-0.128	FLM5	FLM8	-0.070
CF6	CF8	-0.062	CFM6	CFM8	-0.133	FL7	FL9	-0.042	FLM6	FLM8	-0.134
CF7	CF8	-0.009	CFM7	CFM8	0.103	FL8	FL9	-0.072	FLM7	FLM8	-0.128
CF1	CF9	-0.018	CFM1	CFM9	0.000	FL1	FL10	-0.047	FLM1	FLM9	-0.098
CF2	CF9	-0.116	CFM2	CFM9	0.055	FL2	FL10	-0.119	FLM2	FLM9	-0.067
CF3	CF9	-0.092	CFM3	CFM9	-0.061	FL3	FL10	-0.053	FLM3	FLM9	-0.067

Chee Fah Chicken						Fah Luang Chicken					
CRRBC			MLRBC			CRRBC			MLRBC		
Specimen 1	Specimen 2	<i>r</i>	Specimen 1	Specimen 2	<i>r</i>	Specimen 1	Specimen 2	<i>r</i>	Specimen 1	Specimen 2	<i>r</i>
CF4	CF9	-0.077	CFM4	CFM9	0.024	FL5	FL10	-0.147	FLM4	FLM9	0.012
CF5	CF9	-0.098	CFM5	CFM9	-0.076	FL6	FL10	-0.095	FLM5	FLM9	-0.087
CF6	CF9	-0.087	CFM6	CFM9	-0.030	FL7	FL10	-0.029	FLM6	FLM9	-0.043
CF7	CF9	-0.123	CFM7	CFM9	-0.075	FL8	FL10	-0.100	FLM7	FLM9	0.011
CF8	CF9	-0.017	CFM8	CFM9	-0.050	FL9	FL10	-0.016	FLM8	FLM9	-0.107
CF1	CF10	-0.049	CFM1	CFM10	0.026	-	-	-	FLM1	FLM10	-0.041
CF2	CF10	-0.082	CFM2	CFM10	-0.140	-	-	-	FLM2	FLM10	-0.083
CF3	CF10	-0.067	CFM3	CFM10	-0.084	-	-	-	FLM3	FLM10	0.003
CF4	CF10	-0.123	CFM4	CFM10	-0.080	-	-	-	FLM4	FLM10	-0.079
CF5	CF10	-0.123	CFM5	CFM10	-0.070	-	-	-	FLM5	FLM10	-0.067
CF6	CF10	-0.113	CFM6	CFM10	-0.021	-	-	-	FLM6	FLM10	-0.048
CF7	CF10	-0.006	CFM7	CFM10	-0.080	-	-	-	FLM7	FLM10	0.024
CF8	CF10	-0.080	CFM8	CFM10	-0.127	-	-	-	FLM8	FLM10	-0.124
CF9	CF10	-0.110	CFM9	CFM10	-0.054	-	-	-	FLM9	FLM10	-0.071

Table S15 Inbreeding coefficients (F_{IS}) of 39 individuals of Chee Fah and Fah Luang chicken individuals in Chiang Rai Livestock Research and Breeding Center (CRRBC) and Mae Hong Son Livestock Research and Breeding Center (MLRBC) populations. Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1

Chee Fah Chicken				Fah Luang Chicken			
CRRBC		MLRBC		CRRBC		MLRBC	
Specimen	F_{IS}	Specimen	F_{IS}	Specimen	F_{IS}	Specimen	F_{IS}
CF1	0.164	CFM1	-0.3023	FL1	0.0102	FLM1	-0.1219
CF2	0.121	CFM2	-0.268	FL2	0.1256	FLM2	-0.2085
CF3	-0.305	CFM3	-0.2623	FL3	0.023	FLM3	-0.1835
CF4	-0.050	CFM4	-0.1928	FL5	0.1226	FLM4	-0.1983
CF5	-0.022	CFM5	-0.3397	FL6	0.0077	FLM5	-0.1082
CF6	-0.002	CFFM1	-0.2646	FL7	0.0856	FLFM1	-0.2078
CF7	0.053	CFFM2	-0.3013	FL8	-0.0431	FLFM2	-0.1776
CF8	0.099	CFFM3	-0.2881	FL9	0.001	FLFM3	-0.1909
CF9	-0.002	CFFM4	-0.3016	FL10	-0.0914	FLFM4	-0.1076
CF10	0.019	CFFM5	-0.2764	-	-	FLFM5	-0.1219

Table S16 Molecular variance (AMOVA) results for Chee Fah and Fah Luang chickens based on 28 microsatellite loci using Arlequin version 3.5.2.2 (Excoffier and Lischer 2010). Detailed information on all of the Chee Fah and Fah Luang chicken individuals is presented in Table S1.

Breeds	Source of variation	df	Sum of squares	Variance components	Percentage of variation
Chee Fah	Among populations	1	127.100	127.100	34%
	Within populations	18	377.200	20.956	66%
	Total	19	504.300		100%
Fah Luang	Among populations	1	57.261	57.261	20%
	Among individuals	17	198.133	11.655	16%
	Within individuals	19	147.000	7.737	64%
	Total	37	402.395		100%

1. Excoffier, L.; Lischer, H.E. Arlequin suite ver 3.5: a new series of programs to perform population genetics analyses under Linux and Windows. *Mol. Ecol. Resour.* **2010**, *10*, 564–567. doi: 10.1111/j.1755-0998.2010.02847.x