Genetical classification of Asian Red junglefowls and chickens, *Gallus gallus*

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Chicken (*Gallus gallus*) became domesticated from Red junglefowl (*Gallus gallus*) in Asian nearly 10,000 years ago. The Red junglefowl is divided into 5 subspecies (*G.g.gallus*, *G.g.spadiceus*, *G.g.jabouillei*, *G.g.murughi*, and *G.g.bankiva*) based on their phenotypes and distribution. However, it is still unclear about recognition of these subspecies genetically, and their contribution to chicken domestication. Miao *et al*. (2013) reported that a fine-gained complete mitochondrial DNA (mtDNA) phylogeny was investigated by defining 13 haplogroups A-I and W-Z. Common haplogroups A-G were shared by domesticated chickens and Red junglefowls, especially in Southeast Asian haplogroups A, B and E that were dominants. In this study to survey the genetic diversity, and restore the original state and the history of domestication, we carried out a largescale molecular phylogenetic analysis using mtDNA complete D-loop sequences of Red junglefowls and commercial chickens in Asian countries. Nucleotide sequences of complete D-loop were determined, and aligned to calculate genetic distances to construct Neighbor-joining tree using MEGA7. The tree showed that many individuals of the *G.g.gallus* and *G.g.spadiceus* existed in Southeast Asia and distributed in 8 of 13 clades. Many of the Asian native and commercial chickens were grouped in the same clade with these two subspecies (*G.g.gallus* and *G.g.spadiceus*) as well as *G.g.murugi*. This result suggested the possibility that *G.g.gallus* and *G.g.spadiceus* in Southeast Asia and *G.g.murugi* in South Asia were closely related to the domestication of chickens. In this study, we firstly reported a new haplogroup “V” in only a *G.g.gallus* with white

ear-lobe at northeast Thailand.