

Description of Additional Supplementary Files

Supplementary Data 1: A summary of all the ancient samples screened in this study.

Individuals in bold are subject to further 1240K-based analyses.

Supplementary Data 2: A list of groups used for the population genetic analyses in this study.

A. This list includes 109 ancient groups used as an analysis unit in the analyses, such as PCA, ADMIXTURE, outgroup-f3, f4 and qpAdm. For all groups, we provide mean latitude and longitude across individuals. We also provide the original study reporting the samples and the individual IDs for convenient tracking of ancient samples. In part of f4 and qpAdm analyses, some populations are combined for higher depth as marked in the "Combine group" column. B. This list includes 82 co-analyse modern groups.

Supplementary Data 3: Two-way admixture modeling of BLG, We use multiple populations from Northern East Asian(Shandong_EN,AR13-10K,WLR_MN,DevilCave_N,Boisman_MN and YR_MN) and Southern East Asian(Qihe,Fujian_EN,Fujian_LN.Longlin, Dushan,Baojianshan and Guangxi_LBIA) as two separate sources to test the population admixture events of BLG-MN-YS. Our base set of outgroups("Base") include Mbuti, Natufian, onge, Iran_N , WHG, Anatolia_N, Mixe, Taiwan_Hanben, Itelmen and Tianyuan. (A). Base models with P-value >0.05 provide an adequate model fit and are highlighted in bold face. (B). estimated admixture proportions and their SEs for base models (use base outgroups) with P-value >0.05, we use rotate strategy to test the best model from these similarly well-fitness models by adding each potential source to outgroups respectively. (C). estimated admixture proportions and their SEs for each period of Baligang using the best model in B. (D). estimated admixture proportions and their SEs of the proximal model connecting the earlier and later Baligang populations.

Supplementary Data 4: Genetic affinity of newly genotyped Baligang populations with Eastasian and Southeast asian populations by f3 statistics, with >15000 SNPs.

Supplementary Data 5: The KIN pairwise analysis reveals the kinship relationships among 30 Baligang M13 individuals with coverage exceeding 0.1X.

Supplementary Data 6: Calculated posterior probabilities of the type and directions of 2nd-degree pairs in BLG-M13. For the “direction” column, a value of 1 indicates that the individual in column iid1 is genetically older than iid2, while a value of 2 indicates the reverse. The values in parentheses in the titles of the “Posterior Probability” columns represent the same meaning.

Supplementary Data 7: Pairwise IBD (Identity-by-descent) sharing between all Baligang individuals with more than 0.15X coverage (n = 47).