Supplementary Information 1. Supporting Tables and Figures.

Table S1. The 19 bioclimatic variables from CHELSA. While all variables were included in initial models, we marked those retained for downstream analyses after sequential filtering with "V"

Bioclimatic variables	**Abbrev.**	**Dark-winged**	**Clear-winged**	**All populations**
Annual Mean Temperature	bio 1			
Mean Diurnal Range	bio 2			
Isothermality	bio 3	V	V	V
Temperature Seasonality	bio 4	V	V	V
Max Temperature of Warmest Month	bio 5			
Min Temperature of Coldest Month	bio 6			V
Temperature Annual Range	bio 7	V	V	V
Mean Temperature of Wettest Quarter	bio 8	V		
Mean Temperature of Driest Quarter	bio 9			
Mean Temperature of Warmest Quarter	bio 10		V	V
Mean Temperature of Coldest Quarter	bio 11			
Annual Precipitation	bio 12		V	V
Precipitation of Wettest Month	bio 13			V
Precipitation of Driest Month	bio 14			
Precipitation Seasonality	bio 15		V	V
Precipitation of Wettest Quarter	bio 16	V		
Precipitation of Driest Quarter	bio 17	V		V
Precipitation of Warmest Quarter	bio 18			V
Precipitation of Coldest Quarter	bio 19			

Table S2. Number of specimens applied for genomic analysis (N_G) and phenotypic analysis (N_P).

Sample site	N_G	N_P
Alibang	5	6
Daxi	13	13
Longtan	11	11
Guanxi	12	12
Neiwan	5	5
Miaoli	5	4
Lianhuachi	28	28
Maolin	7	7
Shizi	8	8
Nangang	9	9
Fushan	27	24
Xiulin	6	6
Haiduan	4	4
Total	140	137

Note: Sampling sites are ordered by locations from north to south and west to east.

Table S3. The change of potential distribution range under different future Shared Socioeconomic Pathways (SSPs). Positive values indicate an increase, while negative values indicate a decrease in the future potential distribution range.

Scenario	**SSP126**			**SSP370**			**SSP585**		
Period	2011-2040	2041-2070	2071-2100	2011-2040	2041-2070	2071-2100	2011-2040	2041-2070	2071-2100
Dark-winged	48.5%	24.9%	46.1%	-4.4%	-5.9%	-22.9%	42.4%	39.5%	37.3%
Clear-winged	54.8%	76.6%	102.3%	76.7%	58.5%	41.1%	65.4%	23.7%	50.8%
All Populations	39.2%	14.1%	120.6%	22.0%	-9.8%	46.0%	40.1%	81.9%	105.6%

Table S4. Results of variance partitioning analysis following the redundancy analysis (RDA). Partitioning of variance is explained by geographical (geo.) and environmental (env.) factors. The table shows the percentage of variance explained (PVE%) by combined and individual fractions, and *F*-statistics were used to assess the significance of each fraction, with statistical significance indicated as: $p < 0.05$ (*), $p < 0.01$ (**), $p < 0.001$ (***).

Combined fractions	PVE(%)
F~geo.	1.27**
F~env.	1.29***
Individual fractions	
F~geo.| env.	1.54***
F~env.| geo.	1.56***
Total explained	2.83***
Total unexplained	97.17
Total	100

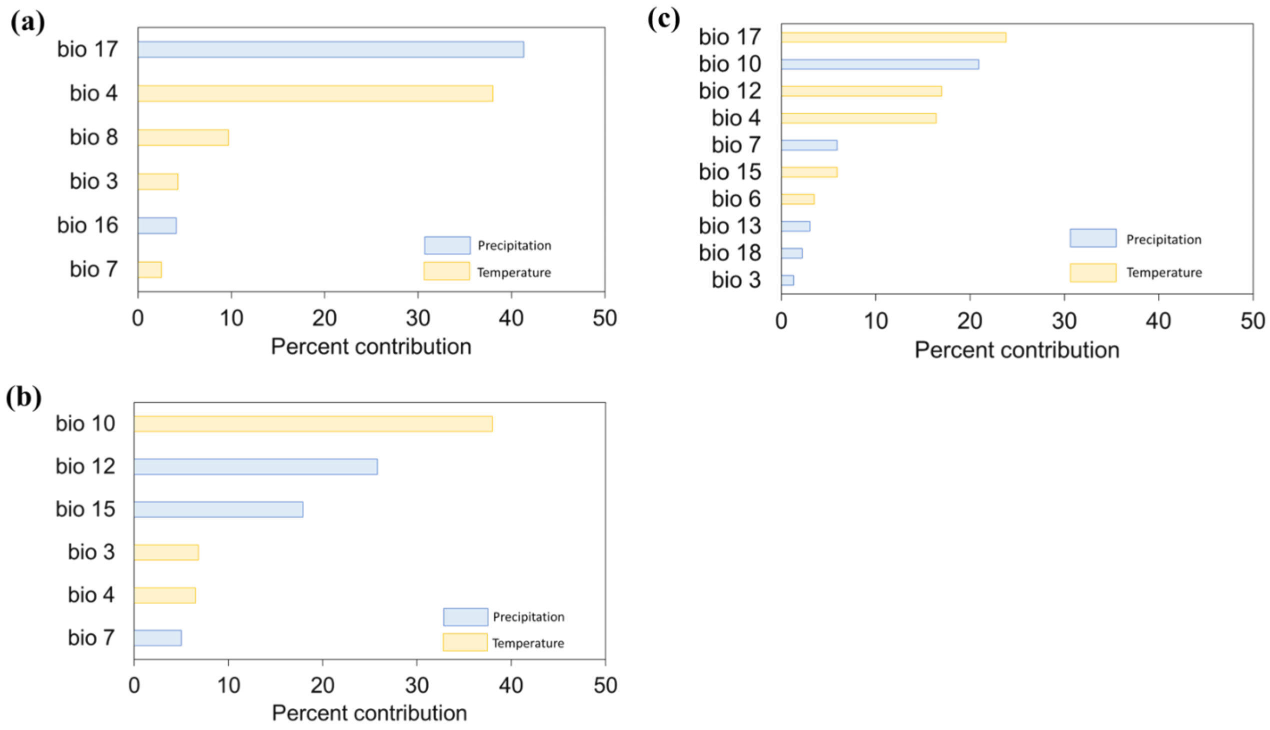

Figure S1. The variable contribution of distribution models for (a) Dark-winged individuals, (b) Clear-winged individuals and (c) all individuals.

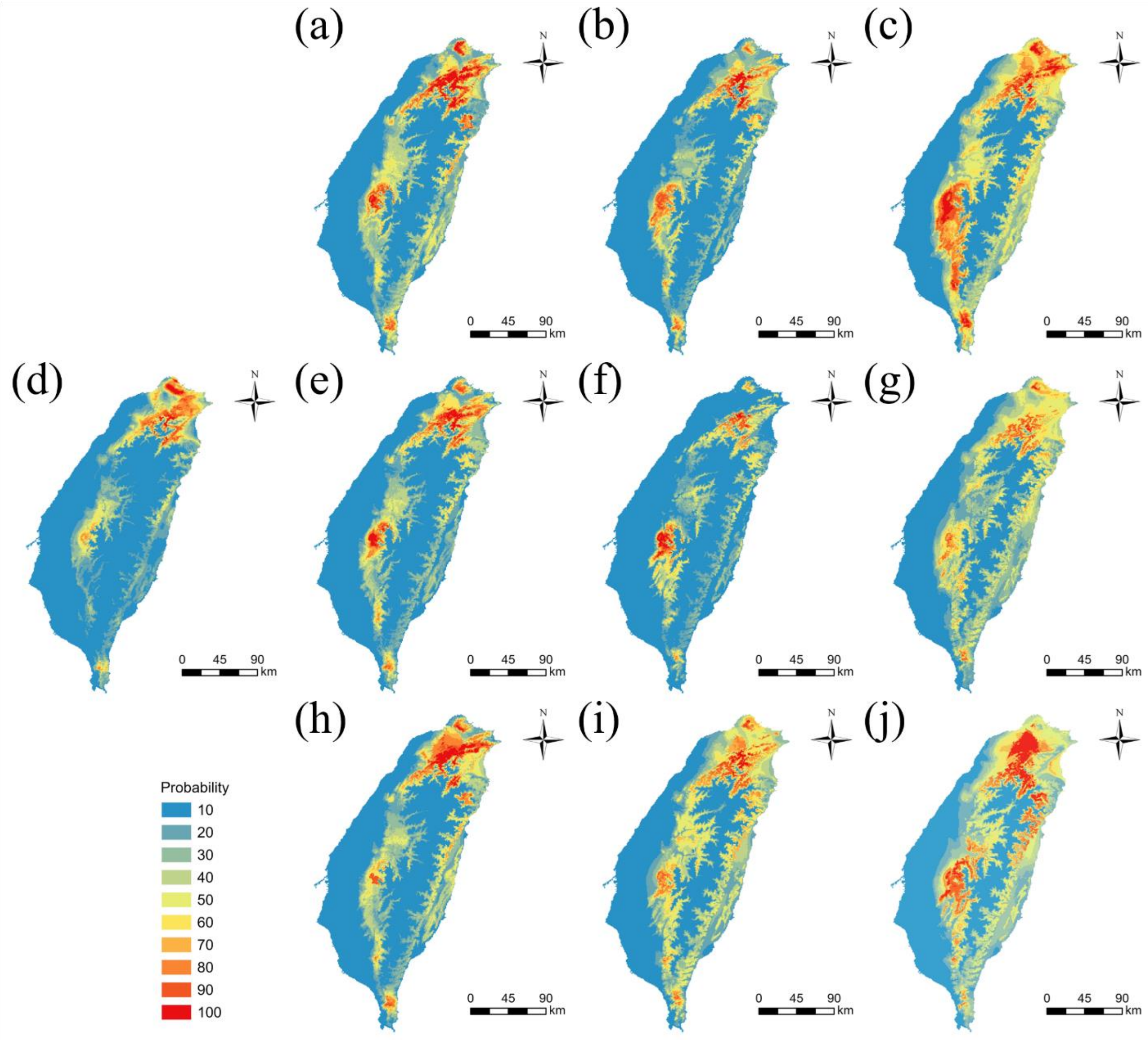

Figure S2. Projected distribution of *Psolodesmus mandarinus* (jointly with all individuals regardless of phenotypes) under current time (d); future distribution under SSP126 in (a) 2011-2040, (b) 2041-2070, and (c) 2071-2100; (d) current time; future distribution under SSP370 in (e) 2011-2040, (f) 2041-2070, and (g) 2071-2100; and future distribution under SSP585 in (h) 2011-2040, (i) 2041-2070, and (j) 2071-2100.

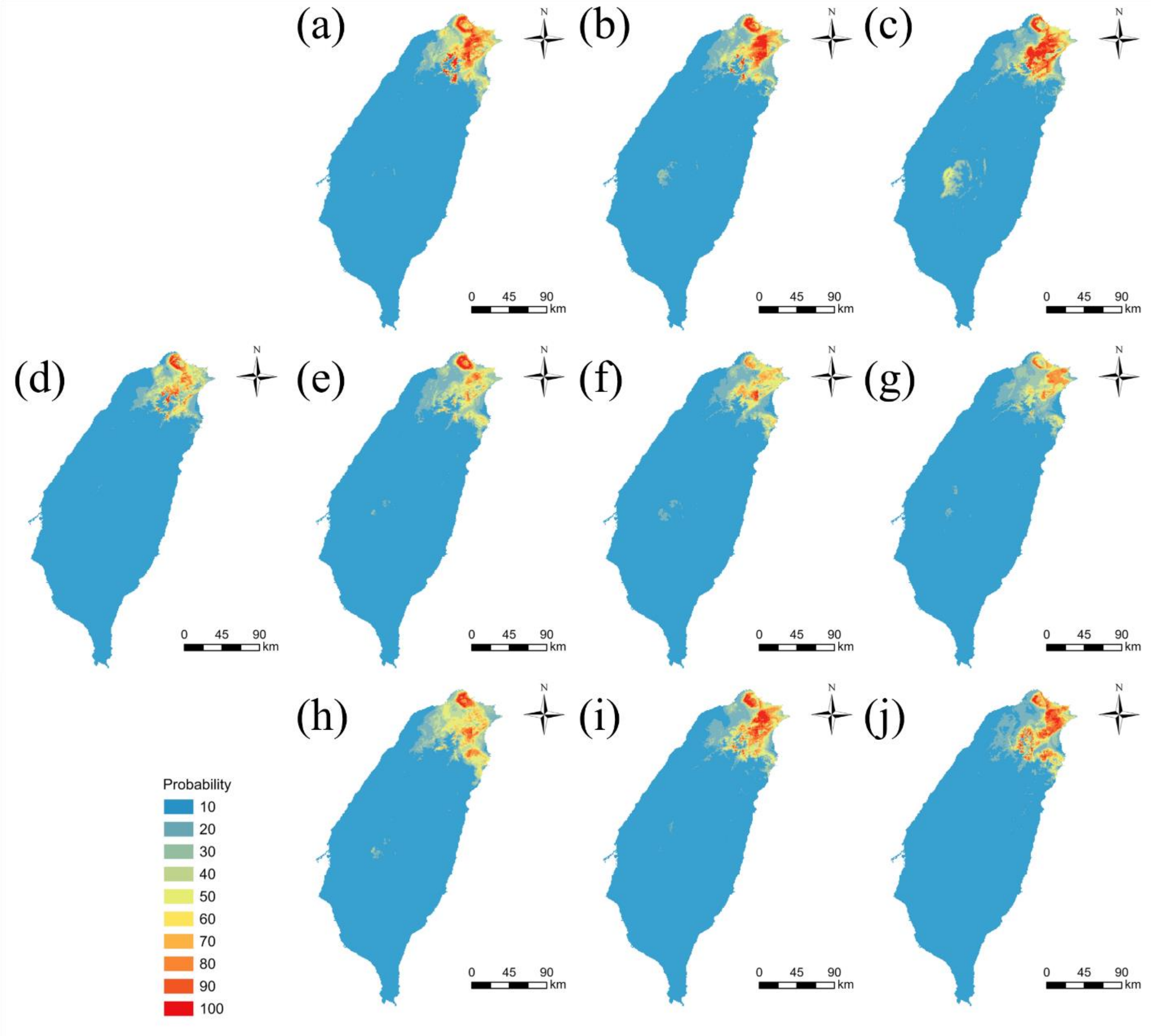

Figure S3. Projected distribution of clear-winged individuals of *Psolodesmus mandarinus* under current time (d); future distribution under SSP126 in (a) 2011-2040, (b) 2041-2070, and (c) 2071-2100; (d) current time; future distribution under SSP370 in (e) 2011-2040, (f) 2041-2070, and (g) 2071-2100; and future distribution under SSP585 in (h) 2011-2040, (i) 2041-2070, and (j) 2071-2100.

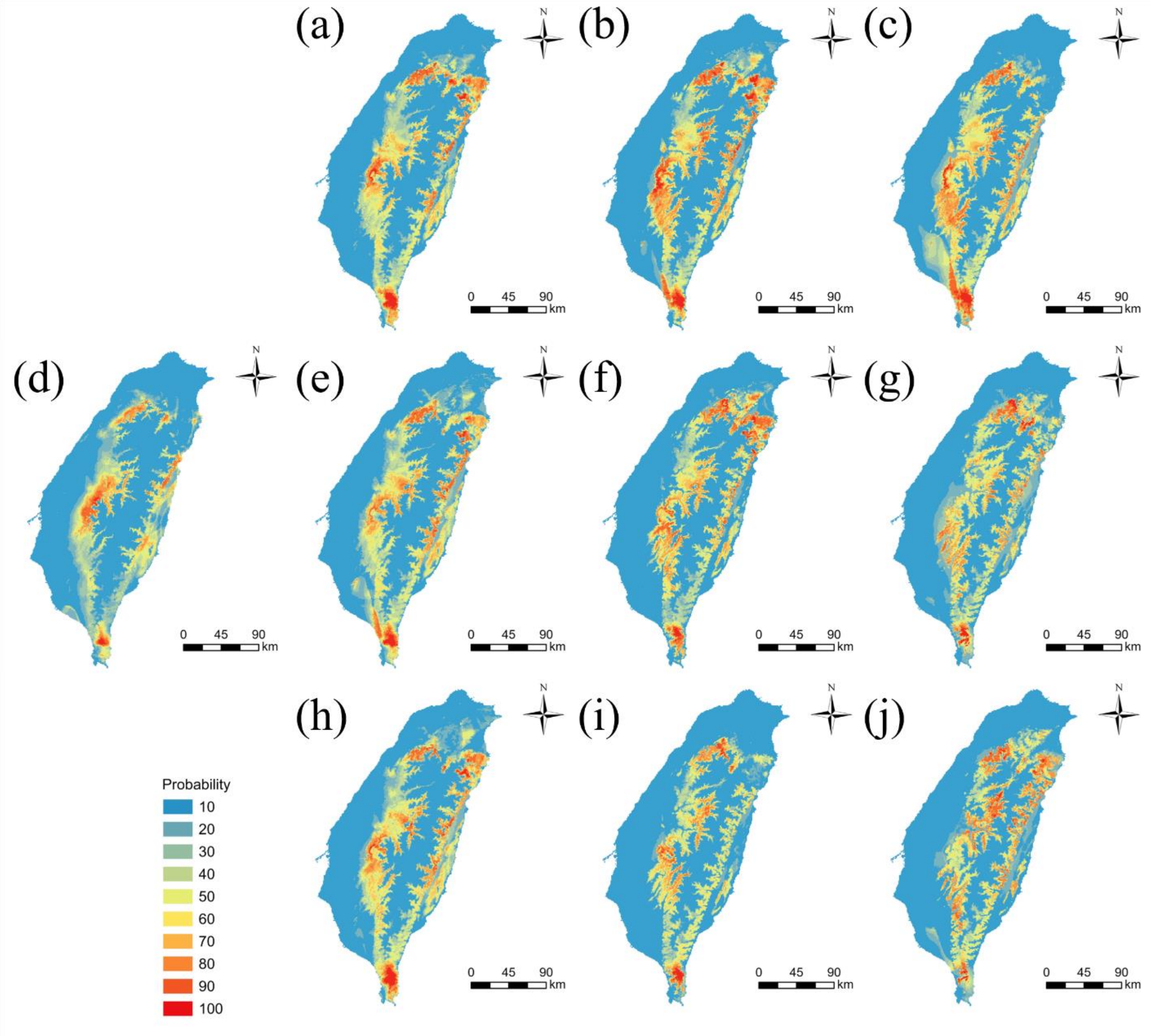

Figure S4. Projected distribution of dark-winged individuals of *Psolosdesmus mandarinus* under current time (d); future distribution under SSP126 in (a) 2011-2040, (b) 2041-2070, and (c) 2071-2100; (d) current time; future distribution under SSP370 in (e) 2011-2040, (f) 2041-2070, and (g) 2071-2100; and future distribution under SSP585 in (h) 2011-2040, (i) 2041-2070, and (j) 2071-2100.

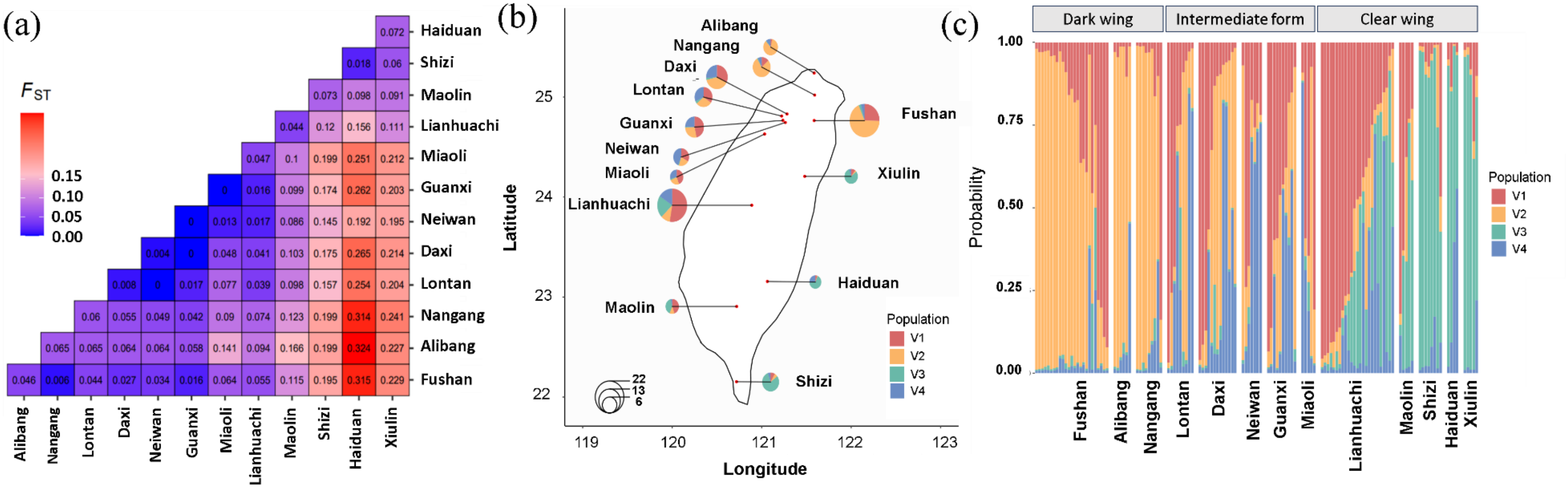

Figure S5. Population structure analysis based on the OutCombo dataset: (a) Pairwise F_{ST} values, (b) Pie chart from STRUCTURE analysis, and (c) Bar chart from STRUCTURE analysis. The OutCombo approach, which filters loci deviating from Hardy-Weinberg equilibrium across all populations combined, minimises artefacts by detecting subtle population structure while accounting for potential biases in individual population-level deviations.

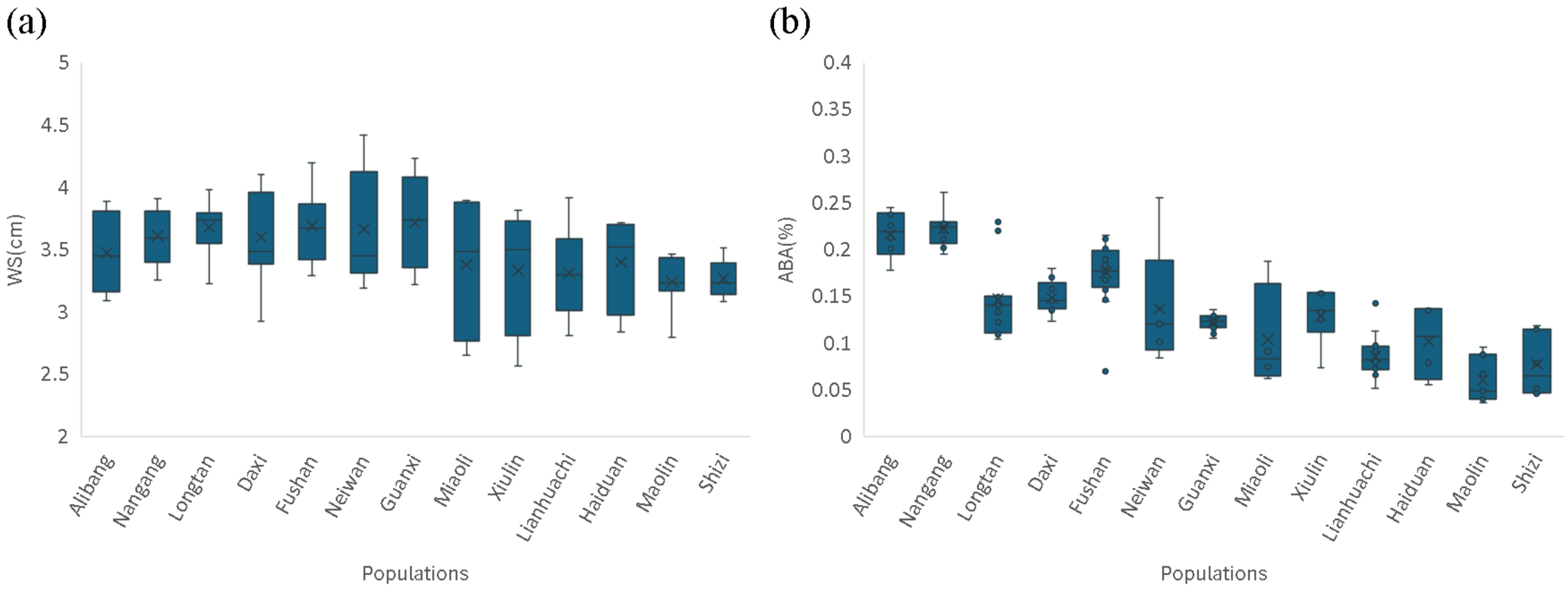

Figure S6. Phenotypic variations of (a) wing size (WS) and (b) the ratio of the apical blackish area of the whole wing (ABA%) are different among populations (WS, $F = 3.34$, $p < 0.001$; ABA%, $F = 24.61$, $p < 0.001$).