

Capturing response differences of species distribution to climate and human pressures by incorporating local adaptation: Implications for the conservation of a critically endangered species

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- 1 Capturing response differences of species distribution to climate and human
- 2 pressures by incorporating local adaptation: implications for the conservation of
- 3 a critically endangered species
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Abstract: Considering local adaptation has been increasingly involved in forecasting species distributions under climate change and the management of species conservation. Herein, we take the critically endangered Chinese giant salamander (*Andrias davidianus*) that has both a low dispersal ability and distinct population divergence in different regions as an example. Basin-scale models that represent different populations in the Huanghe River Basin (HRB), the Yangtze River Basin (YRB), and the Pearl River Basin (PRB) were established using ensemble species 24 distribution models. The species ranges under the future human population density (HPD) and climate change were predicted, and the range loss was evaluated for local 2526 basins in 2050 and 2070. Our results showed that the predominant factors affecting 27 species distributions differed among basins, and the responses of the species 28 occurrence to HPD and climate factors were distinctly different from northern to 29 southern basins. Future HPD changes would be the most influential factor that engenders negative impacts on the species distribution in all three basins, especially in 30 31 the HRB. Climate change will likely be less prominent in decreasing the species range, 32 excluding in the YRB and PRB under the highest-emissions scenario in 2050. Overall, the high-emissions scenario would more significantly aggravate the negative impacts 33 34 produced by HPD change in both 2050 and 2070, with maximum losses of species 35 ranges in the HRB, YRB, and PRB of 83.4%, 60.0%, and 53.5%, respectively, under the scenarios of the combined impacts of HPD and climate changes. We proposed 36 adapted conservation policies to effectively protect the habitat of this critically 37 38 endangered animal in different basins based on the outcomes. Our research addresses 39 the importance of incorporating local adaptation into species distribution modeling to 40 inform conservation and management decisions.

41 Keywords: local adaptation; Chinese giant salamander; species distribution models;
42 human population density; climate change; range loss

43 **1 Introduction**

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Determining where and how species will respond to climate change is currently

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a pivotal topic in biogeography and conservation biology research, which can provide 45 great knowledge to help formulate conservation and management strategies to 46 47 mitigate the extinction risks of endangered species (Chardon et al. 2019). Species distribution models (SDMs) are commonly employed approaches that explore how the 48 49 distribution of a species of concern will shift in space and time with a changing 50 climate (Pacifici et al. 2015). Such models correlate species occurrences with bioclimatic factors to predict the relative probability of occurrence by assuming that 51 52 species track alongside the changing climatic conditions (Elith and Leathwick 2009, 53 Booth et al. 2014). Given their simplicity and flexibility (Thuiller et al. 2009), as well as the easy accessibility of species occurrence records and climate datasets, SDMs are 54 widely utilized to predict species' range shifts across the globe and guide the 55 56 conservation management of species in all earth spheres (García-Alegre et al. 2014, Gobeyn and Goethals 2019, Pecchi et al. 2019). 57

Despite their widespread use, SDMs have been criticized for involving 58 59 assumptions that ignore many ecologically relevant factors (Araújo and Peterson 2012). One of the potential sources of model error that has been of increasing concern 60 61 is the assumption that species across populations are ecologically uniform in their climatic tolerances within their range (Wiens et al. 2009). Typically, SDMs treat a 62 species as a single entity (Busby 1988) and are developed utilizing all the occurrence 63 64 data of a species in the whole area to project its potential distribution (Merow et al. 65 2013). Substantial evidence has shown that the distribution limits of many species vary among populations and that climate tolerances differ among distribution areas 66

due to adaptation to local climate conditions (Sheth and Angert 2014, Lee - Yaw et al. 67 2016). most models assume that species' 68 Despite this. tolerances 69 to climate changes do not differ across distributional ranges (Valladares et al. 2014). 70 Uncertainties and errors in geographic distribution predictions can be produced by not considering local adaptation (Pearman et al. 2010, Peterson et al. 2019), which 71 72 preclude the analysis of genetic variation in ecologically important traits (Marcer et al. 73 2016).

74 Local adaptation most likely exists within species whose distribution, dispersal, 75 and population dynamics are affected by natural barriers, including physical and biological barriers (Cozzi et al. 2013). Relevant physical barriers may include 76 77 geographical and topographical events that result in discontinuous habitats (Aliaga -78 Samanez et al. 2020) and biological barriers that may include interspecific 79 competition and changes in the trophic habitat (Hallfors et al. 2016, Aliaga - Samanez et al. 2019). Very recent research indicated that a growing number of studies are 80 81 emphasizing the importance of incorporating different forms of local adaptation or intraspecific variation in climate responses (Chardon et al. 2019, Peterson et al. 2019). 82 83 When modeling range shifts under climate change with the incorporation of local adaptation, individuals within species were divided into groups with different climate 84 responses based on taxonomic units, populations, geographic regions, phenotypes or 85 genetic groups (Pearman et al. 2010, Kapeller et al. 2012, Marcer et al. 2016, 86 Schwalm et al. 2016, Meynard et al. 2017, Peterson et al. 2019). Among the existing 87 studies that incorporated local adaptation, few examined the adaptation patterns of 88

nonclimatic variables that could characterize the environmental tolerances of a species(Peterson et al. 2019). At least three studies have considered adaptations to local environmental conditions other than climate factors (Wang et al. 2010, Schwalm et al. 2016, Hu et al. 2017); however, all of them assumed the nonclimatic variables to remain static over time when predicting future conditions. Therefore, how differences in local adaptation to human-related pressures could affect future predicted range shifts remains poorly documented.

96 Since SDMs are widely used to support conservation or management decisions, 97 not taking local adaptation into account may lead to inaccurate descriptions of species responses to environmental changes across their geographic ranges and, therefore, 98 misplaced conservation efforts, especially for critically endangered species (Hamann 99 100 and Aitken 2013). Amphibians represent the most threatened vertebrates around the world (Zhang et al. 2019). especially salamanders, which are highly sensitive to 101 climate change because of their low vagility and restrictive physiological demands 102 103 (Barrett and Guyer 2008). Unlike species that can track varying climates, salamanders will suffer range shrinkage when the climate condition in their distribution areas 104 105 become unsuitable to sustain their populations (Araújo et al. 2006). Therefore, 106 salamanders are likely to have distinct local adaptations because of their strong climatic requirements, and their wild populations are varied in community structure 107 108 and ecosystem function in different biogeographic regions (Kozak and Wiens 2006, 109 Ficetola et al. 2016). Human pressures from anthropic activities serve as yet another threat to salamanders' wild population and are likely to aggravate existing stresses 110

(Hof et al. 2011). Therefore, it is fundamental to figure out how the salamanders' ranges will respond to future disturbances from exacerbated human pressures and future climate change to ensure efficient management and conservation.

114 In the present study, we addressed intraspecific variation in responses to climate 115 and human-related factors in distribution models to explore how it will affect 116 conservation management. We take the critically endangered Chinese giant salamander (CGS; Andrias davidianus (Blanchard, 1871)) as a case. It is known to be 117 118 historically distributed in most of mainland China. Its wild populations and habitat 119 have been declining due to habitat destruction and hunting for use in medicinal herbs and foods, and the species is currently critically endangered (Yan et al. 2018). We 120 121 separated the region into three basins, i.e. the Huang River (Yellow River) basin and 122 its adjacent Hai River Basin, the Yangtze River basin, and the Pearl River basin. Basin-scale SDMs were constructed by considering the effects of both climate and 123 human-related factors on the range shifts. This study aims to: (1) test whether 124 125basin-scale models describing separate populations are reliable in species distribution modeling; (2) describe whether the species responses to climate and human-related 126 127 variables varied among geographical regions; (3) quantify the species range shifts impacted by human pressures and climate change in separate areas; and (4) to help 128 guide management and conservation efforts for the CGS based on these outcomes. 129

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130 **2 Methods**

131 **2.1 Species occurrence and data grouping**

The CGS is recognized as the world's largest amphibian. It is one of the three 132 extant giant salamanders that are Cryptobranchidae living in aquatic habitats (Zhang 133 134 et al. 2019). Due to habitat loss and human consumption, their population has sharply declined over the past decades. The species has been classified as a critically 135 endangered animal by the Chinese government, included in the Appendix I listed 136 137 species of CITIES and listed as "CR" in the IUCN Red List of Threatened Species (Yan et al. 2018). The occurrence data of CGS were collected from the literature (Wen 138 2015, Turvey et al. 2018), the Global Biodiversity Information Facility (GBIF; 139 140 http://www.data.gbif.org/), and the geodatabase of the natural reserves 141 (https://www.osgeo.cn/data/). The period covered by these data was from the late 20th century to the early part of this century. The occurrence data were located mainly in 142 the Huang River (Yellow River) basin (HRB), the Yangtze River basin (YRB), and the 143 Pearl River basin (PRB), as well as adjacent rivers and basins (Figure 1). We retained 144 259 occurrence records after discarding erroneous (e.g., records far from waters) and 145 146 duplicate records. We selected only one record in each model grid to diminish the spatial autocorrelation of presence records (i.e., more than one presence record in one 147 environmental grid cell with a 30 arc-second spatial resolution, ca. 1.0 km² at the 148 equator) through a spatial thinning method provided by Boria et al. (2014), and 253 149 occurrences datasets finally remained for model construction. 150

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Due to its limited ability to disperse, particularly between river systems, the CGS

distributions were geographically partitioned and confined in neighboring regions 152(Liang et al. 2019). Considerable studies have found genetic diversity and variability 153154 among the CGS populations across the whole distribution area based on molecular analysis (Liang et al. 2019). For instance. Tao et al. (2005) discovered significant 155156 genetic differentiation between populations in the PRB and the YRB and between populations in the YRB and the PRB by applying mitochondrial DNA sequencing. 157 Yang et al. (2011) used AFLP makers and found significant genetic diversity from 158 159 northern to southern China The high population differentiation likely originated in 160 association with their lower dispersal ability and geographical barriers (including mountains and drainages), as well as their specific habitat requirements(Liang et al. 161 162 2019). Based on these studies, we divided all the occurrences into three populations 163 from north to south. The northern population involved the occurrence located in the HRB and its adjacent Hai River Basin (n=33); the central population included the 164 occurrence located in the YRB (n=172), and the southern population contained the 165 occurrence located in the PRB (n=28). Other occurrences located in Huai River Basin 166 167 (HuRB, n=8) and South-eastern River Basin (SRB, n=12) were classified as unknown 168 populations. We developed a model at the species level with all the occurrences for the whole area (model name "M Whole") and three separate basin-scale models for 169 the populations in the HRB and Hai River Basin, the YRB, and the PRB (model 170171names: "M_HRB", "M_YRB" and "M_PRB"). The basin-scale models were used to 172 test the spatial transferability to other basins and compared with the model including the whole occurrence dataset. 173



We applied the ensemble modeling technique to develop SDMs of the CGS by 178 179 considering their reliability in reducing the uncertainties from a single modeling 180 algorithm and providing robust projections of species distribution (Grenouillet et al. 2011). We used four model algorithms, i.e. the generalized linear model (GLM), 181 generalized boosting model (GBM), random forest (RF), and multiple adaptive 182 regression splines (MARS) model, which have been frequently employed in SDMs to 183 develop the ensemble models (Zhang et al. 2020a). All the model algorithms and the 184 ensemble model were implemented by the biomod2 package in the software R 185 3.6.1(Thuiller et al. 2009). Since we used presence-absence algorithms and reliable 186

absence data are not available, pseudo-absence records with the same number of 187 presence records within the local basin for each model scenario were generated using 188 189 a random method that can exclude pixels in the presence locations (Barbet-Massin et 190 al. 2012). Afterward, all the presence and pseudo-absence records were combined and 191 shuffled for ultimate use in model construction (Senay et al. 2013). For each model 192 algorithms, 70% of all records were randomly chosen for model calibration, and the remaining 30% was used to assess the algorithm performance. Each model algorithm 193 194 was run 10 times to avoid bias from the splitting of the total records. The predictive 195 abilities of each model were evaluated using the true skill statistic (TSS) and the area under the receiver operating characteristic curve (AUC) (Swets 1988). To ensure the 196 optimal predictive ability, algorithms with a TSS score greater than 0.6 and AUC 197 198 score greater than 0.8 (Allouche et al. 2006) were selected to develop ensemble models by the committee-averaged method. We also determined the relative 199 importance of the selected predictors using an inbuilt randomization procedure 200 201 (Thuiller et al. 2016) and the response curves of species occurrence for each algorithm 202 using the evaluation strip method (Elith et al. 2005).

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204 **2.2 Predictor selection**

The selection of predictors in SDMs can strongly affect the reliability of the predicted niche and spatiotemporal transferability (Peterson et al. 2007). Recent research tested 19 bioclimatic variables and 11 nonclimatic variables, including eight human-related variables, to predict the species distribution of the CGS for the whole 209 potential distribution area in China (Zhang et al. 2020a). Through analysis of the variable collinearity, contribution, and reasonability, four climate variables, and three 210 211 nonclimatic variables were finally selected as important predictors and showed a good 212 performance in distribution modeling and prediction of the species in that study. In the 213 present study, however, as only about forty occurrence data points were used for 214 model calibration for the HRB and PRB (70% of the whole presence and pseudoabsence data), we selected the four most important variables from the seven 215 variables (see Table 1 in Zhang et al. (2020)) to meet the empirical rule of the use of a 216 217 maximum of one predictor for ten data points to avoid overparameterization of the models(Harrell Jr et al. 1984, Petitpierre et al. 2017). The four predictors included 218 three bioclimatic variables, i.e., the temperature seasonality (TS), the mean 219 220 temperature of the coldest quarter (MTCQ), and the precipitation of the warmest (PWQ) 221 quarter accessed from the WorldClim data website (https://www.worldclim.org/data/index.html), and the human population density 222 223 (HPD) from SEDAC (http://sedac.ciesin.columbia.edu). Despite the small number of predictors, these four variables were regarded as the most relevant factors affecting 224 225 the distribution of the CGS, as the contributions of the other three variables to species occurrence were all less than 5% (Zhang et al. 2020a). We used the four 226 selected variables in the four basal model algorithms and ensemble models to predict 227 current and future species distributions at the basin-scale and over the whole area. 228

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230 **2.4 Model prediction and evaluation**

The CGS distributions under the current (1950-2000) and future (2050 and 2070) 231 232 climate conditions with and without the impact of future HPD change for three separate basins and the whole area were projected. We considered two representative 233 234 concentration pathways (RCPs) for climate change, the optimistic scenario with stringent mitigation (RCP 2.6) and the pessimistic scenario (RCP 8.5). Future climate 235 236 data were derived from three global circulation models (GCMs) (MIROCESM-CHEM, CCSM4, and BCC-CSM1-1) that are widely used in Asia. To 237 238 reduce uncertainties in the prediction of the species occurrence probability, the averaged outputs of the three GCMs were used as future climates. We obtained future 239 HPD data at a spatial resolution of 1 km for 2050 and 2070 from the global population 240 241 dataset of the Socioeconomic Data and Applications Center (SEDAC) (Jones and O'Neill 2016). 242

For real application and model evaluation, species presence and absence maps 243 244 are required and obtained through transforming the continuous suitability predictions 245 produced by SDMs to binary outputs using threshold values. We applied the mean of 246 the predicted probabilities of species occurrences that can objectively maximize the agreement between observed and predicted distributions (Cramer 2003, Liu et al. 247 2005), as the threshold to determine the species range (Zhang et al. 2020a). This 248 method was suggested to be reliable in transforming SDM results from presence 249 probabilities to presences/absences binary maps (Liu 2005, Liu et al. 2013, França 250 and Cabral 2019). For each basin-scale model, the threshold was calculated separately, 251

and range sizes under current and future conditions were quantified based on the presence/absence map. The changes of the range size in the scenarios of HPD and climate changes relative to the current condition were calculated and compared among the three basins.

256 **3 Results**

3.1 Model performance

For each basin-scale model, most model algorithms performed well when 258 assessed with AUC and TSS, with their median values being greater than 0.8 and 0.6, 259 260 respectively (Supplementary Figure S1). Of the four model algorithms, RF always performed better compared to others for all basin-scale models. Among the 40 basal 261 models, 31, 36, and 29 basal models were respectively selected to develop the 262 263 ensemble SDMs for the HRB, YRB, and PRB (Table 1). For the model with all the occurrences for the whole area, it is not surprising that all basal models performed 264 better compared to those in the basin-scale models, and all the basal models were 265 266 retained to establish the ensemble models. However, the ensemble model for each basin-scale model also showed high accuracy, with AUC \ge 0.94 and TSS \ge 0.0.80 for 267 268 all the basins, indicating that basin-scale ensemble models could be reliable in species 269 distribution modeling. In terms of predicted mean probabilities (MP) of species 270 occurrence (Table 1), the whole-area model performed slightly better for the YRB 271 (0.93) than the YRB model (0.90). The predicted MP values for the HRB and PRB 272 (0.75 and 0.79), however, were lower than those by the local basin models (0.83 and 0.88), indicating the improved capabilities of basin-scale models in modeling the local
distribution of the CGS.

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Table 1 Statistics of model performance, the number of models used in ensemble modeling (NME), and the predicted mean probabilities (MP) of species occurrence. MP_Basin: MP of local species occurrence in each basin-scale model; MP_Whole: MP of species occurrence in each basin in the whole-area model; MP_HuRB: MP of species occurrence in the Huai River Basin in Basin-scale and whole-area models; MP_SRB: MP of species occurrence in the Southeastern River Basin in the basin-scale and whole-area models

					MP_Whol			
Models	AUC	TSS	NME	MP_Basin	e	MP_HuRB	MP_SRB	
	0.95	0.81						
M_HRB	2	2	31	0.83	0.75	0.73	0.40	
	0.97	0.83						
M_YRB	5	3	36	0.90	0.93	0.84	0.83	
	0.94	0.80						
M_PRB	4	4	29	0.88	0.79	0.62	0.82	
M_Whol	0.98	0.86						
e	3	2	40	0.89	0.89	0.92	0.93	

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285 **3.2 Variable importance and response curves**

For the whole-area model, the importance of all four predictors was greater than 10%, with the MTCQ ($32.6\pm2.5\%$) and HPD ($26.8\pm1.9\%$) being more important than the other two (Table 2). However, the allocation of the variable importance considerably changed for the basin-scale models. For the HRB model, the most important variable was the HPD (mean of 40.7%), while the MTCQ played a less pivotal role (mean of 7.8%). The second-most important variable was the PWQ, and

292	the contribution of TS became less. The variable importance pattern produced by the
293	YRB model was similar to that of the whole-area model, despite a significant decrease
294	in the HPD (mean of 11.0%). The MTCQ was the most crucial factor for the species
295	occurrence in the YRB (mean of 37.8%), surpassing all other variables. The most
296	important predictor for the PRB was the PWQ (mean of 35.3%), while the HPD and
297	MTCQ were less important (both mean values were less than 8%). These results
298	revealed that the importance of each variable in the whole-area model seemed
299	balanced by the occurrences in different basins from north to south. The findings from
300	basin-scale models indicated that the environmental conditions affecting the
301	distribution and survival of populations in different basins were likely to greatly differ
302	from each other.

Table 2 Variable importance (%) and the optimal range of the variables (species presence
 probability>0.8) produced by different models. The units for the range of the TS, MTCQ,
 PWQ, and HPD are Celsius, Celsius, millimeters, and people per km², respectively.

	Predictors	M_HRB	M_YRB	M_PRB	M_Whole
	TS	3.3±0.8	12.1±1.1	10.6±1.3	10.9±1
Variable	MTCQ	7.8±0.9	37.8±2	6.2±0.9	32.6±2.5
importance	PWQ	18.8±2.1	8.0±0.6	35.3±4.3	15.2±0.4
	HPD	40.7±3	11.0±0.9	7.6±0.5	26.8±1.9
	TS	[8.6, 11.9]	[6.6, 8.4]	[6.2, 7.5]	[6.1, 10.1]
Optimal	MTCQ	[-10.8, -1.1]	[-1.5, 9.1]	[9.6, 12.1]	[-3.9, 9.7]
range	PWQ	[134.8, 447.7]	[346.5, 576.2]	[557.5, 911.6]	[239.7,721.2]
	HPD	<441.7	<437.6		<414.6

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For each predictor, the response curves among different algorithms were similar in all basin-scale models and the whole-area model (Supplementary Figure S2). A comparison of the response curves produced by the ensemble models showed that the 310 species occurrence exhibited a unimodal response to three climate factors for all basins, but the responses were different among basins for each variable (Figure 2). 311 312 This demonstrated that the curves of both the MTCQ and PWQ moved from the left 313 to the right of the horizontal axis from the HRB to the YRB and the PRB, indicating 314 that the requirements for these two variables were gradually enhanced for populations 315 from north to south. The requirements for the TS of different populations, however, decreased from northern to southern basins. This revealed the response curves of the 316 climate variables produced by the whole-area model failed to reflect the peak 317 318 occurrence probabilities of different basins despite their wider range of high occurrence probabilities. The optimal ranges for the climate variables were distinctly 319 320 different from each other, although they slightly overlapped between connected basins 321 (Table 2). The optimal range increased for the MTCQ and PWQ and decreased for the TS from northern to southern basins. The optimal MTCQ for the HRB was less than 322 the freezing temperature (-10.8~-1.1°C), while it was greater than 9°C for the PRB 323 (9.6~12.1°C). The optimal range of the MTCQ, the most important variable for 324 species in the YRB, was above and below 0°C for this basin (-1.5~9.1°C). As the most 325 326 important variable for species in the PRB, the optimal PWQ (557.5~911.6 mm) was significantly greater than those in the other two basins. It should be noted that the 327 whole-area model did not produce an optimal range covering those in HRB and PRB. 328 For all basins, the occurrence probability decreased with the increase of the HPD 329 330 (Figure 2), suggesting that the species is inclined to occur in regions where the HPD is less than 450 people in one square kilometer (Table 2). The requirement for human 331

interference of the species occurrence in the PRB is stricter, as HPD was less than 75
people per km² when its occurrence probability was above 0.6. Generally, the
requirements of the species distribution varied distinctly in different basins, especially
for climate factors, and these differences could only be detected by separate
basin-scale species distribution models.

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Figure 2. Response curves of predictor variables for separate and whole populations

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341 **3.3 Current distribution**

The species occurrence probabilities predicted by the basin-scale models and the whole-area model under current conditions were compared (Figure 3). Generally, the species distribution areas predicted by the basin-scale model were constrained to local basins, despite some areas with medium species occurrence probability transferred

346	around basin boundaries. Figure 4 shows that the range of the climate predictors
347	clearly varied from northern to southern basins, which could have resulted in confined
348	projections in local areas, considering the distinct responses of the species occurrence
349	to climate factors (Figure 2). Comparisons showed consistent species distributions in
350	the YRB predicted by the whole-area and YRB models (Figure 3b and 3d), but this
351	was not observed in the basin-scale models in the HRB and PRB (Figure 3a and 3c).
352	The mean occurrence probability of the species occurrence data predicted by the
353	whole-area model was less than 0.8 (Table 1, 0.75 and 0.79 for the HRB and PRB,
354	respectively), while it was 0.93 for the YRB, indicating that the whole-area model had
355	a better performance for the YRB but a poor performance in predicting species
356	occurrence for the HRB and PRB. As a result, compared with the local basin models,
357	the whole-area model significantly underestimated the species distribution area by
358	93.4% and 80.3% for the HRB and PRR, respectively. Therefore, these results implied
359	that the basin-scale model could be locally adapted and would be better in projecting
360	the CGS distributions in different basins.



Figure 3. Comparison of projected current occurrence probabilities for the basin-scale
 models and whole-area model, with a, b, c, and d representing the modeling results of
 the HRB, YRB, HRB and the whole basin, respectively. Low: occurrence probability
 below 0.6; Medium: occurrence probability from 0.6 to MH in Table 1 (MH_Basin);
 High: occurrence probability from MH to 1.



Figure 4. Range comparison of the four predictors among the three basins and the whole

area

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371 **3.4 Species range shifts**

Future species distributions were predicted for separate basins using basin-scale models (Supplementary Figure S3), and species range shifts were compared (Figure 5). HPD change caused similar impacts on species distribution for the three basins in both 2050 and 2070 (Figure 5a, 5b) and evidently decreased the species range by over 26% (Table 3), especially in the HRB (range loss of 55.8% and 61.3% in 2050 and

377	2070, respectively). Compared with the current status (Figure 3), future HPD changes
378	would fragment the habitat in all the basins. The species range extended westward,
379	and new habitat was gained in the YRB due to the impact of HPD change (Figures 5a
380	and 5b). The species range was not obviously altered in the HRB and YRB due to the
381	impact of climate change (Figures 5c-5f), and the species ranges were slightly
382	decreased or even slightly increased (due to climate change with RCP2.6 in 2050,
383	Table 3), excluding an obvious range loss of 11.0% in the YRB under climate change
384	with RCP8.5 in 2050. The species range loss was obvious in the northern PRB, while
385	the species ranges expanded southward to the coastal area of the PRB in the
386	climate-change scenarios. The overall range loss in the PRB, however, was more
387	significant in 2050 than in the 2070s in both RCP scenarios (Table 3). When
388	overlapping the impacts from HPD and climate changes, the range loss was
389	aggravated in RCP 8.5 scenarios for all basins (Figure 5i, 5j), especially in 2070 with
390	stable habitat nearly disappearing in the HRB and only remaining in the west and the
391	south coast, respectively, in the YRB and PRB (Figure 5j). The maximum losses of
392	species ranges in the HRB, YRB, and PRB were 83.4%, 60.0%, 53.5%, respectively,
393	indicating a significant negative impact of the combined effect of HPD and climate
394	changes on the species distributions. Despite this, slight offset effects induced by
395	climate change with RCP 2.6 were identified in the HRB and YRB (Table 3).
396	Generally, the effects of HPD and climate changes on species ranges varied among
397	watersheds and periods. HPD variation was likely the most influential factor that
398	engendered negative impacts on species distributions in all three basins, especially in

the HRB. Climate change was probably less prominent in decreasing the species range, excluding the YRB and PRB in high emission scenario in 2050. Overall, the high-emissions scenario would more significantly aggravate the negative impacts produced by HPD change under the superimposed impacts of future climate changes and human pressures.



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Figure 5. Species distribution shifts predicted by the basin-scale models in different scenarios, in which (a) and (b) are HPD change scenarios in 2050 and 2070, respectively; (c) and (d) are climate change scenarios with RCP 2.6 in 2050 and 2070, respectively; (e) and (f) are climate change scenarios with RCP 8.5 in 2050 and 2070, respectively; (g) and (h) are HPD and climate changes with RCP 2.6 in 2050 and 2070, respectively; and (i) and (j) are HPD and climate changes with RCP 8.5 in 2050 and 2070, respectively; and and (h) are HPD and climate changes with RCP 8.5 in 2050 and 2070, respectively; and

412 Table 3. The relative losses of species ranges (%) for the three basins in different scenarios.

C	Models	RCP2.6		RCP8	RCP8.5	
Scenarios		2050	2070	2050	2070	
	HRB	-55.8	-61.3			
HPD	YRB	-28.1	-33.0			
	PRB	-26.9	-27.9			
	HRB	3.9	-0.7	-3.5	-1.7	
CC	YRB	1.9	-1.2	-11.0	-3.2	
	PRB	-13.3	-2.1	-41.8	-2.1	
	HRB	-53.7	-60.9	-56.1	-83.4	
HPD+CC	YRB	-26.5	-32.5	-30.8	-60.0	
	PRB	-34.6	-30.3	-53.5	-37.2	
	HRB	2.1	0.4	-0.3	-22.1	
Difference*	YRB	1.6	0.5	-2.7	-27.0	
	PRB	-7.7	-2.4	-26.6	-9.3	

CC: climate change; HPD+CC: climate change with HPD change.

414 *The difference is the range loss in scenarios HPD+CC minus that in scenario HPD. A positive 415 value indicates offset effects by climate change, while a negative value means aggravated 416 negative impacts due to climate change.

417 **4 Discussion**

413

418 **4.1 Model comparison and consideration**

In the present study, we selected the most important variables based on the model that used all species occurrence records across the whole study area. We used the same variables in the basin-scale models to make the models in separate basins comparable. Only four variables were used to avoid overparameterization because of the relatively limited occurrence records in the HRB and YRB. Although we acknowledge that the species occurrence size in these two basins was tiny and that the inference ability of the SDM could be subsequently influenced, previous studies 426 indicated that SDMs based on small samples size can also produce useful predictions (Hernandez et al. 2006, Wisz et al. 2008, Zhang et al. 2020b). Given the assumed 427 428 niche transferability of SDMs, projections in space could be useful in identifying 429 potential distributions in other geographical regions (Randin et al. 2006, Wenger and 430 Olden 2012). However, the differences of environmental conditions among different 431 study regions can be distinct in species' range, thus, the regional model can result in a generally low transferability across regions. It should be noted that the aim of this 432 study was not to explore the model transferability of different regional models but to 433 434 probe local differences in species distribution responses to environmental changes, specifically for the CGS that have a limited dispersal ability and distinct population 435 divergence among basins. We found distinctly different responses of species 436 437 occurrence to climate conditions and similar responses to HPD among the three basins (Figure 2), which could be an adaptation to local environments (Figure 4). 438 Additionally, our results showed that species distribution area from the whole-area 439 440 model did not completely cover the species occurrences in the HRB and YRB (Figure 3d), while their occurrence probability was corrected to be higher by the local basin 441 442 models, indicating that the local model could outperform the whole-area model. Considering the additional finding that basin-scale models could provide more detail 443 about species distribution, basin-scale models that incorporated local adaption were 444 suggested as more reasonable model strategies. However, to improve or validate the 445 ability of the model to predict species distribution, independent geographically or 446 temporally separated data should be collected (Bahn and McGill 2013). Considering 447

the difficulty and high cost of filed investigation, the emerging environmental DNA method can be employed to determine the presence in the potential distribution area of the CGS predicted by our study and incorporate the data into future SDM work.

Selecting a model-specific threshold to transform model outputs into binary 451 452 presence/absence maps has been essential in various aspects of conservation 453 applications and management (Guisan et al. 2013). Maximizing the sum of sensitivity and specificity (MaxSSS) is regarded as an efficient method for threshold selection for 454 455 presence-only SDMs when compared with various other existing methods (Liu et al. 456 2013), and this method is also commonly used in real applications. However, it is stated that specificity and commission error cannot be calculated without true absence 457 data when using the MaxSSS method to select the threshold (Braunisch and Suchant 458 459 2010). In this study, we tested the MaxSSS method to generate the binary map for all three separate basins and the whole area and found the resulted presence area of the 460 461 CGS continuously spread over almost all of the basins. The predicted distribution 462 distinctly deviated from the real distribution of this species that is limited in dispersal ability and has a habitat highly impacted and isolated by human modification of the 463 464 environment. It is indicated that the predicted distribution generated by MaxSSS could not characterize the potential distribution if information about the biotic and 465 anthropogenic factors that affect the distribution of specific species is not 466 incorporated in the SDM (Liu et al. 2013). For a given species with populations that 467 are geographically confined due to dispersal limitation or species interactions, 468 the occupied geographic range will be smaller than its full potential distribution 469

470 (Leathwick 1998, Svenning and Skov 2004, Soberon and Arroyo-Pena 2017). Furthermore, limited climate availability is also expected to reduce the fundamental 471 472 niche to a smaller realized niche (Soberón and Nakamura 2009). Although no direct 473 biotic and human factors were considered in our model, we constrained the model 474 area in the separate basin for this species with a limited dispersal ability and included 475 the human population as an important predictor in the model. Therefore, we hypothesized that our model-estimated distribution was closer to the realized 476 distribution, which is more consistent with the actual distribution of the CGS. To 477 478 achieve this, we used a more rigorous threshold, which was the predicted mean probability of the occurrence data, for the studied critically endangered species. 479 Satisfactory agreements between occurrence sites and the predicted high occurrence 480 481 probabilities were also achieved with this method (Figure 3, Table 1). The predicted current species distribution was also generally consistent with the results from the 482 county-scale habitat model produced by Chen et al. (2018). Further work is still 483 needed to test and compare other threshold methods (e.g. kappa maximization and 484 prevalence approaches) (Liu 2005) to select the optimal thresholds for different basins 485 486 to better support model evaluation and application.

487

488 **4.2 Difference among populations in local basins**

Our research revealed a distinct response variation of species occurrence to climate factors from northern to southern basins. As the basins changed from temperate areas to subtropical monsoon regions, the preferred MTCQ and PWQ of the

492	CGS were found to increase (Figure 2) with increases in the air temperature and
493	precipitation from north to south. As the HRB is a mountainous region with complex
494	landforms and is partly controlled by a continental dry climate, its annual temperature
495	differences are very large (Lu et al. 2014). This may explain why the preferred TS of
496	the CGS in the HRB was higher than those in the other two basins. For the studied
497	ancient animal with poor dispersal potential, mountains and rivers blocked its
498	migration with the formation and evolution of geographic structures, which has led to
499	a rather high level of population differentiation in different geographic regions (Liang
500	et al. 2019). At the same time, the distributions of the species could have adapted to
501	local climate conditions, as indicated by our research. Such local adaptation evidence
502	was also shown in the difference in the contributions of climate factors to species
503	occurrence (Table 2). The most important climate factor in the HRB and PRB was the
504	PWQ, while it was the MTCQ in the YRB. Like most amphibians, the CGS needs to
505	hibernate in cold months to reduce energy consumption and protect them from the
506	frozen period. Unlike the HRB and PRB, where the preferred MTCQ of CGS
507	occurrence is either below-zero temperatures or higher-than-zero temperatures (Figure
508	2), the optimal range of the MTCQ in the YRB is around the freezing temperature
509	(Table 2), revealing that the CGS in the YRB could be more sensitive to the variation
510	of winter temperatures required for hibernating. As the breeding month of the CGS is
511	mainly in wet June and July and the quantity of precipitation is a dominant factor
512	influencing the biomass and health of aquatic ecosystems (Grimm et al. 2013), a
513	suitable PWQ could afford a suitable habitat and enough food for CGS reproduction

in the HRB and PRB. Although the TS was found to be relatively less important to CGS occurrence in the three basins, studies revealed that the seasonal variation of climatic conditions may influence the phenology and spatial distributions of salamanders (Kirk et al. 2019).

518 As the life attributes of ectothermic animals are highly linked to the climate, 519 climate change may cause profound impacts on salamanders (Bartelt et al. 2010). However, as indicated in this study, future HPD variations were primarily accountable 520 for the loss of the species' range, especially for the HRB, where HPD played an 521 522 important role in the occurrence of the species. Future increasing human populations may advance the harvesting rate of the CGS, where it is popularly believed that they 523 are nutrient-rich foods. As salamanders have low dispersal abilities and rigorous 524 525 habitat requirements, they are susceptible to human-induced environmental changes (e.g., urbanization and river reconstruction) (Price et al. 2011). The obvious range loss 526 of the CGS resulting from future HPD changes will probably be caused by the 527 528 booming expansion of urban areas in China in the future. As the CGS prefers to live in habitats with clean and fast-flowing waters(Chen et al. 2018), urbanization can 529 530 destroy suitable habitats by changing the land cover, altering catchment hydrology, and contaminating river water (Price et al. 2011). Additionally, our study revealed 531 distinct habitat fragmentation caused by HPD change, which would decrease the 532 genetic diversity of populations by obstructing movement among species ranges 533 534(Marsh et al. 2005) and ultimately increase the risk of species extinction (Noël et al. 535 2006).

536

537 **4.3 Insights for conservation and management**

538 The endangered CGS has attracted considerable conservation attention, while the baseline data on its distribution status is often limited for identifying conservation 539 540 activities and management policies (Fellowes et al. 2009). The spatiotemporal species 541 distribution produced by our study could provide helpful guidance to surveys of the species' presence and could detect key habitats and populations throughout its ranges. 542 Setting up nature reserves has been acknowledged as an effective strategy for 543 544 protecting natural populations of the CGS (Liang et al. 2013). However, effective management to prohibit human access to habitats has been lacking in some of the 545 protected areas (Pan et al. 2015). Our research elucidated that future HPD change 546 547 would result in a significant range loss of the CGS, which is basically following the accepted view that their population decline in the wild is primarily attributed to 548 human-induced habitat destruction and overexploitation. Therefore, tighter measures 549 550 that prevent human interference should be addressed, especially for the existing nature 551 reserves of the CGS. To do this, public education campaigns should be enhanced to 552 provide better information about the survival status of the CGS and the importance of conserving their habitat. The government should implement severer penalties and 553 regulations to prohibit hunting wild CGS. We recognize that climate change would 554 induce relatively fewer negative impacts on the CGS distribution; however, it is likely 555 556 to evidently aggravate the adverse impacts from human pressure in the future.\, as indicated in our study. Therefore, climate factors that heavily influence the habitat and 557

survival of the CGS should not be neglected when formulating conservation
 measures.

560 We revealed local differences in climate variable importance and range shift responses to HPD and climate changes among the three basins using basin-scale 561 562 models. Therefore, we suggest that local adaptive management strategies should be 563 employed for populations in different regions in the future. For the HRB, it is especially important to eliminate the impact of human activities on the habitat of the 564 CGS, as the variation of the used human-related factor would cause distinct range loss. 565 566 For this relatively dry basin, we reported that precipitation in the wet season is a dominant climate factor since it may affect its breeding activities. Water 567 replenishment to the key habitat streams and rivers in the reproduction season could 568 569 be an effective measure. If no urgent conservation measures are implemented, the suitable habitats would be devastated by HPD and climate changes (Figure 5j). For 570 the YRB, we advocate strengthening the conservation of existing nature reserves, as 571 572 most of them are in this basin, and new reserves could be established in the west of 573 the range since the habitat there is more stable; thus, new habitats would be colonized 574 in this region with the changes of HPD and the climate (Figure 5). Mitigating the environmental temperature in the winter is needed for the reserves, as the temperature 575 is crucial in influencing the hibernation of the CGS. For the PRB, compared to the 576 impact of human pressure, climate change would seriously reduce the species range in 577 578the northern part of the basin, although new habitat could be gained in the south (Figure 5c-5f). This would force the habitat and populations in the PRB to be more 579

580 isolated from those on the north side. As precipitation in the wet season was found to be notably more important for species occurrence compared to other climate factors 581 582 and the human factor, similar measures in the HRB should be particularly enforced to support the successful breeding of the species. As the species ranges of the three 583 584 basins would distinctly be detached from each other in the future (Figure 5g-5j), specific mitigation strategies at the population level should be further addressed in 585 future studies, and our findings concerning the local adaptation differences of species 586 ranges provide beneficial information. 587

588 It is worth mentioning that the release of farmed salamanders has been increasingly approved as a conservation measure for the CGS in recent years. 589 Although it could help restore its populations, the introduction of non-native 590 591 individuals might induce severe genetic homogenization in local populations (Liang et al. 2019). Therefore, we suggest that environmental tolerance and genetic lineage 592 should be tested before releasing farmed individuals into the wild. In any case, our 593 study highlights the importance of local adaptation in generating more robust 594 management and conservation plans for this critically endangered species of special 595 596 interest.

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