中国農業大學
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iPRRG

Genetic-Ecological Integration for Adaptive Potential Assessment: Case Studies of Two Invasive *Bactrocera* species

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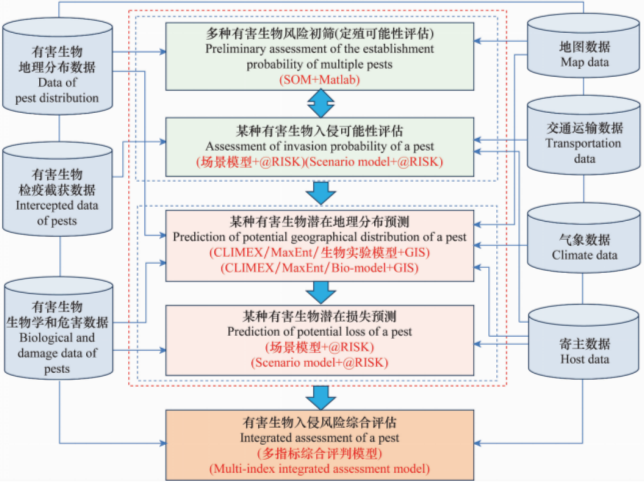
Background



有害生物地理分布数据
Data of pest distribution

有害生物检疫截获数据
Intercepted data of pests

有害生物生物学和危害数据
Biological and damage data of pests

多种有害生物风险初筛(定殖可能性评估)
Preliminary assessment of the establishment probability of multiple pests
(SOM+Matlab)

某种有害生物入侵可能性评估
Assessment of invasion probability of a pest
(场景模型+@RISK)(Scenario model+@RISK)

某种有害生物潜在地理分布预测
Prediction of potential geographical distribution of a pest
(CLIMEX/MaxEnt/生物实验模型+GIS)
(CLIMEX/MaxEnt/Bio-model+GIS)

某种有害生物潜在损失预测
Prediction of potential loss of a pest
(场景模型+@RISK)
(Scenario model+@RISK)

有害生物入侵风险综合评估
Integrated assessment of a pest
(多指标综合评判模型)
(Multi-index integrated assessment model)

地图数据
Map data

交通运输数据
Transportation data

气象数据
Climate data

寄主数据
Host data

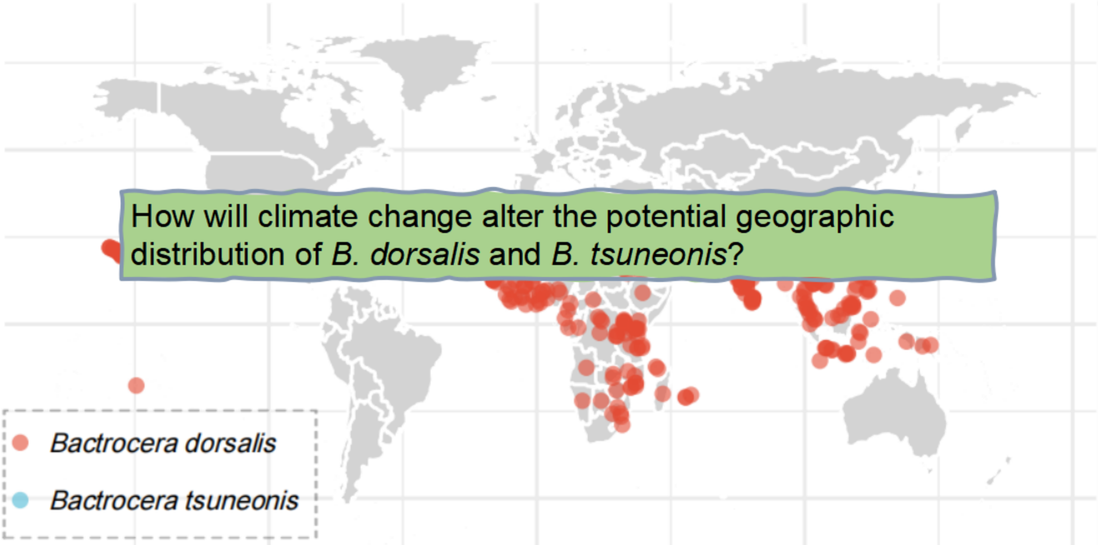
The intergrated technical system of quantitative risk assessment of PRA

Study Object

- Human-caused climate change, particularly gradual shifts in temperature and precipitation, may promote the spread, colonization, and adaptation of invasive species to new geographic areas.
- Fruit flies (*Tephritidae*) exemplify this problem, they cause significant crop losses, threaten food security, create horticultural trade barriers, and lead to substantial direct and indirect economic losses.

Bactrocera tsuneonis

Bactrocera dorsalis

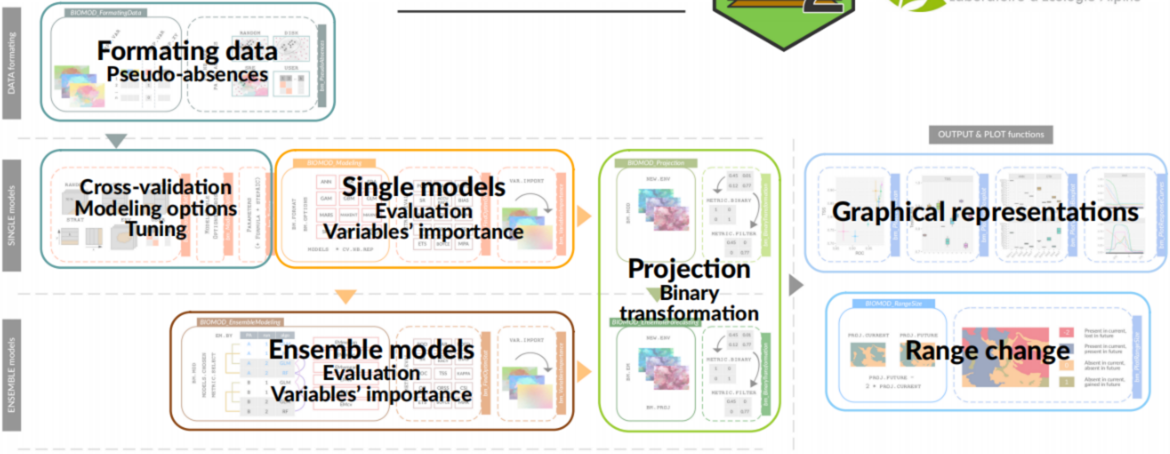


How will climate change alter the potential geographic distribution of *B. dorsalis* and *B. tsuneonis*?

SDM

Species distribution modeling,
calibration and evaluation,
ensemble modeling

Laboratoire d'Ecologie Alpine



Formating data
Pseudo-absences

Cross-validation
Modeling options
Tuning

Single models
Evaluation
Variables' importance

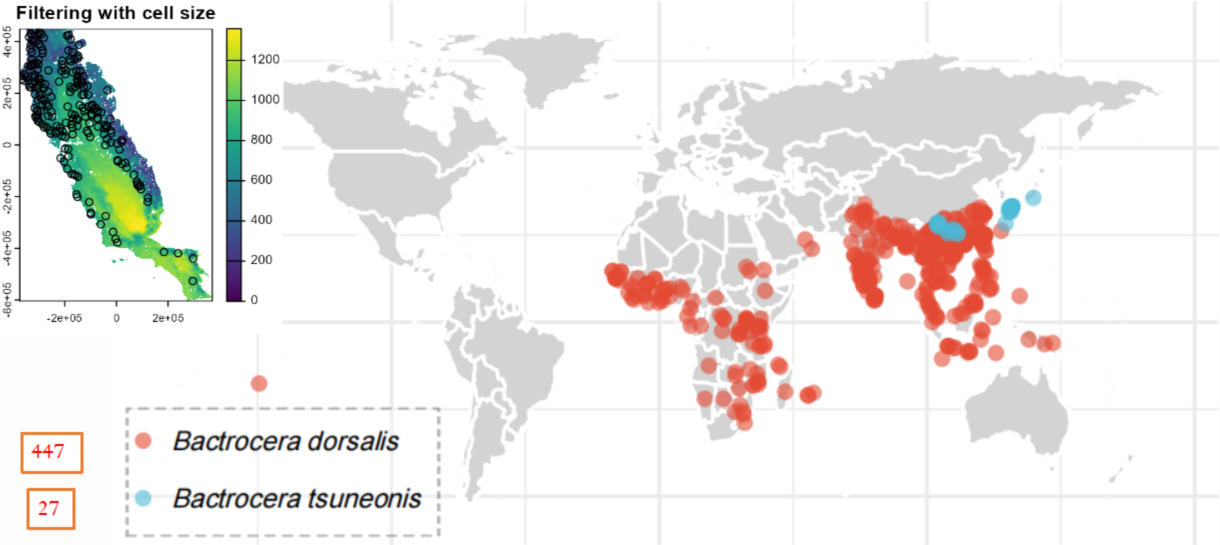
Ensemble models
Evaluation
Variables' importance

Projection
Binary
transformation

Graphical representations

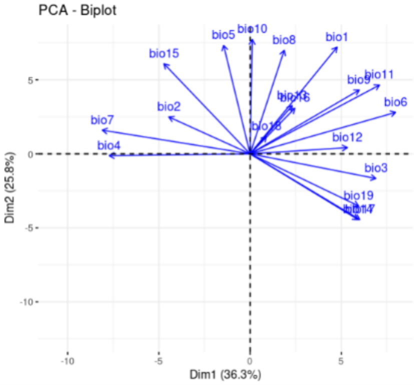
Range change

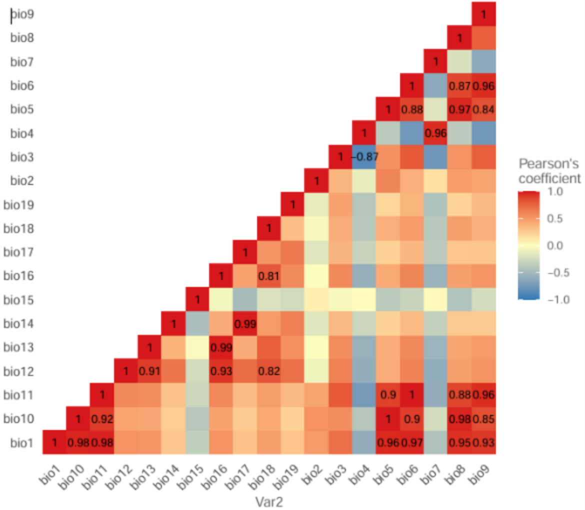
Data



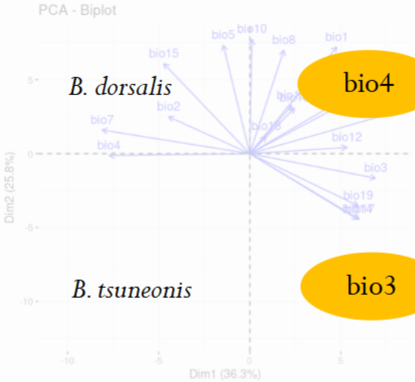
Filtering with cell size

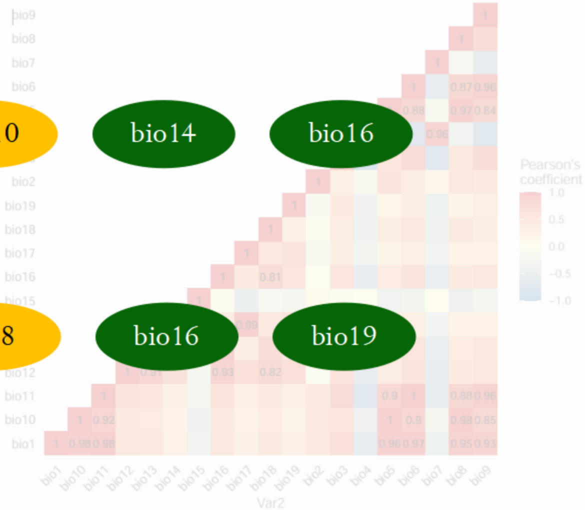
Data


PCA - Biplot
bio5
bio10
bio8
bio1
bio15
bio9
bio11
bio13
bio16
bio6
bio2
bio7
bio18
bio12
bio4
bio3
bio19
bio17
bio14
5
0
-5
-10
-10
-5
0
5
Dim1 (36.3%)
Dim2 (25.8%)


bio9
bio8
bio7
bio6
bio5
bio4
bio3
bio2
bio19
bio18
bio17
bio16
bio15
bio14
bio13
bio12
bio11
bio10
bio1
1
1
1
1
0.87
0.96
1
0.88
0.97
0.84
1
0.96
1
-0.87
1
1
1
1
1
0.81
1
1
0.99
1
0.99
1
0.91
0.93
0.82
1
0.9
1
0.88
0.96
1
0.92
1
0.9
0.98
0.85
1
0.98
0.98
0.96
0.97
0.95
0.93
bio1
bio10
bio11
bio12
bio13
bio14
bio15
bio16
bio17
bio18
bio19
bio2
bio3
bio4
bio5
bio6
bio7
bio8
bio9
Var2
Pearson's coefficient
1.0
0.5
0.0
-0.5
-1.0

Data

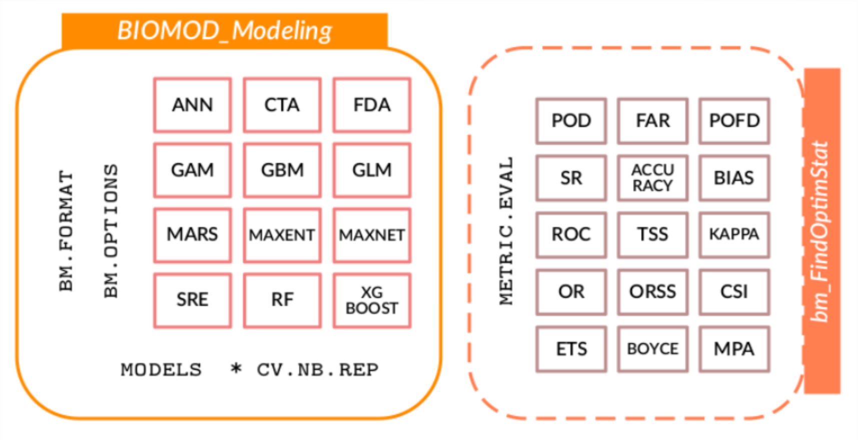




B. dorsalis bio4 bio10 bio14 bio16

B. tsuneonis bio3 bio8 bio16 bio19

Data

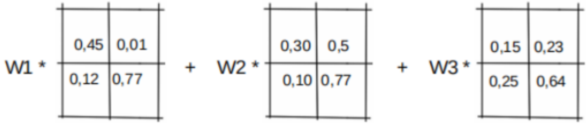


Pseudo absents: 3 * n(occ)

Run: 10 reps

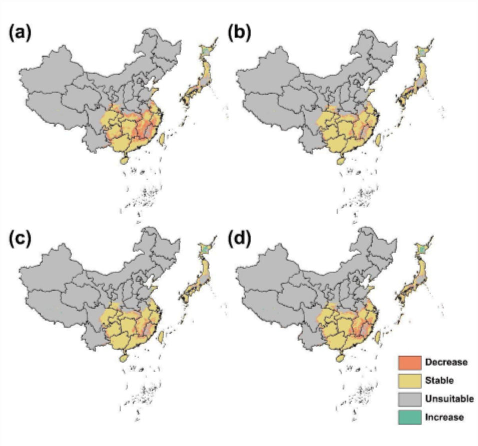
Models: GLM, GBM, MAXNET, MARS

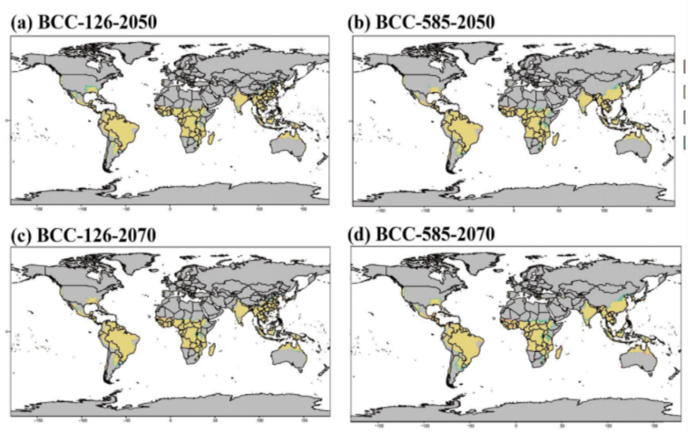
EM: Probability weighted mean



$$W1 * \begin{array}{|c|c|}\hline 0,45 & 0,01 \\ \hline 0,12 & 0,77 \\ \hline\end{array} + W2 * \begin{array}{|c|c|}\hline 0,30 & 0,5 \\ \hline 0,10 & 0,77 \\ \hline\end{array} + W3 * \begin{array}{|c|c|}\hline 0,15 & 0,23 \\ \hline 0,25 & 0,64 \\ \hline\end{array}$$

Results


(a)
(b)
(c)
(d)
🟧 Decrease
🟨 Stable
⬜ Unsuitable
🟩 Increase


(a) BCC-126-2050
(b) BCC-585-2050
(c) BCC-126-2070
(d) BCC-585-2070

Conclusion

- ✓ The suitable habitat shows high stability across all future climate scenarios, with very limited areas of increase or decrease.
- ✓ This stability may suggest that the BD has a wide tolerance to various climate conditions.
- ✓ The limited changes in suitable habitat may reflect the Japanese fruit fly's specificity to certain climate conditions.

Are there internal mechanisms that enable them to cope with varying climates?

Population genetics

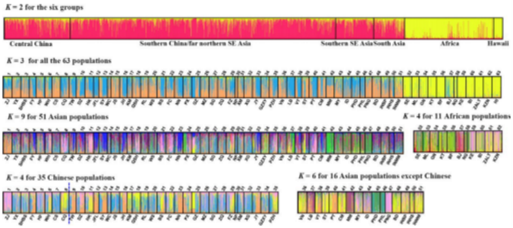
Received: 16 April 2018 | Revised: 8 July 2018 | Accepted: 7 August 2018
DOI: 10.1111/eva.12701

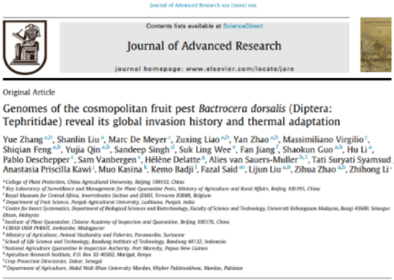
ORIGINAL ARTICLE

WILEY Evolutionary Applications

Population structure of a global agricultural invasive pest, *Bactrocera dorsalis* (Diptera: Tephritidae)

Yu-jia Qin[1]* | Matthew N. Krosch[2]* | Mark K. Schutze[2] | Yue Zhang[1] | Xiao-xue Wang[1] | Chandra S. Prabhakar[2,3] | Agus Susanto[4] | Alvin K. W. Hee[5] | Sunday Ekesi[6] | Kemo Badji[7] | Mahfuza Khan[8] | Jia-jiao Wu[9] | Qiao-ling Wang[1] | Ge Yan[1] | Li-huan Zhu[1] | Zi-hua Zhao[1] | Li-jun Liu[1] | Anthony R. Clarke[2] | Zhi-hong Li[1]





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journal homepage: www.elsevier.com/locate/jare

Original Article

Genomes of the cosmopolitan fruit pest *Bactrocera dorsalis* (Diptera: Tephritidae) reveal its global invasion history and thermal adaptation

Yue Zhang[a,b], Shanlin Liu[a], Marc De Meyer[c], Zuxing Liao[a,b], Yan Zhao[a,b], Massimiliano Virgilio[c], Shiqian Feng[a,b], Yujia Qin[a,b], Sandeep Singh[d], Suk Ling Wee[e], Fan Jiang[f], Shaokun Guo[a,b], Hu Li[a], Pablo Deschepper[c], Sam Vanbergen[c], Hélène Delatte[g], Alies van Sauers-Muller[h,1], Tati Suryati Syamsud Anastasia Priscilla Kawi[j], Muo Kasina[k], Kemo Badji[l], Fazal Said[m], Lijun Liu[a,b], Zihua Zhao[a,b], Zhihong Li

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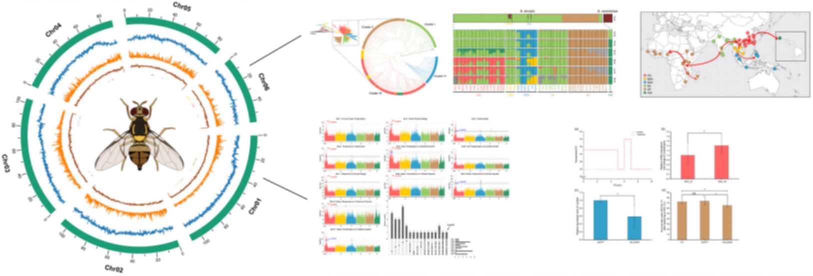
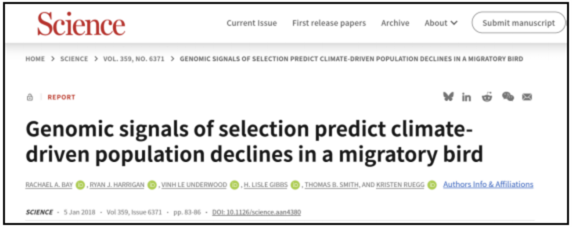
[l] Crop Protection Directorate, Dakar, Senegal
[m] Department of Agriculture, Abdul Wali Khan University Mardan, Khyber Pakhtunkhwa, Mardan, Pakistan



Genomic vulnerability

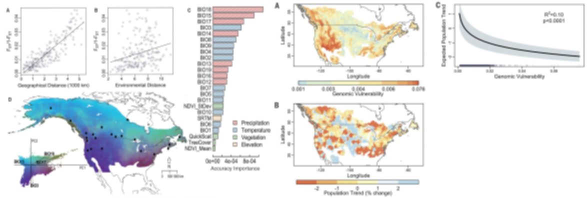
Genomic offset was used quantify the genetic variation that a population needs to undergo in order to maintain adaptability in response to future environmental changes.



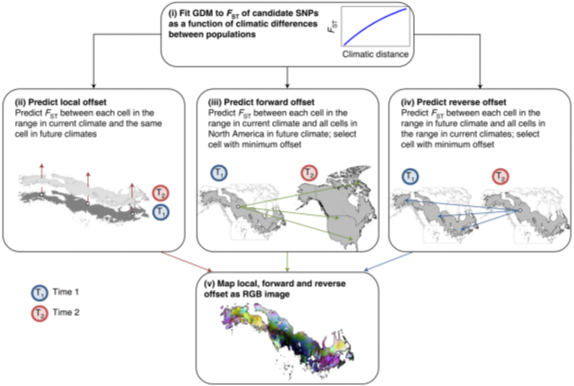
Genomic signals of selection predict climate-driven population declines in a migratory bird

RACHAEL A. BAY, RYAN J. HARRIGAN, VINH LE UNDERWOOD, H. LISLE GIBBS, THOMAS B. SMITH, AND KRISTEN RUEGG Authors Info & Affiliations

SCIENCE · 5 Jan 2018 · Vol 359, Issue 6371 · pp. 83-86 · DOI: 10.1126/science.aan4380



(Bay et al., 2018)



(i) Fit GDM to F_{ST} of candidate SNPs as a function of climatic differences between populations

(ii) Predict local offset
Predict F_{ST} between each cell in the range in current climate and the same cell in future climates

(iii) Predict forward offset
Predict F_{ST} between each cell in the range in current climate and all cells in North America in future climate; select cell with minimum offset

(iv) Predict reverse offset
Predict F_{ST} between each cell in the range in future climate and all cells in the range in current climates; select cell with minimum offset

(v) Map local, forward and reverse offset as RGB image

(Gougherty et al., 2021)

Genetic-Ecological Integration

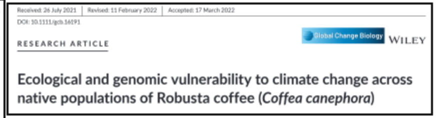
Received: 13 July 2023 | Revised: 15 March 2024 | Accepted: 28 March 2024
DOI: 10.1111/ddi.13847

REVIEW ARTICLE

Diversity and Distributions WILEY

The integration of whole-genome resequencing and ecological niche modelling to conserve profiles of local adaptation

Jong Yoon Jeon[1] | Yucheol Shin[2] | Andrew J. Mularo[3] | Xiao Feng[4] | J. Andrew DeWoody[1,3]

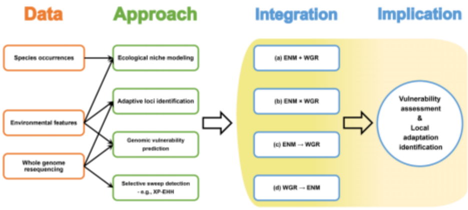


Received: 26 July 2021 | Revised: 11 February 2022 | Accepted: 17 March 2022
DOI: 10.1111/gcb.16191

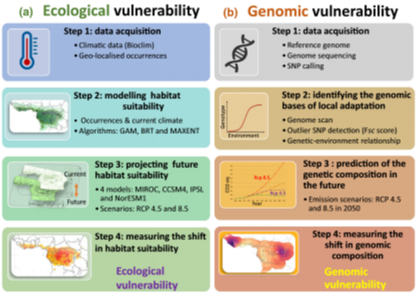
RESEARCH ARTICLE

Global Change Biology WILEY

Ecological and genomic vulnerability to climate change across native populations of Robusta coffee (*Coffea canephora*)



(Jeon et al., 2024)



(a) Ecological vulnerability

Step 1: data acquisition
- Climatic data (Bioclim)
- Geo-localised occurrences

Step 2: modelling habitat suitability
- Occurrences & current climate
- Algorithms: GAM, BRT and MAXENT

Step 3: projecting future habitat suitability
- 4 models: MIROC, CCSM4, IPSL and NorESM1
- Scenarios: RCP 4.5 and 8.5

Step 4: measuring the shift in habitat suitability

Ecological vulnerability

(b) Genomic vulnerability

Step 1: data acquisition
- Reference genome
- Genome sequencing
- SNP calling

Step 2: identifying the genomic bases of local adaptation
- Genome scan
- Outlier SNP detection (Fsc score)
- Genetic-environment relationship

Step 3 : prediction of the genetic composition in the future
- Emission scenarios: RCP 4.5 and 8.5 in 2050

Step 4: measuring the shift in genomic composition

Genomic vulnerability

(Tournebize et al., 2024)

Data

whole genome sequencing-SNP

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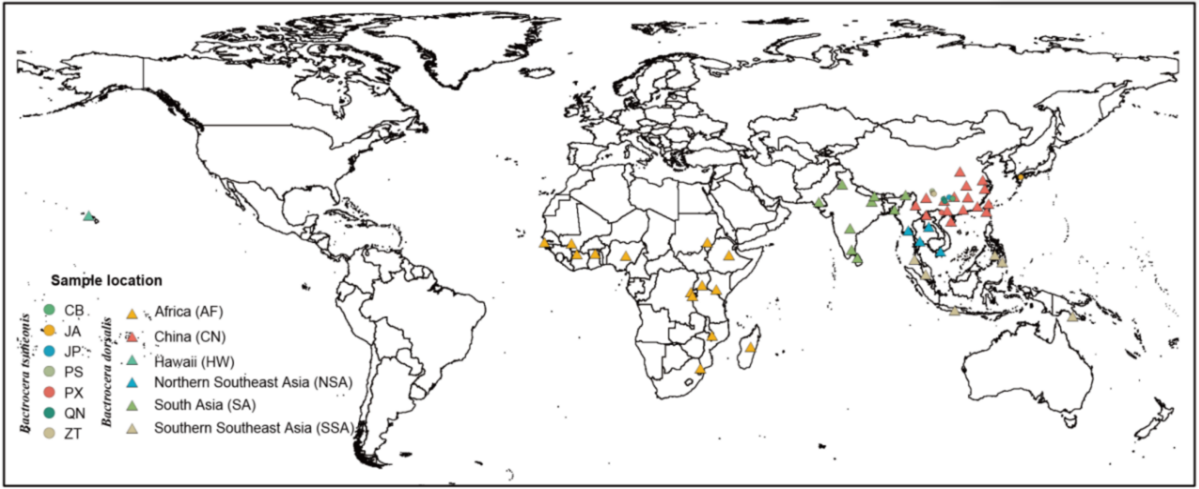

Results

Identification of genomic variants associated with local climate adaptation

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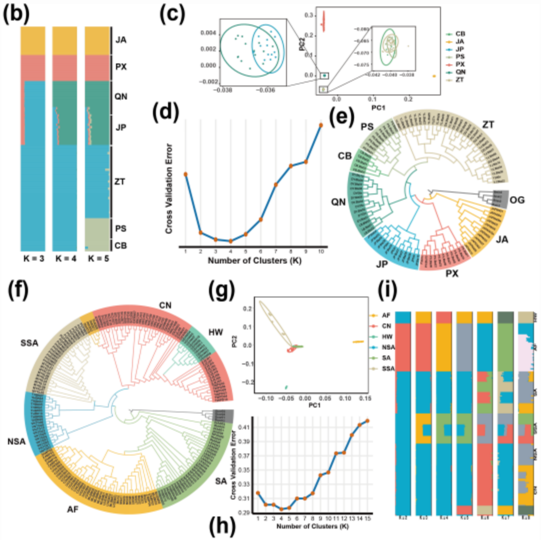
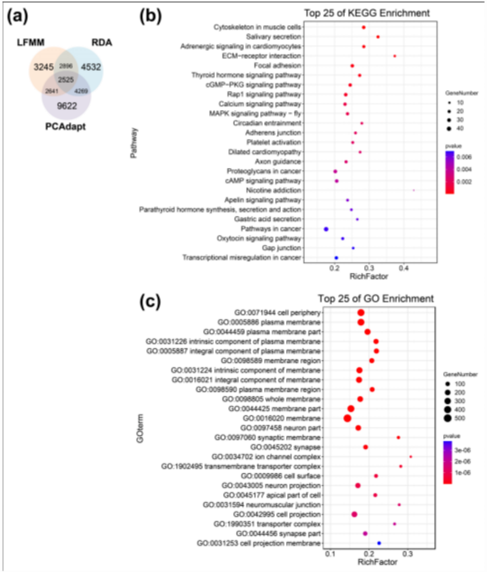
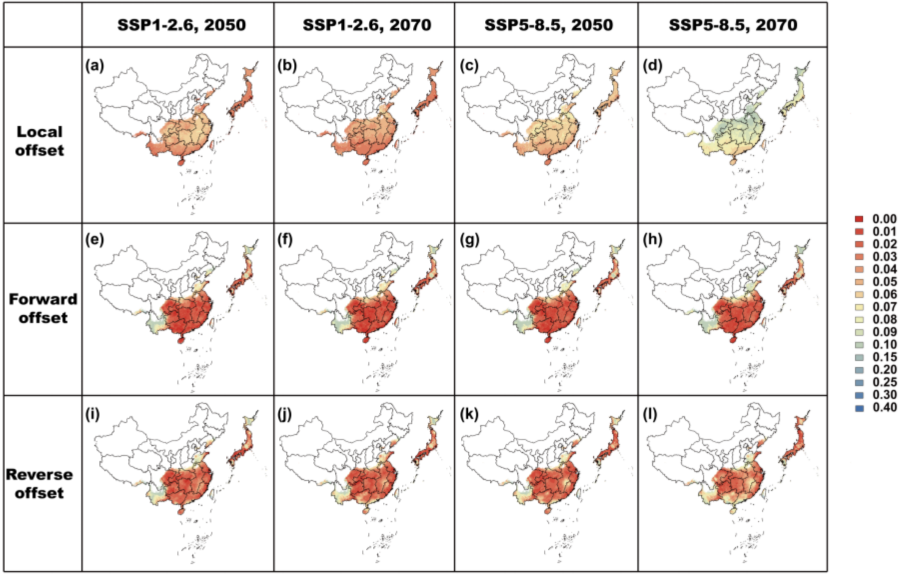
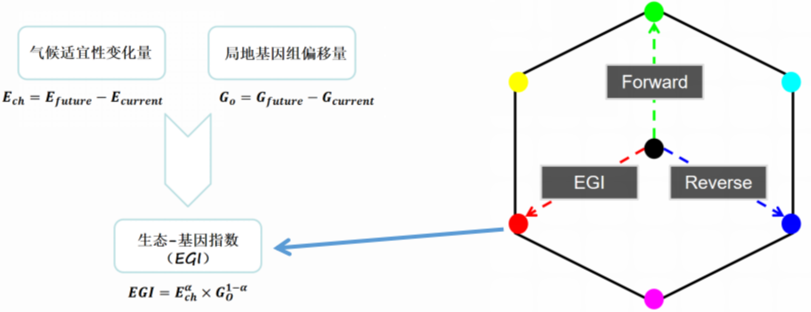




Genomic vulnerability



Ecological-Genetic Index



气候适宜性变化量

$E_{ch} = E_{future} - E_{current}$

局地基因组偏移量

$G_o = G_{future} - G_{current}$

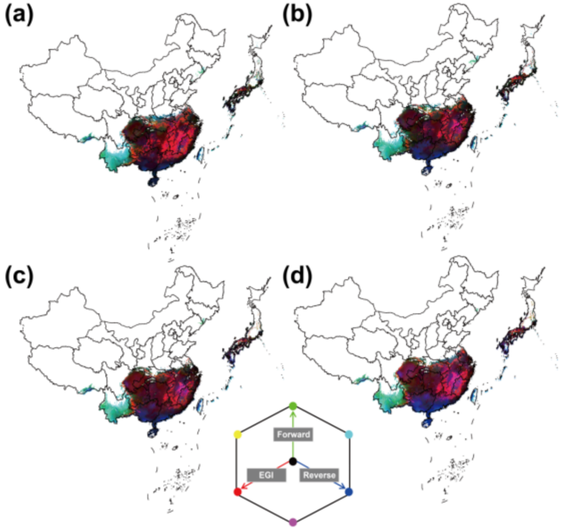
生态-基因指数（EGI）

$EGI = E_{ch}^{\alpha} \times G_O^{1-\alpha}$

- Red: both ecological unsuitability for the species and genomic divergence are relatively small, making it suitable for the stable existence of the population;
- Green: the current population can adapt to the climate through migration;
- Blue: in the future environment, there will be populations that have already expanded and adapted in the current area.

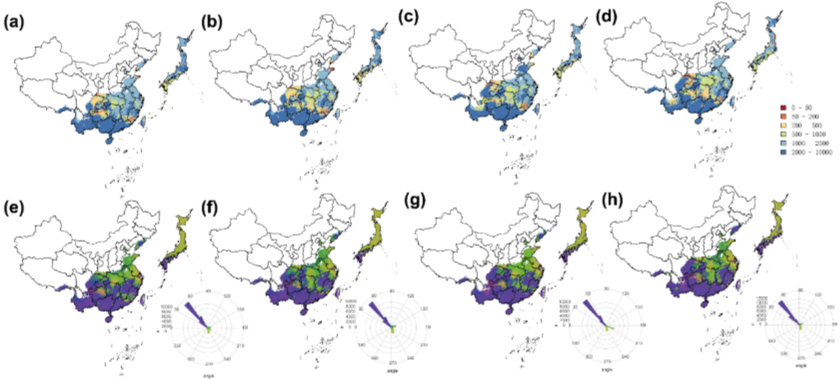
- Additionally, the brighter the color, the higher the values in all three channels, meaning a lack of both ecological and genetic suitability, and a high degree of vulnerability; black indicates that all performances in this area are strong, with low vulnerability.

Adaptive potential from RGB map



RGB map of EGI (red), forward (green) and reverse (blue) offsets under four greenhouse gas emission scenarios, (a) SSP1-2.6 in 2050, (b) SSP1-2.6 in 2070, (c) SSP5-8.5 in 2050, (d) SSP 5-8.5 in 2070. Darker cells (close to black) have relatively low values along each of the three axes.

Adaptive migration distance and direction



Distance and initial bearing to locations that minimize forward offset. Distance (a-d) and initial bearing (e-f) were calculated from the focal cell to the location in the future climate that minimizes the predicted allele frequence from the GF.

Results

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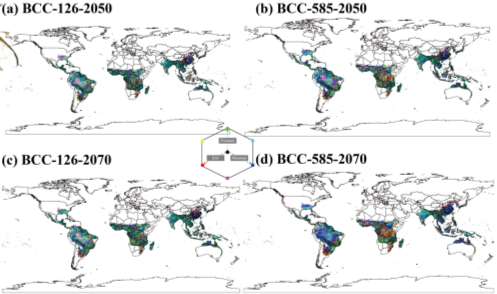
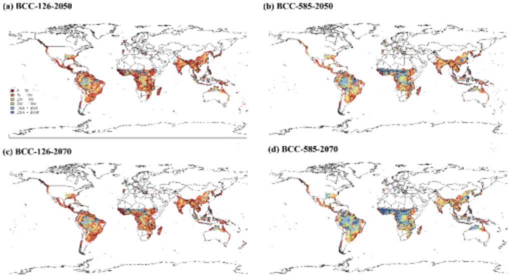


(a) BCC-126-2050

(b) BCC-585-2050

(c) BCC-126-2070

(d) BCC-585-2070

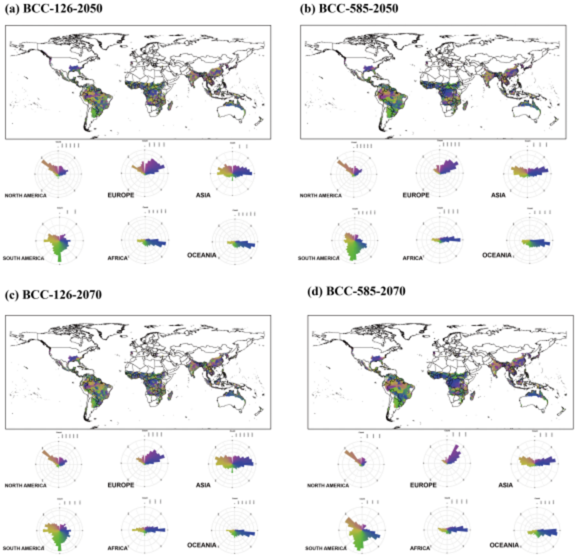


(a) BCC-126-2050

(b) BCC-585-2050

(c) BCC-126-2070

(d) BCC-585-2070



(a) BCC-126-2050

(b) BCC-585-2050

(c) BCC-126-2070

(d) BCC-585-2070

Conclusion

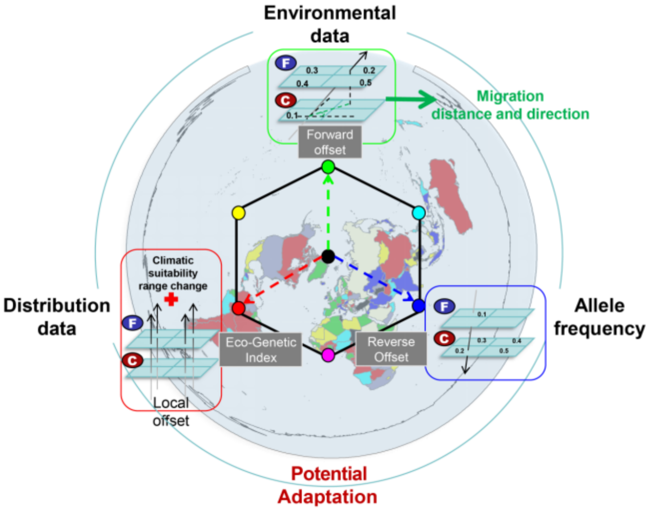
- ✓ The contrasting adaptive trajectories of *B. tsuneonis* and *B. dorsalis* exemplify how genetic connectivity and environmental tolerance jointly shape invasion outcomes under global change.

In Yunnan Province, most areas are predicted by ecological niche models to be unsuitable under future climate scenarios. However, the local offset results indicate that many grid cells in this region exhibit low offset values, suggesting that *B. tsuneonis* has a strong potential to adapt locally.

- ✓ By incorporating local genomic offset, migration-associated adaptation costs, and shifts in climatic suitability, this framework improves the predictive resolution for identifying range shifts and high-risk invasion zones under future climate change.

Framework

Framework for Quantifying Adaptive Potential of Invasive Species



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Plant Quarantine and Invasion Biology Laboratory

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Thank you for your attention!