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POTENTIAL DISTRIBUTION OF THE MONOPHAGOUS LONGHORN BEETLE *ROSALIA COELESTIS* SEMENOV, 1911 (COLEOPTERA: CERAMBYCIDAE: CERAMBYCINAE) IN NORTHEAST ASIA UNDER CLIMATE CHANGE

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Summary. Using MaxEnt algorithms, this study provides the first assessment of the potential distribution range of *Rosalia coelestis* Semenov, 1911, a longhorn beetle with a narrow trophic specialization in Northeast Asia. According to the modeling results, the current area of the most suitable habitats for the species is estimated at 3,554,100 km². It was demonstrated that, according to three climate models MRI-ESM2-0, MPI-ESM1-2-HR, and BCC-CSM2-MR by 2080–2100, under different greenhouse gas emission scenarios (SSPs), a reduction in the area of habitats suitable for *R. coelestis* will occur in Northeast Asia. The core of the monophagous species' range will be concentrated in the valley broad-leaved forests of southern Primorye and in certain regions of Northern and Eastern China, which may be associated with a sufficient availability of the beetle larvae's primary host plant, *Acer tegmentosum*.

Key words: Coleoptera, monophagous longhorn beetle, *Rosalia coelestis*, rare species, northeast Asia, distribution, climate change, spatial modeling, MaxEnt, potential area, climatic parameters.

А. В. Куприн, Н. Е. Шевченко, М.-И. Лин. Потенциальное распространение жука-монофага *Rosalia coelestis* Semenov, 1911 (Coleoptera: Cerambycidae: Cerambycinae) в Северо-Восточной Азии в условиях изменения климата // Дальневосточный энтомолог. 2026. N 548. С. 1-23.

Резюме. С использованием алгоритмов MaxEnt впервые проведена оценка потенциального ареала жука-усача *Rosalia coelestis* Semenov, 1911 с узкой трофической специализацией в Северо-Восточной Азии. По результатам моделирования установлено, что в настоящее время площадь наиболее пригодных для вида мест обитания составляет 3554100 кв.км. Показано, что трем климатическим моделям MRI-ESM2-0, MPI-ESM1-2-HR и BCC-CSM2-MR к 2080-2100 годам при разных сценариях увеличения выброса парниковых газов (SSP) в Северо-Восточной Азии будет происходить уменьшение площади пригодных для *R. coelestis* мест обитания. Основное ядро ареала монофага будет находиться в долинных широколиственных лесах юга Приморского края и отдельных районах Северного и Восточного Китая, что может быть связано с достаточным запасом кормового растения личинок жука – *Acer tegmentosum*.

INTRODUCTION

Longhorn beetles (Coleoptera: Cerambycidae) represent one of the key groups of xylophilous insects in forest ecosystems, participating in wood decomposition, the transformation of dead organic matter, and the maintenance of biodiversity within saproxylic communities (Kuprin, Baklanova, 2025). The distribution of many Cerambycidae species is determined not only by macroclimatic conditions but also by the availability of suitable host trees, the condition of woody substrates, and the preservation of old-growth forests (Kuprin, Yi, 2019). For longhorn beetles in general the characteristics of the larval substrate and host plant are closely associated with reproductive strategy, adult behavior, and the spatial structure of populations; consequently, trophic specialization may act as one of the principal factors limiting the geographical range of a species (Hanks, 1999).

In this regard, the genus *Rosalia* Audinet-Serville, 1833 is of particular interest, as it includes endemic saproxylic longhorn beetles predominantly associated with deciduous tree species. The best-studied representative of the genus is *Rosalia alpina* (Linnaeus, 1758), which is regarded as an indicator species of old-growth broadleaved forests in Europe. This species has been shown to be closely associated with beech stands, the presence of dead or dying wood, and well-warmed, sun-exposed habitats (Campanaro *et al.*, 2017). At the same time, recent studies indicate that the ecological plasticity of *R. alpina* within its range may be greater than previously assumed: in lowland regions of Central Europe the species is capable of utilizing other deciduous

tree species, and the configuration of its distribution range is determined by a combination of climatic, landscape, and phytocoenotic factors (Čížek *et al.*, 2009; Drag *et al.*, 2018; Bosso *et al.*, 2013).

Other representatives of the genus *Rosalia* also demonstrate considerable variation in the degree of trophic specialization. The Japanese endemic *Rosalia batesi* Harold, 1877 develops in the dead wood of various deciduous tree species and occurs from Hokkaido to Kyushu, indicating relatively broad ecological amplitude within the genus (Kiryama *et al.*, 2018; Fukaya *et al.*, 2023). The North American *Rosalia funebris* Motschulsky, 1845 is likewise associated with a wide range of deciduous hosts; the larvae of this species develop in weakened or dying branches and trunks of broadleaved trees, including alder, ash, laurel, oak, and willow (Sylvester *et al.*, 2024). Thus, the genus *Rosalia* as a whole encompasses a spectrum of strategies ranging from relatively broad utilization of deciduous hosts to more pronounced trophic specialization, making it a convenient model for analyzing the relationship between host specificity and the spatial organization of species ranges.

Against this background, *Rosalia coelestis* Semenov, 1911 is of particular interest as an East Asian species characterized by a narrower ecological association. The species is distributed in the southern part of the Russian Far East, northeastern China, and the Korean Peninsula (Kuprin, 2016; Kuprin & Danilevsky, 2025). According to available literature data, *R. coelestis* is associated with the maple *Acer tegmentosum*; therefore, the larvae of this species should be regarded as monophagous, for which host specialization may significantly restrict the set of suitable habitats and increase dependence on the spatial coincidence of climatic conditions with the distribution of the host plant *A. tegmentosum*. In addition, the relevance of studying *R. coelestis* is determined both by its rarity and by the vulnerability of its habitats. According to the Red Data Book of the Republic of Korea, the species is known from only a few localities in Gangwon Province and is assessed as Vulnerable; among the probable threats are excessive harvesting of the host plant for medicinal purposes and climate change (Red Data Book, 2024). For saproxylic longhorn beetles in general, forest fragmentation, sanitary logging, removal of standing dead trees, and the reduction of old-growth forests lead to the loss of suitable microhabitats even in areas where overall climatic conditions remain favorable (Campanaro *et al.*, 2017; Kuprin *et al.*, 2024).

In recent years, ecological niche modeling and the assessment of potential distribution ranges have become among the most widely used tools in biogeography and the conservation of rare insects. For species represented primarily by presence-only records, the MaxEnt approach is particularly widely applied, allowing the estimation of habitat suitability based on a set of environmental predictors and enabling the identification of both known and potentially underexplored areas within the species range (Li *et al.*, 2020; Tan *et al.*, 2025; Yong *et al.*, 2025; Zhang *et al.*, 2025). For *R. alpina*, MaxEnt models have already been used to evaluate geographic distribution and to identify gaps in the network of protected areas in Italy (Bosso *et al.*, 2013). In Northeast Asia, bioclimatic range modeling has been conducted for polyphagous species associated with both deciduous and coniferous trees, allowing

characterization of their present potential distribution and possible changes under climatic influences. These studies have demonstrated that distribution models are informative both for invasive species and for rare longhorn beetles with fragmented ranges and a limited number of reliable records (Kuprin *et al.*, 2024).

The aim of the present study is to evaluate the potential distribution of the monophagous beetle *R. coelestis* in Northeast Asia under conditions of global climate change using MaxEnt algorithms.

MATERIAL AND METHODS

Input data for modeling

A matrix data of more than 100 georeferenced occurrence records of *R. coelestis* was compiled for distribution modelling and used to prepare the distribution map (Fig. 1). The dataset was based on the authors' own material, specimen records deposited in major scientific institutions, including the Federal Scientific Center of the East Asia Terrestrial Biodiversity, Far Eastern Branch of the Russian Academy of Sciences (Vladivostok), the Zoological Institute of the Russian Academy of Sciences (St. Petersburg), the Zoological Museum of M.V. Lomonosov Moscow State University (Moscow, Russia), and the Institute of Zoology, Chinese Academy of Sciences (Beijing, China), as well as published data from available literature sources (Pu, 1980; Zhou *et al.*, 1988; Qi, 1999; Wang, 2003, 2014; Hu *et al.*, 2011; Zhang, 2013; Lin, 2017; Yu, 2020; Zong *et al.*, 2021; Di & Ren, 2021; Tian, 2023). Additional records from Northeast Asia were retrieved from GBIF.org and parameterized for subsequent analysis (GBIF Occurrence Download, accessed 12 March

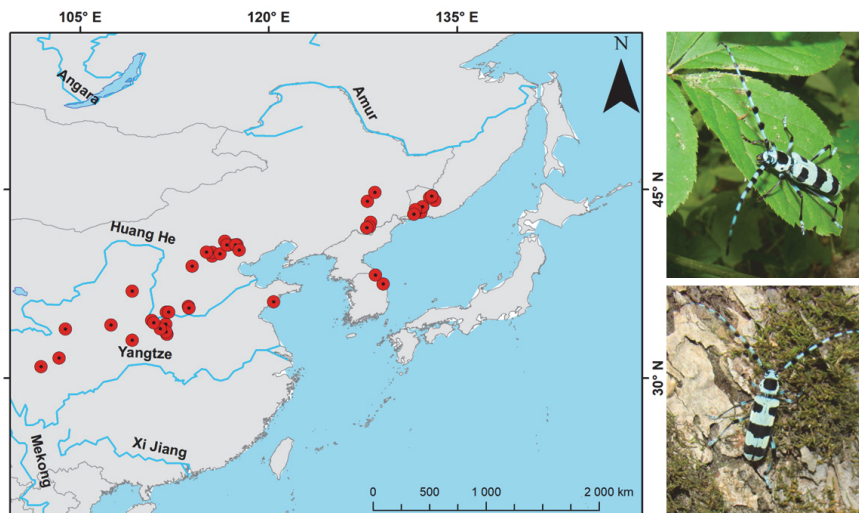


Fig. 1. Known geographical distribution of *R. coelestis* in northeast Asia.

2026, <https://doi.org/10.15468/dl.4h49q4>). Records lacking coordinates were georeferenced based on locality data using the portal <https://www.bchrt.com> (accessed 12 March 2026).

Climate models and predictors

To predict the potential distribution range of *R. coelestis*, open-access data from three global climate models (GCMs) were used: MRI-ESM2-0 (Japan Meteorological Research Institute Earth System Model version 2.0), MPI-ESM1-2-HR (Max Planck Institute Earth System Model), and BCC-CSM2-MR (Beijing Climate Center), based on CMIP6 projections for the 2080-2100 time interval (Mauritsen *et al.*, 2020; IPCC, 2021; World Data Center for Climate, 2026). These models constitute a reliable tool for forecasting temperature and precipitation variables under four shared socioeconomic pathway scenarios: SSP126, SSP245, SSP370, and SSP585 (O'Neill *et al.*, 2016; Kriegler *et al.*, 2017; Vaghefi & Abbaspour, 2019). This set of scenarios covers a wide range of possible future climate trajectories, from low-emission to extremely high-emission pathways (Gutjahr *et al.*, 2019; Wu *et al.*, 2019; Yukimoto *et al.*, 2019; Mauritsen *et al.*, 2019). In species distribution modeling studies, this makes it possible to assess the robustness of projections, compare the degree of ecological niche shift under different climatic conditions, and identify areas in which habitat suitability is maintained regardless of scenario (Eyring *et al.*, 2016; Gutjahr *et al.*, 2019).

To assess the current distribution of *R. coelestis* and to predict its potential range, 19 bioclimatic variables (bioclim) and elevation were used: bio1, annual mean temperature (°C); bio2, mean diurnal range (mean of monthly [maximum temperature – minimum temperature]); bio3, isothermality ($(\text{bio2}/\text{bio7}) \times 100$); bio4, temperature seasonality (standard deviation $\times 100$); bio5, maximum temperature of the warmest month (°C); bio6, minimum temperature of the coldest month (°C); bio7, annual temperature range (bio5 – bio6, °C); bio8, mean temperature of the wettest month (°C); bio9, mean temperature of the driest quarter (°C); bio10, mean temperature of the warmest quarter (°C); bio11, mean temperature of the coldest quarter (°C); bio12, annual precipitation (mm); bio13, precipitation of the wettest month (mm); bio14, precipitation of the driest month (mm); bio15, precipitation seasonality (coefficient of variation, CV); bio16, precipitation of the wettest quarter (mm); bio17, precipitation of the driest quarter (mm); bio18, precipitation of the warmest quarter (mm); and bio19, precipitation of the coldest quarter (mm).

To eliminate multicollinearity among predictors, a correlation analysis was performed using Pearson's correlation coefficient. Pairwise correlation coefficients were calculated for all initial bioclimatic variables, after which, from each pair of highly correlated variables ($r \geq 0.7$), only one predictor was retained for further modeling, namely the one with greater ecological interpretability for the study species (Warren *et al.*, 2010).

Modeling of the potential distribution range

Geospatial modeling of the current and projected potential distribution of *R. coelestis* was carried out using the software MaxEnt v. 3.4.1 (www.cs.princeton.edu/~schapire/maxent/), in which spatial distribution extrapolation is implemented using the maximum entropy method (Elith *et al.*, 2011). During model construction, the default program settings were applied; specifically, all feature classes were enabled, the maximum number of iterations was set to 500, and the number of background points was set to 10,000 (Phillips & Dudík, 2008).

For model validation, 25% of the occurrence records were used as test data. The replicated run type was set to cross-validation, and the threshold rule applied was the 10-percentile training presence.

Model performance was evaluated using the area under the receiver operating characteristic curve (ROC), which reflects both the sensitivity of the modeled object to the predictors included in the model and its specificity. An AUC value above 0.75 and approaching 1.0 indicates a high degree of model reliability (Elith, 2000).

To assess the relative contribution of bioclimatic predictors to model construction, the jackknife analysis method was applied. Visualization of the MaxEnt maps was performed using ArcGIS (Scheldeman & van Zonneveld, 2010). On the resulting maps, only the most probable areas of distribution of the studied species were retained, defined as regions with a habitat suitability threshold greater than 0.5.

RESULTS AND DISCUSSION

Key bioclimatic predictors and their ecological significance

Correlation analysis of the initial set of bioclimatic variables revealed both weak and strong relationships (in absolute magnitude) among individual predictors (Fig. 2). At the threshold value of $|r| \geq 0.7$, variables that duplicated climatic information and could potentially lead to model overfitting were excluded from further analysis. After variable selection, the final set included bio3, bio5, bio12, and bio15, which characterize key aspects of the temperature regime and precipitation patterns within the species' range (Table 1).

The results indicate that the selected predictors adequately reflect the principal climatic constraints on the species' distribution while simultaneously avoiding pronounced multicollinearity within the model. This made it possible to use these variables for further analysis of predictor contributions, the construction of habitat suitability maps, and scenario-based projections of changes in the potential distribution of *R. coelestis*.

The ecological significance of the selected bioclimatic predictors indicates that the potential distribution of *R. coelestis* is determined by a combination of thermal stability of habitats and moisture conditions. The isothermality index (bio3) reflects

the ratio of diurnal to seasonal temperature variability and likely characterizes the degree of thermal stability in forest biotopes. The maximum temperature of the warmest month (bio5) defines the upper summer thermal limits influencing both insect development and the condition of the woody substrate. Annual precipitation (bio12) characterizes the overall moisture availability of the territory, which is important for the persistence of the host plant and the preservation of suitable wood, whereas precipitation seasonality (bio15) reflects the uneven distribution of moisture throughout the year and, consequently, the stability of the moisture regime in forest habitats. Thus, the distribution of the species is determined by a complex of thermal and hydrological conditions that influence not only the beetle directly but also the structure of its trophic and habitat associations.

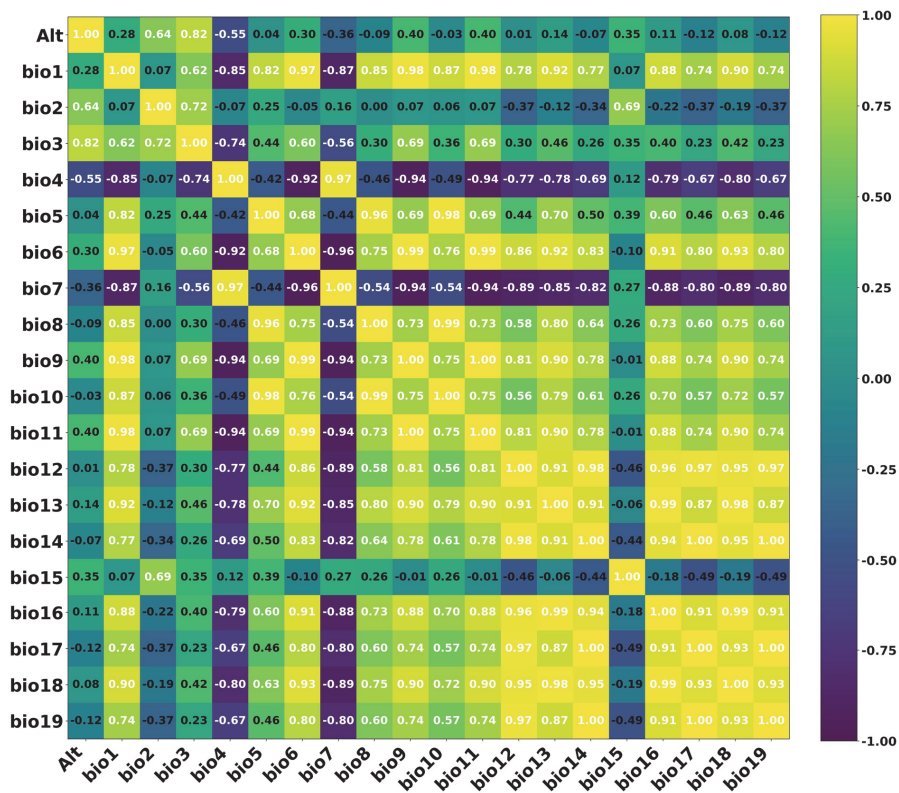


Fig 2. Heatmap of pairwise correlations of bioclimatic predictors.

The identified bioclimatic predictors used in models of potential distribution may affect phytophagous insects with different trophic strategies in different ways. This is because polyphagous, oligophagous, and monophagous species differ in their degree of dependence on host plants, the breadth of their ecological niches, and

their ability to compensate for unfavorable conditions by switching to alternative host plants. For longhorn beetles and other phytophagous insects, it has been demonstrated that host plant characteristics are closely associated with reproductive strategy, substrate selection for larval development, and the spatial organization of populations (Hanks, 1999). On a broader scale, the breadth of the host spectrum determines the resource base of a phytophage and significantly influences its biogeographic and ecological characteristics (Forister *et al.*, 2015).

Table 1. Contribution and suitable range of the leading variable bioclimatic predictors

Estimated parameter		Bioclimatic predictor			
		bio 3	bio 5	bio 12	bio 15
Contribution, %		25,8	21,5	22,3	30,4
Suitable range	min	19	20,6	468	59
	max	41	28,9	1285	127

Polyphagous species typically exploit a wide range of host plants; therefore, the influence of climate on their distribution is more often expressed directly through developmental temperature thresholds, the length of the activity season, survival, developmental rates, and overall population productivity (Bale *et al.*, 2002; Kuprin *et al.*, 2024). Owing to their broad host spectrum, they are more capable of persisting in climatically suitable regions even when vegetation composition changes, provided that alternative hosts remain present in the community.

Oligophagous species occupy an intermediate position. They are associated with a limited set of usually closely related plants, and therefore bioclimatic predictors affect them in two ways: directly through insect physiology and indirectly through the distribution, condition, and phenology of their host plant group. Consequently, for oligophagous species the climatic suitability of a territory is often narrower than for polyphagous species and more strongly dependent on the coincidence of climatic conditions with the distribution of suitable hosts (Hanks, 1999; Kuprin & Baklanova, 2025).

Monophagous species are most strongly dependent on a single plant species or a very narrow host resource. For such insects, the effect of climatic variables is usually strongly mediated through the host plant and habitat structure. Even if climatic conditions are formally suitable for the insect itself, the absence of the host plant or changes in its condition may render the territory entirely unsuitable. As a result, the climatic niche of monophagous species is often the narrowest and the most sensitive to mismatches between the responses of the insect and its host plant to climate change (Forister *et al.*, 2015; Kuprin & Baklanova, 2025).

In general, the influence of bioclimatic predictors on different trophic groups can be viewed as a gradient of increasing dependence on the host plant. In polyphagous beetles, bioclimatic predictors more often reflect the direct influence of climate on physiology, phenology, and geographic distribution, whereas biotic limitations are less pronounced due to the wide range of host plants. In oligophagous

species, predictors simultaneously reflect both the climatic limits of the insect itself and the suitability of a limited group of host plants; therefore, distribution models for such species usually require careful interpretation, especially when host plant distributions are not explicitly included in the model. In monophagous longhorn beetles, bioclimatic variables most often act through a dual constraint the climatic tolerance of the insect and the stability of its single host-making such species potentially the most sensitive to mismatches between the climatic dynamics of the plant and the phytophage.

Thus, the same predictors may have a similar physical meaning but a different ecological significance in species with different trophic specializations. As trophic specialization shifts from polyphagy to oligophagy and monophagy, the importance of biotic environmental factors increases, and climatic suitability becomes progressively more difficult to interpret without considering host plant distribution and habitat structure. For specialized species, this aspect is particularly important when modeling species ranges under both current and future climatic conditions (Hanks, 1999; Parmesan, 2006; Kuprin *et al.*, 2024).

Current potential distribution of *Rosalia coelestis*

A cartographic model of the distribution of *R. coelestis* in Northeast Asia was constructed, demonstrating high model performance for the potential distribution (AUC = 0.96–0.99), which reliably characterizes the distributional features of the studied species (Fig. 3; Table 2).

Table 2. Model parameter optimization results

Model	Scenario	Train AUC	Test AUC	Random prediction
Current	-	0,993	0,987	0,5
MRI-ESM2-0	SSP126	0,968	0,933	0,5
	SSP245	0,955	0,901	0,5
	SSP370	0,963	0,886	0,5
	SSP585	0,955	0,971	0,5
MPI-ESM1-2-HR	SSP126	0,967	0,934	0,5
	SSP245	0,962	0,964	0,5
	SSP370	0,963	0,964	0,5
	SSP585	0,967	0,970	0,5
BCC-CSM2-MR	SSP126	0,954	0,921	0,5
	SSP245	0,964	0,961	0,5
	SSP370	0,975	0,947	0,5
	SSP585	0,955	0,952	0,5

The current bioclimatic potential range of *R. coelestis* exhibits a distinctly East Asian configuration and encompasses the southern Russian Far East, northeastern China, and the Korean Peninsula, as well as several isolated areas in Central and Southwestern China and a single fragment in the southern part of Eastern Siberia.

The principal core of high bioclimatic suitability is associated with the Amur River basin and adjacent regions of Manchuria, whereas the remaining suitable areas are more mosaic and fragmented in character (Fig. 3).

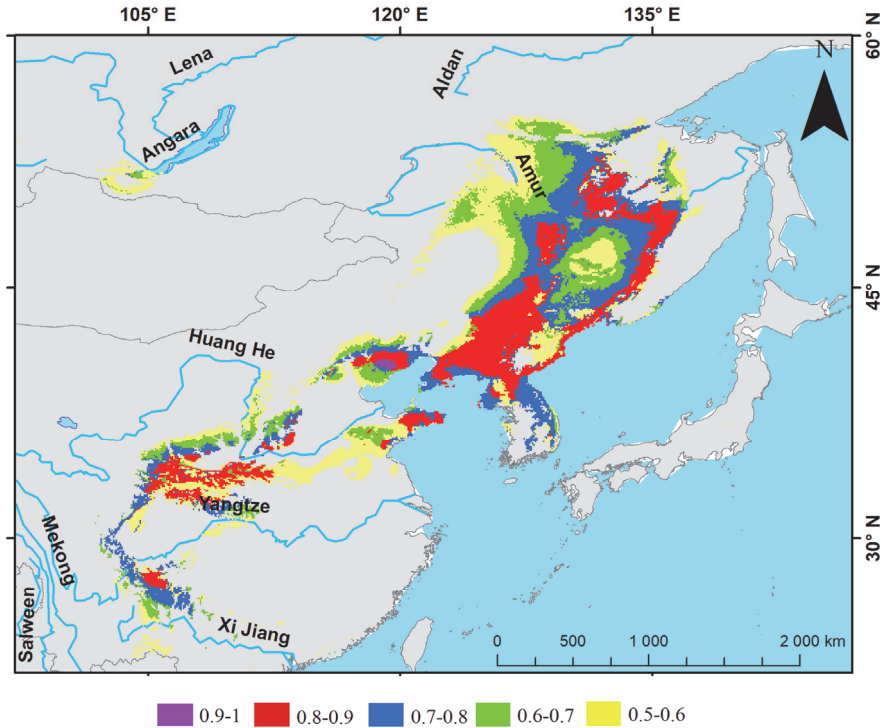


Fig. 3. Potential bioclimatic range of *R. coelestis* in northeast Asia under the current climate conditions.

The most extensive zone of high suitability thresholds (0.8–0.9 and locally 0.9–1.0) extends from northeastern China through southern Amur region to Primorye and further partially covers the Korean Peninsula. Within Russia, this zone is primarily associated with the southern part of Khabarovsk Krai, Amur Oblast, and Primorye. In China, the main suitable territories are located in Manchuria, chiefly in Heilongjiang and Jilin provinces, as well as in adjacent regions of Liaoning and the eastern part of Inner Mongolia. On the Korean Peninsula, areas of moderate and high suitability are more fragmented but generally cover its northern and central parts, with several isolated areas in the south.

The spatial structure of the potential range is clearly associated with the major river systems of East Asia. This relationship is particularly evident in the Amur basin, where areas of high suitability form a broad belt along valley and foothill territories.

In the southern part of the map, bioclimatically suitable areas are also observed in regions associated with the Yangtze and Yellow River basins. In Southwestern China, isolated patches of moderate and high suitability are linked to mountainous territories associated with the upper reaches of the Xi Jiang, Mekong, and Salween rivers. In addition, an isolated suitable area is indicated in the Angara River basin southwest of Lake Baikal. Such a distribution suggests that river valleys, foothills, and adjacent mountain forest regions may represent areas where the most favorable combination of temperature regime and moisture conditions is maintained. However, to date, no confirmed records of the species have been reported from this region (Kuprin & Danilevsky, 2025).

From the perspective of forest zonation, the main contemporary potential range of *R. coelestis* corresponds to the belt of broadleaved, mixed, and Korean pine-broadleaved forests of East Asia. In the Russian Far East, this primarily includes the forests of southern Primorye and the Amur region, comprising Korean pine-broadleaved and broadleaved forest formations. In northeastern China, the most suitable areas coincide with the Manchurian mixed and broadleaved forests, whereas on the Korean Peninsula they correspond to mountain broadleaved and mixed forests. In central and southwestern China, suitable areas appear to be associated with mountain forests of nemoral and hemiboreal types. Thus, in its current bioclimatic expression, the species' range is largely confined to forest landscapes of the temperate and subtemperate zones, characterized by relatively high moisture availability and comparatively mild thermal regimes.

Particular importance in interpreting the resulting map lies in comparing the potential range of the species with the distribution of its host plant, *Acer tegmentosum*. According to Plants of the World Online (accessed 13 March 2026), the range of this host plant includes Amur Oblast, Khabarovsk Krai, Primorye, Manchuria, and Korea – precisely the regions where the principal core of high bioclimatic suitability for *R. coelestis* is concentrated on the map. This correspondence is especially pronounced within the Amur River system, in the southern Russian Far East and northeastern China, supporting the view that the potential distribution of the species is closely linked to the spatial distribution of its host resource (Kuprin & Bezborodov, 2012).

Consequently, the principal Far Eastern–Manchurian–Korean massif of high suitability can be regarded as the most realistic part of the potential range of *R. coelestis*, since it is within this region that favorable climatic conditions coincide with the known distribution of *Acer tegmentosum*. Within this area, the most important regions include the southern part of Khabarovsk Krai, Primorye, the Amur region of Russia, the Chinese provinces of Heilongjiang and Jilin, and forested regions of the Korean Peninsula.

In contrast, the more southern and western areas of the map require more cautious interpretation. Although the model indicates several zones of moderate and high suitability in Central and Southwestern China, their relationship with the distribution

of *A. tegmentosum* is less evident. If the host plant is absent there or occurs only fragmentarily, these territories should rather be regarded as areas of bioclimatic suitability that may not necessarily be realized ecologically. The same applies to the isolated Siberian fragment in the Angara River basin: even if climatic conditions there are formally suitable (habitat suitability threshold 0.5–0.6), the actual possibility of species occurrence would depend on the presence of the host plant and the appropriate forest habitat types.

Thus, the contemporary bioclimatic potential range of *R. coelestis* can be characterized as East Asian, with its principal center located in the Amur basin, Manchuria, the southern Russian Far East, and the Korean Peninsula. This territory most closely corresponds both to the modeled climatic suitability and to the known natural range of the larval host plant, *A. tegmentosum*. Other areas identified on the map, located in Central China, Southwestern China, and the southern part of Eastern Siberia, most likely represent regions that are climatically suitable but less supported by the necessary biotic conditions. Overall, this pattern confirms that the spatial structure of the range of *R. coelestis* is determined not only by temperature and moisture regimes but also by the spatial coincidence of climatically suitable conditions with the distribution of the host plant and the corresponding broadleaved and mixed forest ecosystems.

Projection of bioclimatically suitable space for *Rosalia coelestis* by 2080–2100

The current area of potentially suitable habitats for *R. coelestis* is estimated at 3,554,100 km² (Table 3; Fig. 3). Under all considered future climate scenarios and for all CMIP6 models used in this study, a reduction in the area of the potential range is observed relative to present conditions. Thus, the overall modeling outcome indicates a consistent tendency toward a decrease in climatically suitable space for the species by the end of the 21st century.

The most pronounced reduction in the range is obtained under the SSP585 scenario. In all three models, this scenario is associated with the maximum loss of suitable habitat area: 848,775 km² for the MRI-ESM2-0 model, 862,075 km² for MPI-ESM1-2-HR, and 715,350 km² for BCC-CSM2-MR. This corresponds to reductions of 76.1%, 75.7%, and 79.9%, respectively. Consequently, under the most severe climate change scenario, *R. coelestis* loses approximately three quarters of its current bioclimatically suitable space, with the reduction approaching 80% in the case of the BCC-CSM2-MR model.

Under scenarios with lower or intermediate climatic forcing, the reduction remains substantial, although its magnitude varies among models. For MRI-ESM2-0, the areas of suitable habitat under SSP126, SSP245, and SSP370 amount to 1,792,550 km², 1,841,450 km², and 1,744,650 km², respectively, corresponding to decreases of 49.6%, 48.2%, and 50.9%. These results indicate a relatively stable pattern of estimates within this model: regardless of the scenario (except for SSP585), the projected reduction remains close to half of the present potential range.

Table 3. Changes in the potential range area of *R. coelestis* under current and future climate conditions.

Model / Climatic conditions	Scenario	Area of suitable habitats, km ²	Change relative to the current range, km ²	Change relative to the current range, %
Current	-	3554100	-	-
MRI-ESM2-0	SSP126	1792550	- 1761550	- 49.6
	SSP245	1841450	- 1712650	- 48.2
	SSP370	1744650	- 1809450	- 50.9
	SSP585	848775	- 2705325	- 76.1
MPI-ESM1-2-HR	SSP126	1427100	- 2127000	- 59.8
	SSP245	2073550	- 1480550	- 41.7
	SSP370	2130725	- 1423375	- 40.0
	SSP585	862075	- 2692025	- 75.7
BCC-CSM2-MR	SSP126	2162025	- 1392075	- 39.2
	SSP245	981250	- 2572850	- 72.4
	SSP370	1203700	- 2350400	- 66.1
	SSP585	715350	- 2838750	- 79.9

For the MPI-ESM1-2-HR model, the variation among scenarios is somewhat greater. Under SSP126, the potential range decreases to 1,427,100 km², representing a 59.8% reduction, whereas under SSP245 and SSP370 it amounts to 2,073,550 km² and 2,130,725 km², corresponding to reductions of 41.7% and 40.0%, respectively. Within this model, the most favorable projection for the species occurs under SSP370, rather than under the milder SSP126 scenario. This likely reflects the specific characteristics of the climate model and the spatial configuration of the bioclimatic variables rather than a simple linear relationship between scenario severity and range size.

The BCC-CSM2-MR model indicates the least pronounced reduction under the SSP126 scenario, where the area of suitable habitats remains at 2,162,025 km², or 60.8% of the current range, corresponding to a decrease of 39.2%. However, under SSP245 and SSP370, the reduction becomes considerably stronger, reaching 981,250 km² (-72.4%) and 1,203,700 km² (-66.1%), respectively. Under SSP585, the range decreases further to 715,350 km² (-79.9%). Thus, within the BCC-CSM2-MR model, the most pronounced contrast is observed between the relatively mild scenario and the moderate-to-high emission scenarios.

When averaged across the three models, the mean area of potentially suitable habitats is approximately 1.79 million km² under SSP126, 1.63 million km² under SSP245, 1.69 million km² under SSP370, and 0.81 million km² under SSP585. The mean reduction relative to present-day conditions amounts to approximately 49.5%, 54.1%, 52.3%, and 77.2%, respectively. These results indicate that differences among SSP126, SSP245, and SSP370 are evident but do not form a strictly linear sequence across all models, whereas SSP585 clearly stands out as the most unfavorable scenario.

Comparison of the maps shows that in all three models (BCC-CSM2-MR, MPI-ESM1-2-HR, and MRI-ESM2-0), the transition from present-day conditions to late 21st-century climate scenarios leads to a general contraction and fragmentation of the potential range of *R. coelestis*. However, the degree of contraction and the spatial configuration of suitable territories vary depending on both the climate model and the scenario (Table 3; Figs. 4–6).

Under the SSP126, SSP245, and SSP370 scenarios, the potential range retains its elongated East Asian configuration, although it becomes narrower and more mosaic in structure. Under SSP585, all three models predict the most pronounced reduction in suitable areas, with the range breaking into relatively narrow belts and isolated patches. Thus, regardless of the selected climate model, SSP585 represents the most unfavorable scenario for the species.

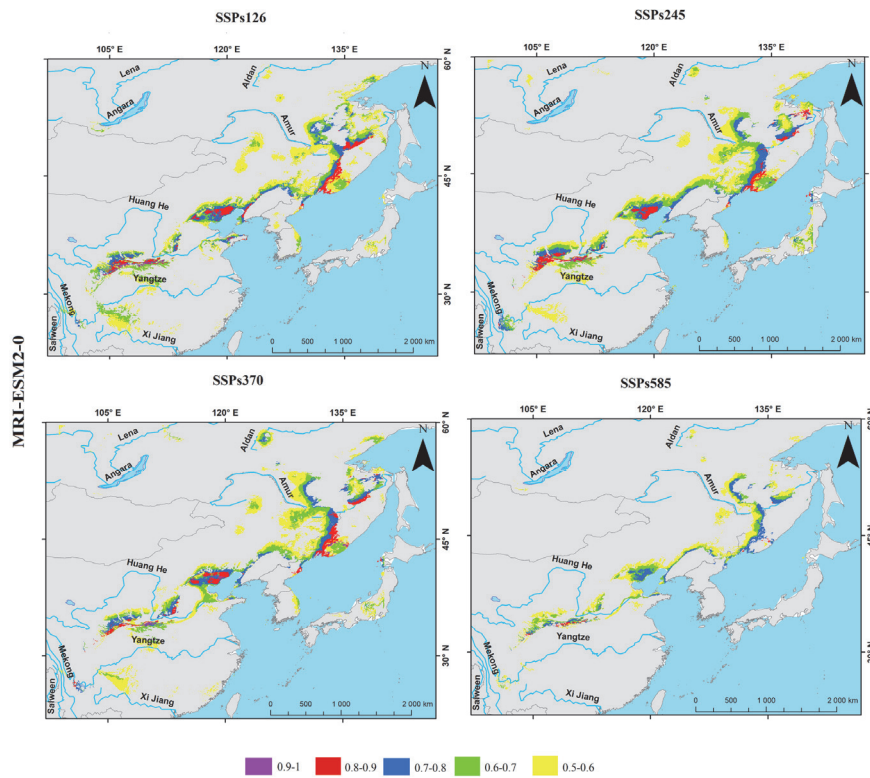


Fig. 4. Projected bioclimatic ranges of *R. coelestis* in Northeast Asia by 2100 according to the MRI-ESM2-0 model under the socio-economic scenarios SSP126, SSP245, SSP370, and SSP585.

The Far Eastern–Manchurian–Korean sector remains the most stable part of the potential range across all three models. Among the areas that maintain the highest suitability under most scenarios are southern Primorye, the southern part of Khabarovsk Krai, adjacent regions of the Amur basin, northeastern China—particularly Heilongjiang and Jilin provinces and the northern and central parts of the Korean Peninsula. These territories correspond most closely with the known natural distribution of the host plant *A. tegmentosum*, making the Far Eastern–Manchurian–Korean core not only climatically suitable but also the most biotically realistic component of the potential range of the species.

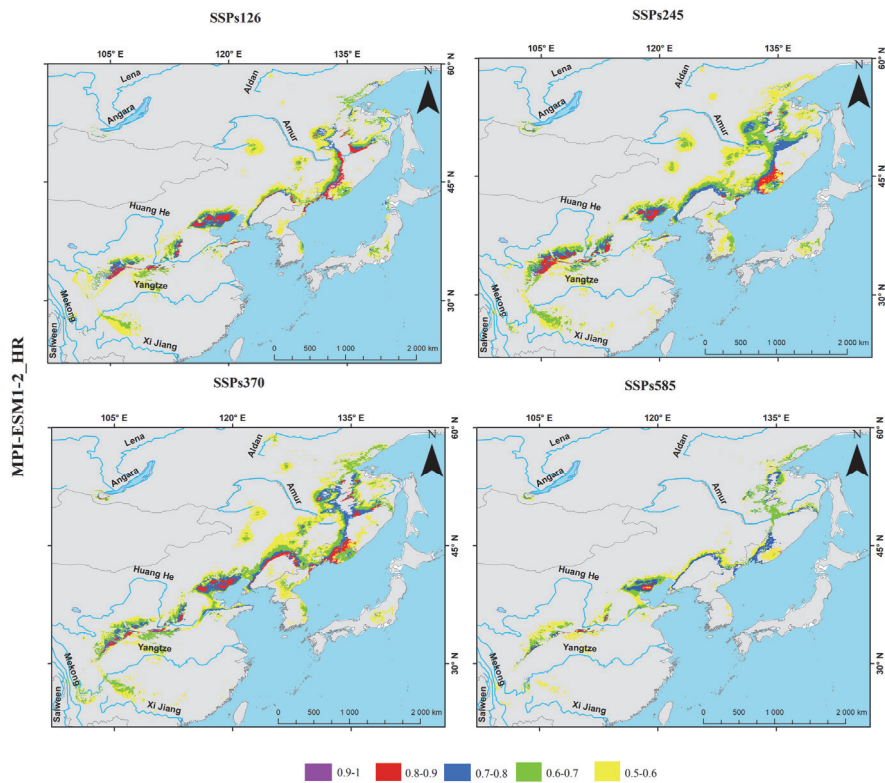


Fig. 5. Projected bioclimatic ranges of *R. coelestis* in Northeast Asia by 2100 according to the MPI-ESM1-2-HR model under the socio-economic scenarios SSP126, SSP245, SSP370, and SSP585.

The BCC-CSM2-MR model demonstrates the most pronounced reduction of the southern and interior portions of the range as scenario severity increases. Under SSP126, northeastern Chinese and Far Eastern zones of suitability remain well preserved, along with several areas within the Yangtze River basin. Under SSP245, and especially SSP370, the range contracts markedly toward the northeastern core, while the southern Chinese fragments become increasingly fragmented. Under SSP585, suitable territories are largely reduced to a narrow belt encompassing the southern Russian Far East, northeastern China, and part of the Korean Peninsula.

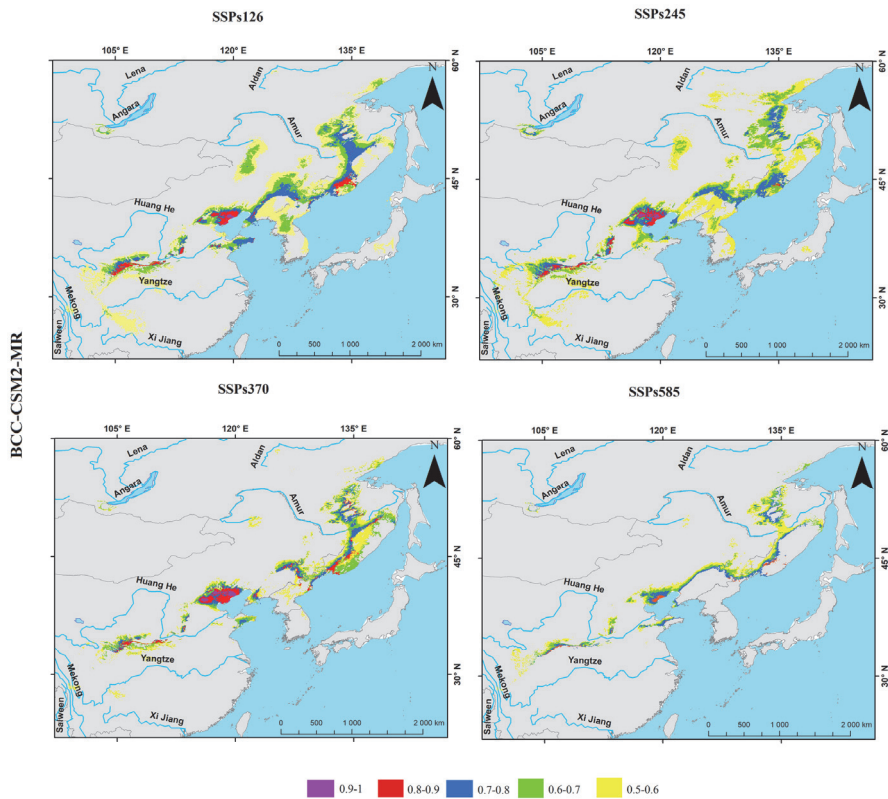


Fig. 6. Projected bioclimatic ranges of *R. coelestis* in Northeast Asia by 2100 according to the BCC-CSM2-MR model under the socio-economic scenarios SSP126, SSP245, SSP370, and SSP585.

The MPI-ESM1-2-HR model, under scenarios SSP126–SSP370, retains a relatively continuous belt of suitable habitats extending from northeastern China and the Amur region toward the Korean Peninsula, as well as several fragments in central China. In this model, certain areas in the middle Yangtze basin and adjacent mountain–valley systems are preserved better than in the BCC-CSM2-MR model. Nevertheless, under SSP585 even this model shows a sharp contraction of the range, with the Primorye–Manchurian and Korean regions remaining the most stable.

The MRI-ESM2-0 model presents a generally similar pattern but is characterized by somewhat greater persistence of certain peripheral areas under mild and intermediate scenarios. Under SSP126, SSP245, and SSP370, not only the principal Far Eastern territories remain suitable, but also several isolated patches in central and southwestern China. However, under SSP585 this model also predicts a general contraction of the range toward the eastern part of the continent, primarily Primorye, northeastern China, and the Korean Peninsula.

A comparison among the scenarios shows that SSP126 and SSP245 generally retain a broader system of potentially suitable territories, although even under these scenarios the range becomes less continuous than under present conditions. SSP370 often results not only in a further reduction in area but also in a more pronounced spatial concentration of suitable habitats within the eastern part of the range. SSP585 differs qualitatively from the other scenarios in that suitable habitats persist mainly in the most stable refugial areas.

From a biogeographical perspective, the most probable refugia for the species are likely to be southern Primorye, adjacent areas of southern Khabarovsk Krai, eastern Manchuria, and certain regions of northern and central Korea. These areas are characterized by a combination of relatively stable climatic suitability, forest landscapes dominated by broadleaved and mixed forest formations, and spatial coincidence with the known range of *A. tegmentosum*. In contrast, regions within the Yangtze and Yellow River basins and southwestern China, although potentially retaining climatic suitability in some models, appear less stable and are likely to depend more strongly on inter-model differences and on the presence of the host plant.

Thus, the future range of *R. coelestis* will be determined not only by the total area of suitable habitats but also by changes in their spatial connectivity. Even in scenarios where a portion of suitable territories is preserved, the range becomes increasingly fragmented. For a species closely associated with *A. tegmentosum* and with specific types of broadleaved and mixed forest ecosystems, this implies an increased dependence on a limited number of spatially stable areas. Consequently, an ensemble modeling approach provides the most appropriate interpretation of the results: all three models converge on the same conclusion –the persistence of the Far Eastern–Manchurian–Korean core and the high vulnerability of peripheral range fragments.

Comparison of the obtained results with published models for other longhorn beetle species indicates that such a pattern is typical for specialized and rare species (Poloni *et al.*, 2022). For *Rosalia alpina* in Italy, MaxEnt modeling likewise revealed limited zones of stable suitability and gaps in the network of protected areas (Bosso *et al.*, 2013). For *Callipogon relictus* in Northeast Asia, it was shown that under various climate scenarios the most stable zones also remain in Primorye and adjacent regions of China and Korea (Kuprin *et al.*, 2024). In contrast, models for the invasive polyphagous species *Anoplophora glabripennis* generally predict much broader and more flexible potential ranges, clearly reflecting the differences between narrowly specialized and trophically more plastic representatives of Cerambycidae (Shim *et al.*, 2020; Zhou *et al.*, 2021; Zhang *et al.*, 2022). Therefore, for *R. coelestis* not only climatic conditions but also the spatial coincidence of future suitable areas with the distribution of the host plant and corresponding forest ecosystems will be of critical importance.

CONCLUSIONS

In the present study, 19 environmental variables, including climatic factors and elevation, were used to predict the potential distribution of the longhorn beetle *R. coelestis* in Northeast Asia based on MaxEnt models under different socioeconomic development scenarios. The greatest contribution to the construction of the species' potential range models was provided by four bioclimatic variables: bio3 (isothermality), bio5 (maximum temperature of the warmest month), bio12 (annual precipitation), and bio15 (precipitation seasonality, coefficient of variation).

According to the climate models MRI-ESM2-0, MPI-ESM1-2-HR, and BCC-CSM2-MR, by 2080–2100 the area of the most suitable habitats for *R. coelestis* in Northeast Asia is projected to decrease under different greenhouse gas emission scenarios (SSPs). The smallest reduction in suitable area is predicted under the mild (SSP126) and intermediate (SSP245) scenarios, whereas the greatest decline is expected under the severe (SSP585) and intermediate-high (SSP370) scenarios.

It was also shown that the core of the species' range, representing the most favorable habitats for the monophagous *R. coelestis* in Northeast Asia under different climate models and emission scenarios by 2080–2100, will be concentrated in valley broadleaved forests, primarily in southern Primorye and certain regions of northern and eastern China. This pattern is likely associated with the sufficient availability of the beetle larvae's host plant, *A. tegmentosum*.

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coelestis finds from a personal data base. The research was carried out within the state assignment of Ministry of Science and Higher Education of the Russian Federation (theme No. 124012400285-7) (for A.V. Kuprin) and 124013000750-1 (for N. E. Shevchenko), and partly supported by the Mianyang Science and Technology Program 2023ZYDF076 and Mianyang Normal University QD2023A30 (for M.-Y. Lin).

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