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ORIGINAL ARTICLE

Biodiversity hotspots for modeled habitat patches and corridors of species richness and threatened species of reptiles in central Iran

Kamran Almasieh[1] · Seyyed Mehdi Mirghazanfari[2] · Shirin Mahmoodi[3]

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Abstract
In recent years, the distribution range of reptiles has greatly shrunk. Reptiles are sensitive to habitat degradation and fragmentation, and are thus ideal focal species for studies on habitat connectivity modeling. In this study, we conducted habitat and corridor modeling for 11 species out of nine families of reptiles and two vulnerable species in Qom province, central Iran, in order to identify biodiversity hotspots of species richness and threatened species for these reptiles and to compare these hotspots with current protected areas. Habitat modeling was carried out using MaxEnt for each species, and habitat patches were obtained from suitable polygons which included occurrence points. Least-cost corridors among these patches were designed using CorridorDesigner. We identified 40 habitat patches and 32 corridors among these patches for the species. The highest species richness was six species for the overlaid map of identified patches and four for the overlaid map of identified corridors. Biodiversity hotspots of species richness and two threatened species for both habitat patches and corridors covered about 22% and 14% of Qom province, respectively. These two hotspots had large overlapping areas (more than half of their areas) and showed the same general pattern. Comparison between the two types of biodiversity hotspots (i.e., species richness and threatened species) and the available protected areas revealed that the hotspots are mainly located outside of the protected areas. Therefore, these hotspots should be given the highest priority for conservation and be taken into consideration by the Department of Environment of Iran.

Keywords Focal species · Habitat connectivity · Least-cost corridors · Protected areas · Qom province

Introduction

Habitat fragmentation, alteration of habitat over the course of time, is characterized by division of a large habitat patch into several smaller isolated patches (Bennett 2003). The process of fragmentation results in habitat loss, smaller habitat patches, and increased isolation (Noss et al. 1996). Animals need to roam within their home ranges in search of food, cover, and mates. In addition, they may move out of their home ranges to find unoccupied habitats and maintain gene flow among population groups (Young and Clarke 2000). Any movement of organisms among habitat patches is regarded as connectivity (Almasieh et al. 2019; Crooks and Sanjayan 2006). If habitat connectivity is not established, fragmented habitat patches will face challenges and will be ultimately lost (Beier et al. 2007). Lack of connectivity constricts the available large patches and intensifies isolation of the remaining smaller habitat patches (Crooks and Sanjayan 2006). A corridor is a narrow continuous area through which individuals of wildlife species are allowed to move between two habitat patches (Beier et al. 2011). Of the three corridor modeling approaches based on the graph theory, least-cost corridor modeling (Adriaensen et al. 2003) is the most widely used (Almasieh et al. 2016; Beier et al. 2008).

Biodiversity hotspots, as one of the most important topics in conservation biology, are applied to identify areas with the highest priority for conservation (Reid 1998; Myers et al.

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✉ Kamran Almasieh
almasieh@asnrukh.ac.ir

[1] Department of Nature Engineering, Agricultural Sciences and Natural Resources University of Khuzestan, Mollasani, Iran

[2] Iranian Herpetological Studies Institute (IHSI), Tehran, Iran

[3] Department of Environmental Sciences, Faculty of Natural Resources, University of Tehran, Karaj, Iran

2000; Araújo 2002). Due to limited budgets, these hotspots are recommended for conservation (Farashi and Shariati 2017; Myers et al. 2000). Biodiversity hotspots refer to heterogeneous areas with high rates of ecosystem loss (Garcia 2006; Myers et al. 2000; Sechrest et al. 2000). In addition, biodiversity hotspots are identified through calculation of biodiversity. Several methods have been used to calculate biodiversity hotspots, including species richness, threatened species, and restricted areas (e.g., endemic species) (Ceballos and Ehrlich 2006; Garcia 2006; Orme et al. 2005; Pascual et al. 2011), among which species richness, as the number of species in a unit of area (Ceballos and Ehrlich 2006), has been widely used to calculate biodiversity (Ceballos et al. 2005; Cincotta et al. 2000; Flather et al. 1998; Hosseinzadeh et al. 2014; Pascual et al. 2011; Reid 1998; Williams et al. 1996).

Another method for determination of biodiversity hotspots is use of threatened species (Ceballos and Ehrlich 2006; Garcia 2006; Pascual et al. 2011; Orme et al. 2005). The International Union for Conservation of Nature (IUCN) has classified 28,338 species as threatened (i.e., vulnerable [VU], endangered [EN], and critically endangered [CR]), which includes 1367 threatened reptile species (IUCN 2019). Habitat fragmentation and degradation, overexploitation, pollution, and climate change are the main reasons behind the decrease in populations of threatened species (Brook et al. 2008; Renwick et al. 2017). Threatened species are in high priority for conservation (Renwick et al. 2017; Brazill-Boast et al. 2018), and their distribution could be considered as a proxy for biodiversity hotspots (Ceballos and Ehrlich 2006; Farashi et al. 2017; Griffin 1999; Orme et al. 2005; Pascual et al. 2011).

Most animals are nocturnal and cryptic, and thus, data deficiency regarding species distribution has been the chief problem in determining species richness and other indicators of biodiversity hotspots (Farashi and Shariati 2017; Mackenzie et al. 2006). Habitat suitability models (HSMs) need little information on species and can serve as a solution to this problem as HSMs can determine potential areas of species distribution using species occurrence records and environmental variables, and therefore, they can be used to determine biodiversity hotspots. By combining suitable habitat patches generated through modeling for different species, we can estimate species richness in a given area (Garcia 2006). Eventually, areas with the highest species richness and the highest number of threatened species are considered as biodiversity hotspots and are given priority for conservation (Ficetola et al. 2012). The incongruence between these hotspots and protected areas is considered as conservation gaps (Araújo et al. 2011; Farashi et al. 2017; Meller et al. 2014).

Reptiles are relatively poorly identified by the IUCN, and only about 80% of all species of reptiles are evaluated by the IUCN (i.e., 7541 from 9084 species) (IUCN 2019; Uetz 2010). Therefore, lack of data on species, such as conservation status, distribution, threats, and population trends, hinders conservation of reptiles. Compared to mammals and birds, reptiles have limited distribution ranges (Anderson 1984; Böhm et al. 2013), rendering them particularly sensitive to human activities which cause habitat degradation and fragmentation (Anderson and Marcus 1992). In addition, changes in environmental conditions have major effects on reptiles as their distribution is under extreme regulation by environmental factors. Consequently, environmental variables can prove useful in modeling of suitable habitats for reptiles (Buckley et al. 2012; Oraie et al. 2015). Based on the definition of focal species (Beier et al. 2007), reptiles can be considered as focal species because they are sensitive to barriers and are among the most area-sensitive species (Hager 1998). Area-sensitive species are highly influenced by habitat degradation and fragmentation. Their sensitivity to barriers and limited distribution make reptiles ideal candidates for habitat connectivity modeling.

Totally, 241 species of reptiles have been identified in Iran so far (Safaei-Mahroo et al. 2015). Among these, 152 species are evaluated by the IUCN, 15 of which are threatened (i.e., VU, EN, and CR) (IUCN 2019). Although some studies have been carried out in Iran to conduct habitat modeling for reptile species (e.g., Chefaoui et al. 2018; Farashi and Shariati 2017; Fattahi et al. 2014; Hosseinian Yousefkhani et al. 2013; Hosseinzadeh et al. 2014; Hosseinzadeh et al. 2017; Sanchooli 2017; Yousefi et al. 2015), none have evaluated habitat connectivity. Therefore, in this study, we performed habitat and corridor modeling for 11 species of reptiles from Qom province in central Iran to determine habitat patches and corridors for each species. Then, we combined habitat patches and corridors for the 11 species. To locate biodiversity hotspots of threatened species and investigate any overlap between the hotspots, the same analyses were done separately for the two available threatened species. We predicted that hotspots for the species richness and threatened species were located mainly in the south and center of the study area and overlapped to a large extent. Finally, to evaluate the coverage of hotspots by protected areas, we compared hotspots of species richness and threatened species with current protected areas in Qom province. We predicted that biodiversity hotspots of reptiles were located mainly outside of protected areas. Lastly, biodiversity hotspots in both patches and corridors were proposed to be taken into consideration for assigning conservation priority in the region.

Materials and methods

Study area

The study area encompassed Qom province, located in central Iran, with an area of about 11,500 km^2 (Fig. 1). The area

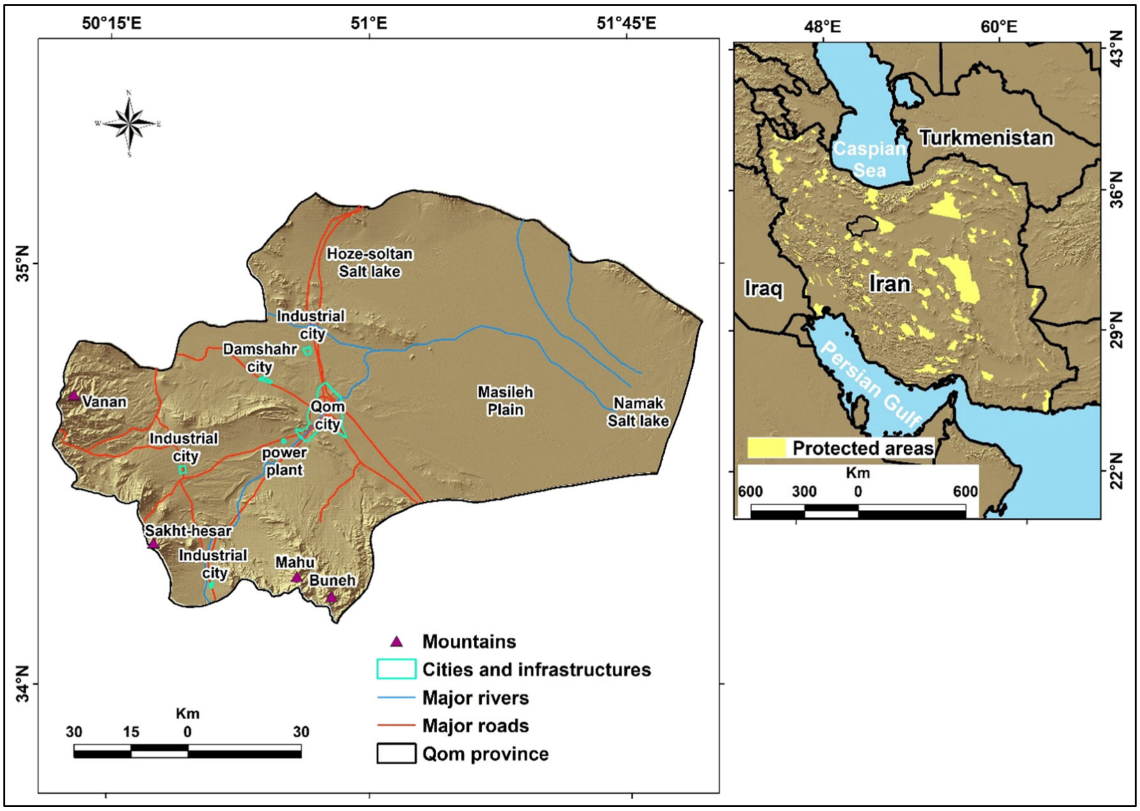

Fig. 1 Study area including Qom province in central Iran for habitat and corridor modeling of the 11 reptile species

mainly includes vast arid plains (e.g., Masileh plain) with high temperatures, averaging 30 °C in summer and 6 °C in winter, with an annual mean precipitation of 150 mm. The mountainous areas southwest of the study area (e.g., Buneh, Mahu, Sakht-hesar, and Vanan mountains) have milder temperatures, averaging 23 °C in summer and 5 °C in winter, with an annual mean precipitation of 250 mm (IRIMO 2010). The city of Qom, a metropolis with a population of about 1,200,000 (SCI 2017), was the main human settlement in the study area. Vast plains and mountainous areas in this relatively small province have given rise to a high diversity of reptile species (Hosseinian Yousefkhani and Rastegar-Pouyani 2011). Therefore, Qom province is representative of the geographic and environmental variation of Iran.

Hosseinian Yousefkhani and Rastegar-Pouyani (2011) reported 33 species of reptiles for Qom province, which was recently raised to 38 species in 11 families based on field surveys done by the Iranian Herpetological Studies Institute (IHSI), an NGO of herpetologists (including the second author of the present study). Of the 38 species, three are endemic, and according to the IUCN Red List of Threatened Species, 18 are evaluated as least concern (LC), 16 are not evaluated (NE), two are vulnerable (VU), and there is no data for the other two species (data deficient, DD). The list of reptile species of Qom province and their conservation status according to the IUCN is available in the supplementary materials (Table S1).

Representative species and field survey

We selected 11 species from nine families as representatives of reptiles in the study area. The species included two vulnerable species, and only six have been evaluated by the IUCN (Table 1). A field survey was done by IHSI during 3 years (2014–2016) from March to October to collect occurrence points for the 11 species. The field survey was conducted randomly in different habitats (mountains and plains, rangelands and agricultural lands, etc.) in Qom province to collect occurrence points for the reptile species based on direct observation. Monitoring did not include absence data because a systematic survey with continuous monitoring is needed to ascertain absence of a species in an area. Therefore, we only used occurrence points collected by IHSI. Specimens were captured by hand. Captured specimens were then identified using *The Lizards of Iran* (Anderson 1999), *A Field Guide for Reptiles and Amphibians of Iran* (Kamali 2013), and *The Atlas of Reptiles of Iran* (Mozaffari et al. 2014). All captured specimens were released into the wild after identification. Occurrence points were recorded by GPS with an error of less than 10 m. In total, 314 occurrence points were collected for 10 reptile species during the field surveys (Table S2). Also, we obtained 17 independent occurrence points for *Phrynocephalus persicus* from bibliographic data (Mozaffari et al. 2014; Rastegar-Pouyani 2010). Spatial autocorrelation between occurrence points was checked, and a circle with a

Table 1 Characteristics of the 11 reptile species, accuracy of MaxEnt models, and relative contribution of each environmental variable to the models of reptile species in Qom province, central Iran, using analysis of variable contributions in MaxEnt models

Scientific name	Family	IUCN status	Number of independent occurrence points	Accuracy of MaxEnt models (from 0 to 1)				Relative contribution of environmental variables (in percentage)					
				AUC	Sensitivity	Specificity	TSS	Elevation	Topographic position	Land cover	NDVI	Distance from rivers	Distance from roads
Agamura persica	Gekkonidae	LC	36	0.861	0.889	0.842	0.731	28.2	7	21.4	6.3	16.7	20.4
Microgecko latifi[a]	Gekkonidae	LC	12	0.978	1	0.967	0.967	22.2	4.2	9.9	19.1	12.3	32.3
Teratoscincus keyserlingii	Sphaerodactylidea	LC	24	0.884	1	0.975	0.975	21.4	10.2	31.8	7.8	12.3	16.5
Eumeces schneideri	Scincidae	NE[b]	25	0.970	0.947	0.932	0.879	33.9	8.5	18.2	19.6	9.2	10.6
Trapelus agilis	Agamidae	NE	28	0.862	1	0.725	0.725	49.7	15.5	4.8	3.7	7.9	18.4
Phrynocephalus persicus	Agamidae	VU	17	0.947	1	0.869	0.869	41.6	15	7.5	8.2	6.1	21.6
Varanus griseus	Varanidae	NE	26	0.901	0.9	0.751	0.651	42	6.1	12.2	6.7	6.2	26.8
Eryx jaculus	Boidae	NE[b]	34	0.934	1	0.943	0.943	30.9	6	18.1	8.6	26.8	9.6
Spalerosophis diadema	Colubridae	NE	38	0.951	1	0.909	0.909	12.3	6.6	60.5	4.5	10.7	5.4
Pseudocerastes persicus	Viperidae	LC	37	0.847	0.914	0.74	0.654	54.1	5.7	19.1	4.9	7	9.2
Testudo graeca	Testudinidae	VU	29	0.97	0.909	0.86	0.869	38.1	9	5	33.5	6.2	8.2

[a] Endemic species

[b] LC in Europe

radius of 0.25 km was placed around each occurrence point to exclude additional points using the Spatially Rarify Occurrence Data tool in the SDMtoolbox (Brown 2014). We set the value at 0.25 km (i.e., 0.25-km radius of a 20-ha circle home range) according to home ranges of similar reptile species in the Arizona project as presented by Majka et al. (2007a). This analysis reduced the initial 331 occurrence points to 306 independent occurrence points for the 11 species (Table 1).

Environmental variables

Environmental variables including two topographic variables (i.e., elevation and topographic position), three variables of water and food resources (land cover, normalized difference vegetation index [NDVI], and distance from river), and two human disturbance variables (distance from roads and distance from villages) were all prepared at 30 m resolution for all species (Table 2). A digital elevation model (DEM) as the elevation variable, generated by 30 m SRTM, was used to create a topographic position map using CorridorDesigner (Majka et al. 2007b). Within a neighborhood with a radius of 200 m, we considered a cell as canyon bottom if its elevation was 12 m lower than the average elevation of the neighborhood, a ridge top if its elevation was 12 m higher than the average elevation of the neighborhood, a gentle slope if the cell was neither a canyon bottom nor a ridge top and the slope was less than 6°, and a steep slope if it was neither a canyon bottom nor a ridge top and the slope was more than 6°. We used all thresholds (i.e., 200 m radius for neighborhood; 12 and − 12 m for ridge top and canyon bottom, respectively; and a 6° threshold for gentle and steep slopes) based on the default settings of the software, which were appropriate for a DEM at a 30-m resolution (Atwood et al. 2011; Beier et al. 2007).

Table 2 Environmental variables used in habitat modeling for the 11 reptile species in Qom province, central Iran

Category	Variable	Unit	Source
Topography	Elevation	Meter	https://earthexplorer.usgs.gov/
	Topographic position	Class	Elevation
Water and food resources	Land cover	Class	FRWMO 2010
	NDVI	− 1 to 1	https://earthexplorer.usgs.gov/
	Distance from rivers	Meter	DoE 2019
Human disturbance	Distance from roads	Meter	NCC 2012
	Distance from villages[a]	Meter	DoE 2019

[a] Removed due to its high correlation with distance from roads

Land cover of Iran with 58 cover types was derived from 30 m Landsat Enhanced Thematic Mapper Plus (ETM+) imagery for Iran (FRWMO 2010). In the study area, there were 18 land-cover types. The land-cover map was converted to raster format, and each 30 × 30 m cell was assigned the class that occupied the majority of the cell. Then, 18 cover types were reduced to six based on their similarity; the simplified cover types consisted of bare lands (44.6% of the study area), rangelands (37.4%), agricultural lands (10.4%), water barriers and salt lakes/lands (6%), mountainous areas (0.9%), and human settlement (0.7%). NDVI was derived from bands 2–5 of 30 m Landsat 8 OLI imagery for July 2016 using the Image Analysis tool in ArcGIS v10.2. Distance from roads and distance from villages were calculated using the Euclidean Distance tool in ArcGIS. Collinearity among variables was checked, and distance from villages was removed because it was correlated with distance from roads (Table S3). All remaining variables had pairwise correlation coefficients less than 0.7. Also, 5000 random points were generated to check multi-collinearity among variables using r-package USDM (Naimi et al. 2014) to exclude multi-correlated variables with variance inflation factor (VIF) > 3 (i.e., the threshold suggested by Zuur et al. 2010). VIF ranged from 1.28 to 2.08 for all variables. Therefore, all variables were retained for subsequent analyses (Table 1).

Habitat modeling

Habitat suitability models of the 11 species were prepared separately (1) to determine areas with high suitability for species, (2) to detect habitat patches, and (3) for use in corridor modeling. Habitat modeling was carried out using MaxEnt v3.3.3k (Phillips et al. 2006), which utilizes a few occurrence points along with randomly created pseudo-absence points. The MaxEnt then compares environmental variables (in both continuous and categorical formats) in occurrence cells with values of the same variables in pseudo-absence cells to discriminate between them (Phillips and Dudik 2008). Finally, the software creates a continuous habitat suitability map.

For modeling each species' suitable habitat, 10,000 pseudo-absence points were generated as the default setting of MaxEnt. Ten thousand points have been shown to be adequate for high predictive accuracy (Phillips and Dudik 2008). Seventy-five percent of the occurrence points were considered as training data and the remaining 25% as test data. Area under the receiver operating characteristic (ROC) curve (AUC) was used to evaluate model performance (values for AUC range from 0 to 1, where 0.5 indicates random assignment and 1 indicates perfect discrimination of occurrence points from pseudo-absence points). To delimit the background area into an informative set of pseudo-absence points, a minimum convex polygon was created around the buffer of each occurrence point for all reptile species (Anderson and Raza 2010; Barbet-

Massin et al. 2012). A 1-km buffer (i.e., about four times the radius of the circular home range of reptiles in the Arizona project) was created around each occurrence point. First, habitat modeling was performed for the background area and was then extrapolated to the entire study area using modeling projection in MaxEnt.

Due to the small data set of occurrence points for each reptile species, (1) linear, quadratic, and hinge features, instead of all features, were considered (Raes and ter Steege 2007; Merow et al. 2013; van Proosdij et al. 2016) and (2) four values, 0.5, 1, 2, and 5, were used for the regularization multiplier and the model with the highest AUC was selected as the final model for each species (Fois et al. 2018). Higher regularization multipliers ease constraints, and consequently, the distribution of species is more spread out (Phillips and Dudik 2008; Fois et al. 2018), and (3) MaxEnt models were done in 10 replicates using bootstrapping. Analysis of variable contribution in MaxEnt results was used to evaluate the relative contribution of each variable to habitat suitability. Response curves of each reptile species occurrences to each environmental variable were used considering the correlation between each variable and other variables. Habitat suitability models were rescaled to 0–100 for use in corridor modeling. Moreover, Qom metropolis, another city (i.e., Damshahr), and four main infrastructures (i.e., three industrial cities and one power plant) (Fig. 1) were assigned a new value (zero) in all habitat suitability models using the Modify HSM 1-Reclassify features tool of CorridorDesigner.

Habitat patches and corridors

We identified habitat patches as polygons of potential distribution for each species. In addition, these patches were considered as start/stop points for corridors. HSMs of 11 reptile species were converted to binary maps (i.e., suitable and non-suitable) based on a threshold obtained by maximum training sensitivity plus specificity of MaxEnt models for each species (Jimenez-Valverde and lobo 2007). Accuracy of binary maps was checked using sensitivity, specificity, and the true skill statistic (TSS). Sensitivity was obtained using results of modeling in MaxEnt (1 minus the omission rate). For specificity, the percentage of the 10,000 random points located in non-suitable polygons was calculated for each species. Finally, TSS was calculated according to the formula presented by Allouche et al. (2006) (i.e., sensitivity plus specificity minus 1). We removed patches with no occurrence points from suitable habitat polygons, and only used polygons where the species had certainly occurred.

We used CorridorDesigner for corridor modeling of each species. This software designs least-cost corridors between two patches with different widths for each corridor (i.e., 0.1–10% of the study area). CorridorDesigner uses a habitat suitability map and converts it to a resistance map (calculated as 100 minus the value of a cell in the continuous suitability map), because cost (i.e., resistance) of cells should be considered when creating a corridor. The resistance map and the suitability map are complementary, and a cell with a perfect suitability score has zero resistance (Beier et al. 2007). Unlike the least-cost path method, least-cost corridor designs a corridor with larger width in high suitability areas and smaller width in low suitability areas (Beier et al. 2007). CorridorDesigner designs corridors using a moving window with a radius of 200 m by selecting contiguous cells within a suitability threshold. We used maximum training sensitivity plus specificity threshold in MaxEnt models for setting the suitability threshold for each species in CorridorDesigner. We only considered corridors among patches with relatively high habitat suitability for species dispersal (Almasieh et al. 2016). We modeled at least one corridor for each habitat patch, and connectivity was maintained among all patches for each species.

Biodiversity hotspots and protected areas

We overlaid identified habitat patches and corridor maps for the 11 reptile species to obtain a map of species richness. We considered patches and corridors with high species richness as hotspots, which covered about 20% of the study area. We chose 20% because the Department of Environment (DoE) of Iran aims to increase protected areas to 20% of the total area of Iran (DoE 2019). Also, we performed these analyses for the two threatened species of reptiles separately, with the main difference that we considered the entire area of the identified habitat patches and corridors of threatened species as biodiversity hotspots because this hotspot covered less than 20% of the study area. We overlaid biodiversity hotspots of species richness and hotspots for the two threatened species to detect the spatial congruence of hotspots. Finally, we compared biodiversity hotspots of species richness and threatened species with protected areas to detect conservation gaps.

Results

Habitat modeling

For different regularization multipliers, our MaxEnt models had AUCs ranging from 0.711 to 0.978 (Table S4). Models with the highest AUCs, i.e., models with the best performance (ranging from 0.861 to 0.978), were chosen for each species (Table 1). Analysis of contribution of variables in MaxEnt revealed that elevation was the most important variable, providing the most useful information in eight of the 11 models (for *Agamura persica*, *Teratoscincus keyserlingii*, *Trapelus agilis*, *Phrynocephalus persicus*, *Varanus griseus*, *Eryx jaculus*, *Spalerosophis diadema*, and *Testudo graeca*).

Distance from roads (for *Microgecko latifi*), NDVI (for *Eumeces schneideri*), and land cover (for *Spalerosophis diadema*) were the most important variables for the remaining models. Relative contribution of each environmental variable to the MaxEnt models for all species is shown in Table 1.

Response curves of the eight aforementioned species to elevation illustrate different ranges of suitable elevation, mainly from 500 to 1500 m. Response curve of *Microgecko latifi* to distance from roads revealed that probability of occurrence increased with distance from roads, with a peak at 0 to 10 km from roads. The response curve of *Eumeces schneideri* to NDVI showed that probability of occurrence increased with increasing vegetation density. Finally, the response curve of *Spalerosophis diadema* to the land-cover variable showed that probability of the species' occurrence increased in agricultural lands. Response curves to environmental variables in the MaxEnt model for the 11 reptile species are available in the supplementary materials (Fig. S1).

HSMs of the 11 species demonstrated various areas of high habitat suitability (Fig. 2). Our habitat modeling showed that *Microgecko latifi* had the most restricted suitable habitat in Qom province. Some other species such as *Trapelus agilis* and *Varanus griseus* had vast suitable habitats in Qom province (Fig. 2).

Identified patches and corridors

For the 11 species, we identified 40 habitat patches that included occurrence points, with a total area covering about 59% of the study area (Table 3, Fig. 3). Suitable polygons, as patches for the 11 species, had sensitivities ranging from 0.889 to 1, specificity ranging from 0.725 to 0.975, and TSS ranging from 0.651 to 0.975 (Table 1), indicating the acceptable accuracy of all models. Only one suitable polygon was modeled as a habitat patch for *Teratoscincus keyserlingii*; therefore, we did not model any corridors for this species. In total, *Varanus griseus* and *Microgecko latifi* had the largest and smallest areas of habitat patches, respectively (Table 3).

We designed 32 corridors among habitat patches, covering about 7% of Qom province (Table 3, Fig. 3).

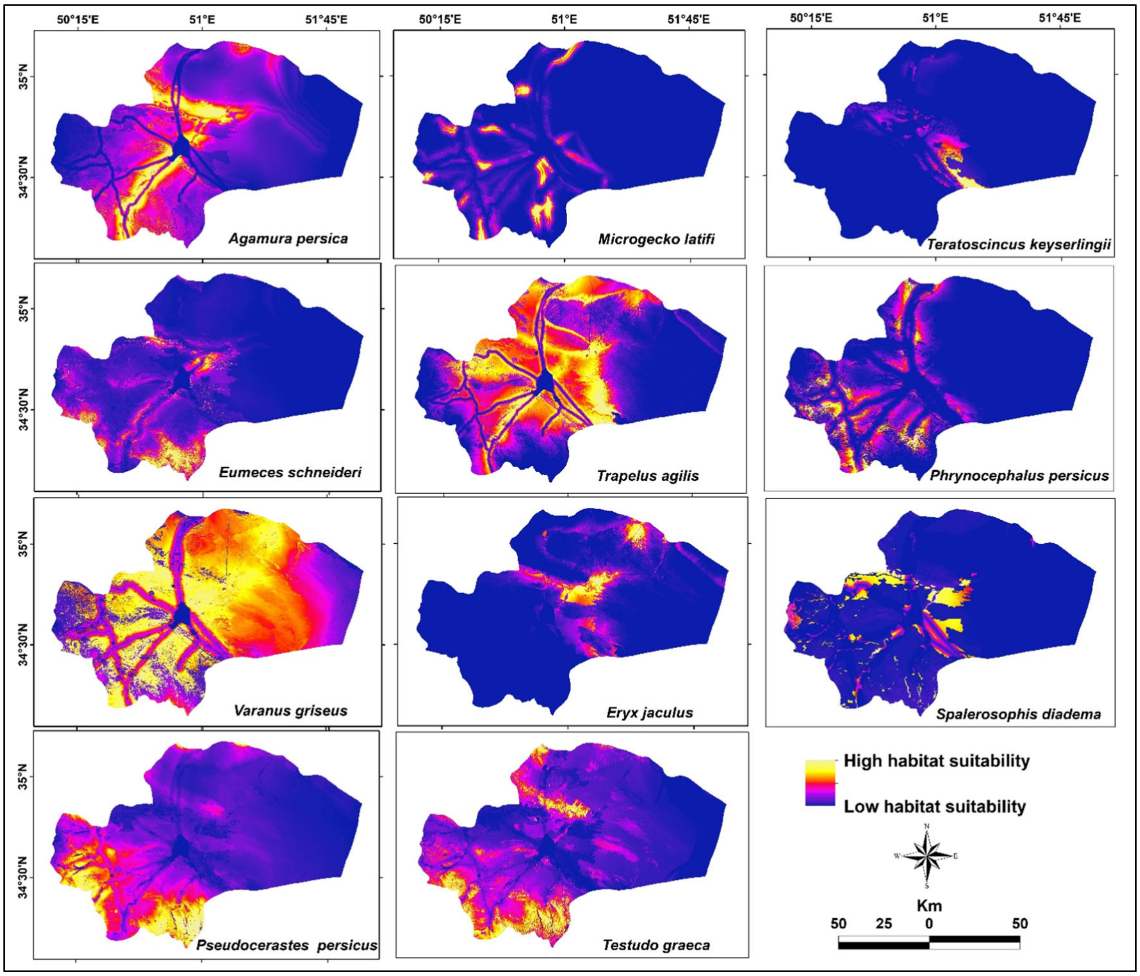

Fig. 2 Habitat suitability modeling of the 11 reptile species in Qom province, central Iran, based on occurrence points and environmental variables using MaxEnt

Table 3 Properties of identified patches and least-cost corridors for the 11 reptile species in Qom province, central Iran

Species	Identified habitat patches with occurrence points		Identified least-cost corridors	
	Numbers	Area (km^2)	Numbers	Area (km^2)
Agamura persica	4	1275.5	3	29.95
Microgecko latifi	2	118.46	1	20.52
Teratoscincus keyserlingii	1	189.8	–	–
Eumeces schneideri	4	510.35	2[c]	83.46
Trapelus agilis	7	2775.77	7	38.31
Phrynocephalus persicus	2	188.77	1[c]	122.55
Varanus griseus	5	3298.69	5	94.56
Eryx jaculus	3	485.84	2	95.17
Spalerosophis diadema	5	472.83	5[c]	150.2
Pseudocerastes persicus	3	2737.05	3	93.36
Testudo graeca	4	1258.88	3[c]	127.28
Total	40	13,310.05[a]	32	861.66[b]

[a] 6836.13 km^2 with consideration of overlapped areas of habitat patches

[b] 766.9 km^2 with consideration of overlapped areas of corridors

[c] Including corridor/corridors with more than one branch

Spalerosophis diadema had the largest area of identified corridors and *Microgecko latifi* had the smallest (Table 3, Fig. 3).

Biodiversity hotspots and protected areas

We prepared species richness maps using habitat patches and corridors separately. The highest species richness was six species for the overlaid map of modeled patches and four for the overlaid map of modeled corridors. We created a map of patches with ≥ 3 species for species richness of habitat patches (in total 1819.93 km^2, roughly 16% of the study area), and a map of corridors with ≥ 1 species for species richness of corridors (in total 706.9 km^2, roughly 6% of the study area). Finally, these two maps were merged to display biodiversity hotspots for the 11 species in the study area. These hotspots, with an area of about 2526.8 km^2, covered about 22% of Qom province and have the highest priority for conservation (Fig. 4, top).

For the two threatened species, we considered the entire area of identified habitat patches (1379.42 km^2, equal to about 12% of the study area) and the entire area of identified corridors (237.3 km^2, equal to about 2% of the study area). Finally, these two maps were merged to illustrate biodiversity hotspots of these two threatened species of reptiles in the study area (Fig. 4, bottom). This hotspot, with an area of about 1600.94 km^2 and covering about 14% of Qom province, should be given priority in conservation. Biodiversity hotspots of species richness and threatened species overlapped in 1070.5 km^2, which was equal to 40% of the biodiversity hotspots of species richness and two thirds of biodiversity hotspots of the two threatened species.

We compared the biodiversity hotspots of species richness and threatened species with the current protected areas in Qom province. For species richness, two patches of biodiversity hotspots (69.97 km^2) were located within protected areas but the majority of hotspots were located outside of protected areas (Fig. 4, top). These habitat patches covered only 7.5% of available protected areas in Qom province. Similarly, for the two threatened species, a single patch of biodiversity hotspots (133.79 km^2) was located within protected areas but the rest were largely located outside of protected areas (Fig. 4, bottom). This habitat patch covered only 14.4% of the current protected areas in Qom province. The overlapped hotspots were 35.67 km^2 in protected areas.

Discussion and conclusions

In this study, we chose reptiles of Qom province as a group of poorly known vertebrate species in Iran to detect areas with the highest priorities for conservation as biodiversity hotspots using two different methods (i.e., species richness and threatened species). Elevation was the most important contributor to habitat suitability maps for most species in this study, and land cover, NDVI, and distance from roads were among other important factors. Response curves illustrated dependence of two species on agricultural lands and vegetation. Our results showed that hotspots of species richness and suitable habitats of threatened species were relatively related and overlapped in more than half of their areas. The main biodiversity hotspots were located in the south of the province and the northeast of the city of Qom.

Ebrahimi et al. (2013) reported that elevation was the most important factor for distribution of 15 species of lizards in Qom province, and our MaxEnt models confirmed their results. Elevation affects temperature (Beier et al. 2007), which is the most vital factor for reptiles as ectothermic animals (Ananjeva et al. 2015; Buckley and Jetz 2010; Hosseinzadeh et al. 2014; Luo et al. 2012; Santos et al. 2009). Elevation also determines the amount and form of precipitation (i.e., rain or snow) (Beier et al. 2007), which affect reptiles' distribution (Fattahi et al. 2014; Hosseinian Yousefkhani et al. 2013; Hosseinzadeh et al. 2017). Land cover and NDVI are related to productivity, food, and cover (Beier et al. 2007; Oraie et al. 2015). NDVI can affect reptiles' diversity; an increase in the density of vegetation increases biodiversity (Hosseinzadeh et al. 2014; Luo et al. 2012). Finally, distance from roads was related to human disturbance (Baxter-Gilbert et al.

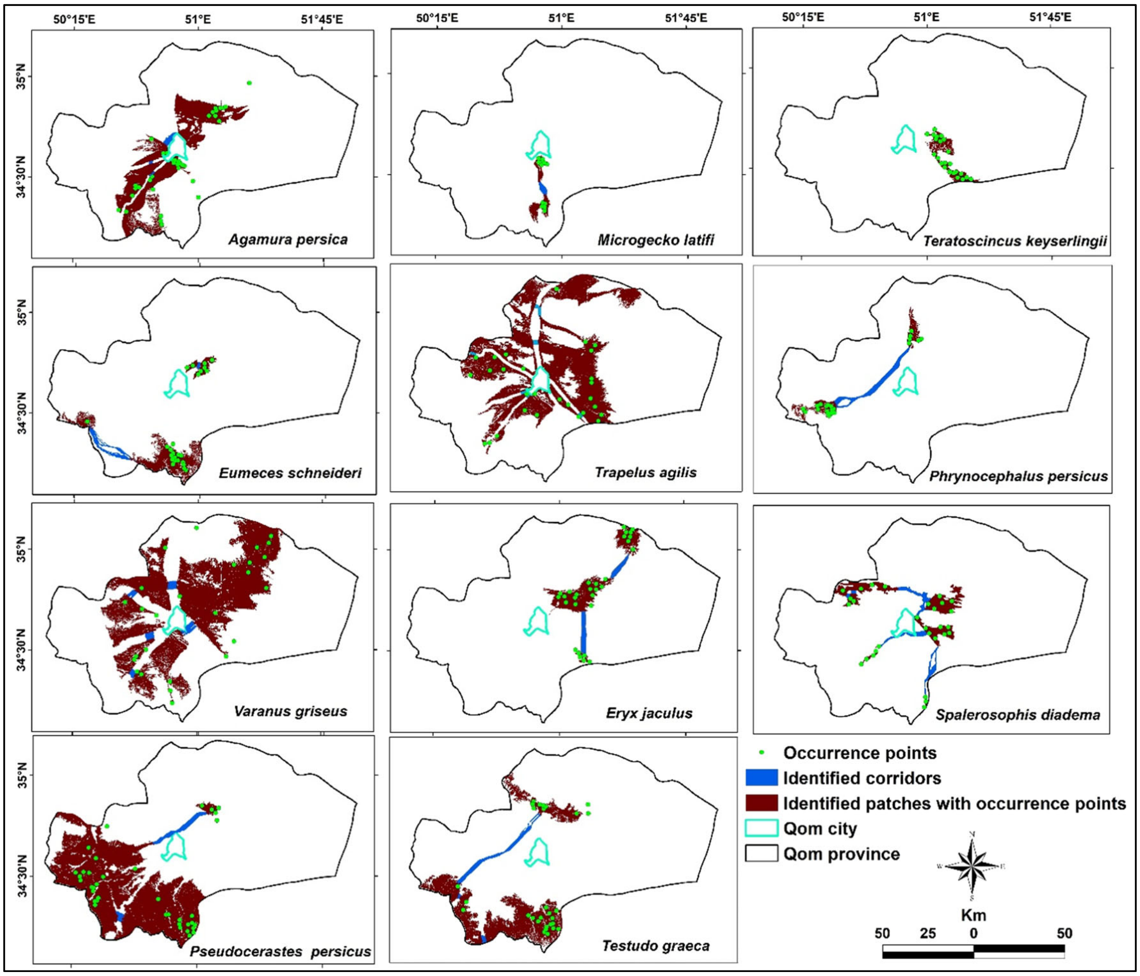

Fig. 3 Identified least-cost corridors among habitat patches for the 11 reptile species in Qom province, central Iran, using MaxEnt and CorridorDesigner

2015; Beier et al. 2008; Mohammadi et al. 2018). Roads threaten reptiles via road mortality or isolation of populations (Baxter-Gilbert et al. 2015; Holderegger and Giulio 2010). *Spalerosophis diadema* was observed near human settlements and agricultural lands (Yadollahvandmiandoab et al. 2018), and *Eumeces schneideri* preferred to hide under the soil near roots of vegetation in areas with relatively high diversity of flora; thus, vegetation is vital for its survival (Mozaffari et al. 2014).

We detected only two confirmed small patches with occurrence points of *Microgecko latifi*. Other patches of suitable habitats with no occurrence points should be investigated in the future. This endemic species (Anderson 1999; Mirghazanfari 2013) was recently discovered in Qom province and has not been reported in previous studies (e.g., Ebrahimi et al. 2013; Mozaffari et al. 2014). *Phrynocephalus persicus* is a threatened species and is under significant pressure, particularly due to habitat fragmentation (Anderson et al. 2009). In our study, HSM of this species in Qom province confirmed reports of Anderson et al. (2009) (Fig. 2). Only two habitat patches with occurrence points were detected for this species, and other suitable habitats should be further investigated in the future. Although *Teratoscincus keyserlingii* had relatively vast suitable habitats in Qom province (Fig. 2), we only detected one patch with occurrence points and hence no corridors were designed for this species (Fig. 3). This species has occurred exclusively in the southeast of Qom province and could be considered as the most isolated species among others in this province.

In this study, we could not assess all 38 reptile species in the study area because of the size of our study area and budget limitations. Therefore, we tried to cover species from different families. Selected species occupied different habitats, from plains to mountains, and can represent other reptile species in the study area. Also, our occurrence points were collected during 3 years which might not seem sufficient but the team sampled all habitat types during this 3-year period. The small number of occurrence points for each reptile species is another limitation which we tried to address by changing the default parameters of MaxEnt to make adjustments for the small sample size. Finally, due to the fine scale of this study (i.e., cell size of 30 m), use of climate data (i.e., WorldClim with cell size $\geq$ 1 km) was not possible. Instead, we used elevation as a representative of temperature and precipitation.

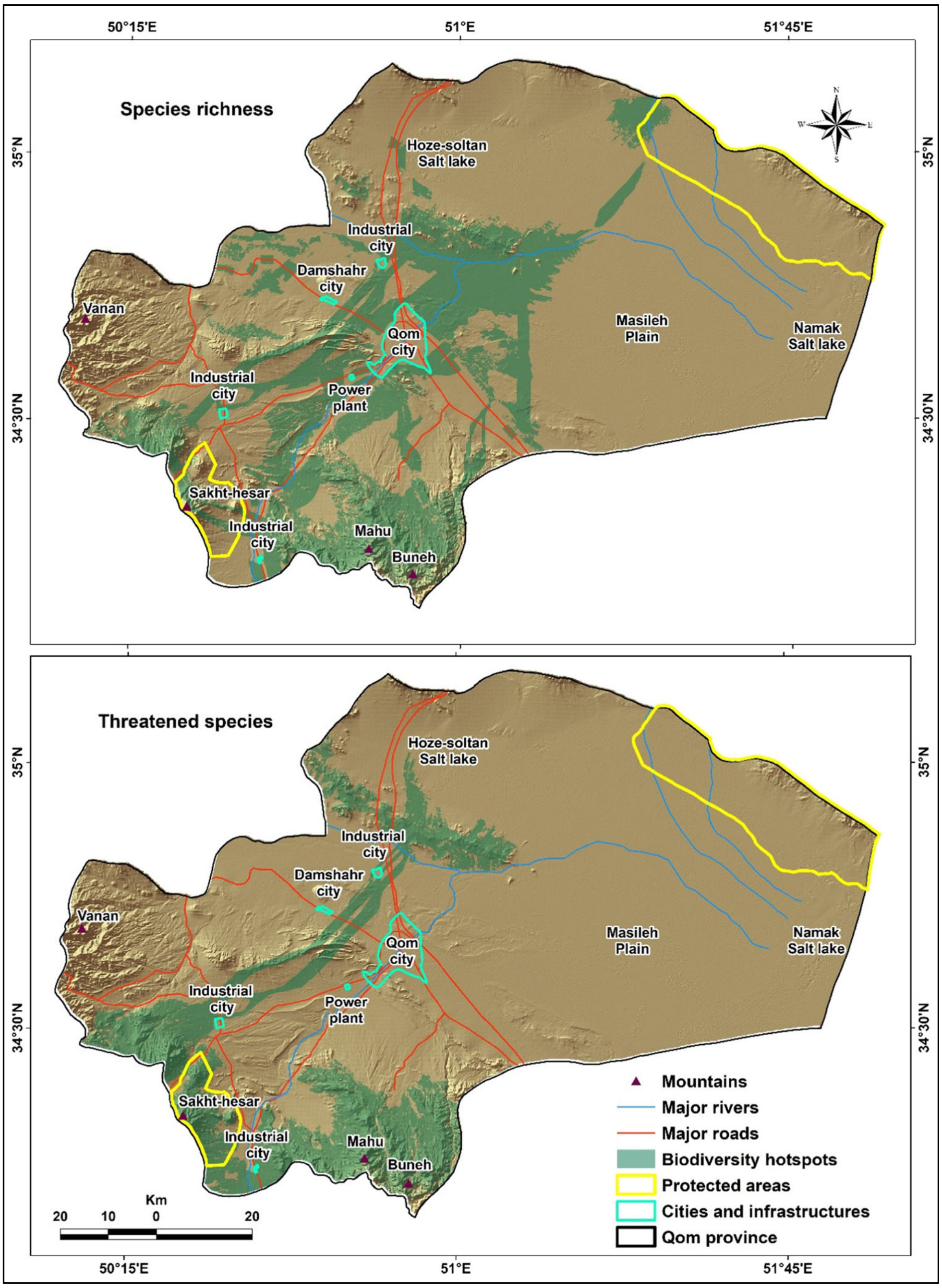

Fig. 4 Biodiversity hotspots of species richness (habitat patches and corridors) for the 11 reptile species (top) and the two threatened species (bottom) in Qom province, central Iran

Keeley et al. (2017) introduced habitat suitability as a poor proxy for resistance in their study on connectivity of a forest-dependent species. Habitat suitability maps are commonly used as a proxy for resistance maps in connectivity modeling as it is assumed that animals select suitable habitats to move across the landscape. Since it is known that animals may be forced to move through unsuitable areas such as paved roads, rivers, etc., this claim needs further support (Beier et al. 2007). Most of our 11 reptile species preferred several cover types (Fig. S1) which helped them move more easily between patches compared to species that depend on a single cover type. In addition, unsuitable habitats may exist in our least-cost corridors, and roads and rivers may cross corridor polygons. In this case, animals prefer to move across these dangerous areas quickly and spend more time in suitable areas as stopover patches (Almasieh et al. 2016).

Regarding the congruence between hotspots of species richness and hotspots for threatened species, Garcia (2006) obtained similar results for herpetofauna in Mexico. However, some of the previous studies such as Pascual et al. (2011) and Orme et al. (2005) reported little overlap between these two types of hotspots in the Iberian Peninsula and the world, respectively. In our study, general patterns for the two biodiversity hotspots were similar (Fig. 4). Garcia (2006) and Pascual et al. (2011) obtained similar results in their study area (i.e., general patterns for the two types of biodiversity hotspots).

Protected areas cover 10.12% of Iran as a whole (Kolahi et al. 2012), but this number is 8.1% in Qom province. Farashi and Shariati (2017) discovered that current Iranian protected areas cover only 10% of the biodiversity hotspots obtained in their study. Our study demonstrated that only 2.7% of biodiversity hotspots of species richness and 8.4% of biodiversity hotspots of threatened species in Qom province were protected by the DoE, which is lower than the results obtained by Farashi and Shariati (2017). Also, Chefaoui et al. (2018) stated that about 27% of occurrence points of a rare reptile species are covered by protected areas in Iran. In similar studies, Pascual et al. (2011) expressed that 5.2% of hotspots of species richness for vertebrates are covered by protected areas in the Iberian Peninsula (i.e., Spain and Portugal), and Venter et al. (2014) reported that this number was 15% for threatened vertebrates in the world.

Protected areas are known mainly for their ability to conserve species diversity (Brooks et al. 2004). Spatial data is also essential for species conservation, particularly on fine scales (Fishpool and Evans 2001). Using relevant environmental variables and occurrence points of lesser-known species, we can predict suitable habitats of species. These data are vital for detecting biodiversity priorities (Ferrier et al. 2002). With comprehensive spatial data on species distribution, protected areas can be chosen more logically (Brooks et al. 2004). Protected areas have been created for several goals, such as nature and ecosystem services, wildlife conservation, and ecotourism (Duran et al. 2013; Xu et al. 2017). However, the primary purpose of protected areas is protection of local to regional biodiversity, especially threatened species (Geldmann et al. 2013; Hoffmann et al. 2018) against the negative effects of human activities (González-Maya et al. 2015). Numerous studies on conservation gaps have revealed that there is little congruence between biodiversity and protected areas (Rodrigues et al. 2004).

Iran initiated its conservation efforts in the 1950s (Makhdoum 2008), and from 1975 to 2018, the number of protected areas has increased from 18 to 282 (DoE 2019; Farashi et al. 2017). Similar to other countries, Iran intends to increase the number and area of its protected areas (Almasieh et al. 2016; Makhdoum 2008). In the establishment of new protected areas, the focus of the DoE should shift towards biodiversity hotspots. Generally, in Qom province, the status of conservation is far worse than that in other parts of Iran, both in terms of the area of protected areas and the congruence of biodiversity hotspots with protected areas. This problem has arisen because parts of the two protected areas located within Qom province near the eastern and western borders (Fig. 4) are managed by the DoE of the neighboring provinces. Qom province needs new protected areas for conservation of biodiversity; thus, hotspots of reptile biodiversity introduced in this study should be taken into consideration by environmental managers of the province.

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Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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