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Research Article

Modelling habitat suitability of the Himalayan monal (*Lophophorus impejanus*) and its connectivity in the Himalayas

Suraj Baral[1*]

[1] Amrit Science Campus, Tribhuvan University, Kathmandu, Nepal
* **Correspondence:** baral.hector@gmail.com

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Abstract

The Himalayan monal *Lophophorus impejanus* is a montane bird exhibiting a seasonal migration to avoid harsh winter. However, the knowledge of the suitable habitat and level of connectivity across the range for the species is not available. To close this knowledge gap relevant for the species' conservation, species distribution modelling with presence-only data and relevant environmental variables was used to determine the range-wide distribution of the species. The distribution of the species is mainly constrained by habitat and climatic variables. The connectivity of the species was modeled using the distribution model output. The study presented a currently contiguous area of suitable habitat available for the species that are well connected with evidence of metapopulation in the range edges. The study also found that the current network of protected areas is not sufficient to ensure the connectivity of the species. Conservation of the currently suitable habitat is necessary to ensure the species is conserved.

Keywords: Ecological niche modelling; Maxent; National bird; Patch importance; Link importance

1 | Introduction

The Himalayan monal (*Lophophorous impejanus*; Phasianidae; Galliformes; hereafter HM) inhabits forests and grasslands at elevations between approximately 2000–4500 m in Afghanistan, Pakistan, India, Nepal, Bhutan, China, and Myanmar (Del Hoyo et al. 1994; Grimmet et al. 2016). Altitudinal migrations, to avoid harsh winter conditions in highly seasonal climates, have been reported (DNPWC & DFSC 2018). While threats, including poaching, forest fires, habitat encroachment by livestock, and climate change, continue to cause population declines and habitat fragmentation throughout its range (DNPWC & DFSC 2018; Fuller & Garson 2000), it continues to be listed as Least Concern as it does not yet meet the criteria of any threat category (Birdlife International 2016).

Quantification of habitat quality within the HM range is one of the first prerequisites for the implementation of an evidence-based conservation measure. However, the exact quantification of habitat quality needs demographic and population parameters along with the response of the species to a certain environmental variable (Thuiller & Munkemuller 2009), which is lacking for the species. Correlative habitat suitability models (HSM; Thuiller & Munkemuller 2009) can be used as an alternative to determine the quality of the habitat available for the species and identify areas of conservation concern. While attempts to identify the suitable habitat for HM has been done, these studies were either limited to a small part of a country (Rai et al. 2020), an ecoregion (Chettri et al. 2021), or used as a proxy for other species (Dunn et al. 2015) with no specific conservation implementation. The present study intends to identify suitable habitats and the degree of connectivity of HM with the objectives specifically to a. determine the habitat suitability of HM across the Himalayas, b. identify important variables that determine the habitat suitability, and, c. quantify the degree of connectivity of the habitat cores as identified from the habitat suitability model and protected area network in the Himalayas.

2 | Materials and methods

2.1 | Study area

The study area encompasses an area of approximately 141,292 sq. km of the Himalayan region with an altitudinal range between 85 m asl to above 7000 m. It consists of the mountainous area of Myanmar, India, Bhutan, China, Nepal, and Pakistan ranging between 71°19' - 98°34' E and 26°28' - 35°34' N.

2.2 | Occurrence data and environmental variables

All the occurrence data used to build the models were retrieved from the GBIF website. All the direct observation and museum specimen datasets from eBird Observation Datasheet and GalliForm: Galliformes occurrence records (GBIF 2021) were used. Occurrence data were removed if the coordinate uncertainty was >5 km. The data points that were between 1500–5000 m which equals the 500 m buffer to the known altitudinal limits of the species (2000–4500 m; Birdlife International, 2016) were added to reduce positional uncertainty. Furthermore, all the duplicated presence points were removed and a bias file using the Gaussian Kernel Density method was created using the *dismo* package in R to reduce the bias in the observations (Boria et al. 2014). A total of 3681 geo-referenced coordinates were retrieved, which was reduced to a final set of 252 unique, geo-referenced presence points available for the analysis.

A candidate set of environment variables that are likely to contribute to the distribution of HM were collected which included bioclimatic variables, habitat-related variables, and topographic variables. All the bioclimatic variables and elevation data with a resolution of 2.5 minutes were retrieved from CHELSA Climatology Database (Karger et al. 2017). The elevational data was used to compute the three topographic variables used for the study- slope, eastness, and northness of the mountain. Net Primary Productivity and Potential Evapotranspiration were used as variables related to productivity. Additionally, distance and proportion of forest, grassland, and a mosaic of grassland and forest as habitat-related variables were used which might affect the distribution of the species. All the presence data and environmental variables were reprojected to Albers Equal Area Conical Projection as the projected coordinate system is suitable to be used in the Himalayan region Multicollinearity between all the variables were checked before proceeding with model training. The Pearson correlation coefficient was used to estimate the correlation between the variables. Finally, 16 environmental variables of which five bioclimatic variables, three topographical variables, and eight habitat-related variables were selected (Table 1, Fig. S1) that were considered uncorrelated (r>|0.75|).

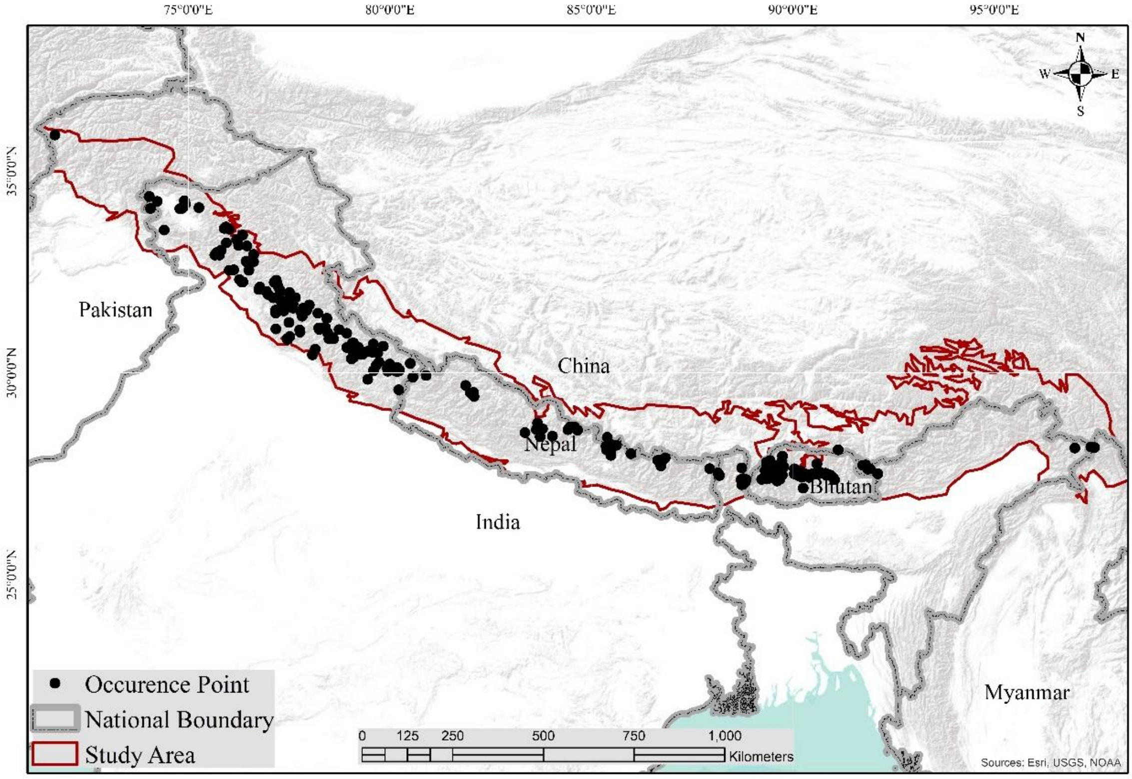

Figure 1. The presence points used for model building, the species range, and the study area

Table 1. Final candidate set of environmental variables selected for the model building.

Variable	Meaning of the Variable	Source
Bio 8	Mean temperature of the wettest quarter	CHELSA Climatology
Bio 11	Mean Temperature of the warmest quarter	CHELSA Climatology
Bio 14	Precipitation of the driest month	CHELSA Climatology
Bio 15	Precipitation seasonality	CHELSA Climatology
Bio 18	Precipitation of warmest quarter	CHELSA Climatology
Slope	Slope of the mountain	SRTM
Eastness	Position of aspect with respect to the East	Calculated From SRTM
Northness	Position of aspect with respect to the North	Calculated From SRTM
NPP	Net Primary Productivity	MODIS
PET	Potential Evapotranspiration	CGAIRCSI
DIST_ECOTONE	Distance from Mosaic vegetation between cropand, grassland and forest	MODIS Landcover Data
DIST_FOREST	Distance from forest (canopy cover >60% and height >2m)	MODIS Landcover Data
DIST_GRASS	Distance to grassland	MODIS Landcover Data
PROP_EDGE	%age of mosaic vegetation in a 3x3 pixels moving window	MODIS Landcover Data
PROP_FOREST	%age of forest in a 3x3 pixels moving window	MODIS Landcover Data
PROP_GRASS	%age of grassland in a 3x3 pixels moving window	MODIS Landcover Data

2.3 | Habitat suitability modelling

The final set of variables (Table 1) was used to train the suitability model. Maximum Entropy Model (Maxent; Phillips et. al. 2006) was used to predict the habitat suitability of the species. The selected model is suitable for presence-only data, has superior predictive power in comparison to other distribution models (Elith et al. 2006; Wisz et al. 2008), and can handle the non-linear relationship between predictors and response variables (Elith et al. 2006).Twenty replicates were ran following Bradsworth et al (2017) for each model using 60% of the available presence points and 2500 background points obtained from the bias file. The remaining presence locations were used for validating the model where True Skill Statistics (TSS; Allouche et al. 2006) and Area of the curve (AUC) under Receiving Operating Curve (ROC, Fielding & Bell 1997) were used. All the models were run in R (R Core team 2021) using the package *sdm* (Naimi & Araujo 2016). Finally, the continuous suitability values were converted into presence and absence using the threshold that maximizes the TSS (Liu et al. 2016). Before running the final model, the regularization multiplier and features in the R environment were fine-tuned using ENMeval 2.0 (Kass et al. 2021). A combination of linear, quadratic, or hinge features with a regularization multiplier ranging from one to five were tested to determine the optimal model to be used for the final run. Delta AICc was used as the criteria for the determination of the optimal model with the ΔAICc value of zero being the best model.

The correlation test available in the *sdm* package (Naimi & Araújo 2016) was used to determine the importance of each variable in each model. The test is performed by randomly permuting the variable under investigation; the correlation between the predicted value and permuted value is calculated. The higher the correlation between the values, the lower is the variable importance; as the permutation affects the prediction (Naimi & Araújo 2016; Thuiller et al. 2009). The measure of variable importance is then expressed as "1-correlation" (Thuiller et al. 2009). The variable importance was calculated from the mean variable importance of all the models pooled.

2.4 | Quantification of landscape and protected area connectivity

Graph-theoretic connectivity analysis was used to quantify the level of connectivity of the landscape and the network of protected areas for the species. Particularly, the total number of components in the landscape and the integral index of connectivity (Pascual-Hortal & Saura 2006) were used to determine the level of connectivity. To define the core area or habitat nodes, the habitat suitability score above 0.5 was used from the obtained habitat suitability model. The available shapefiles of protected areas for the region were used, the suitable habitat core within the protected areas was clipped, and the habitat node was used to quantify the level of connectivity of protected areas. The Euclidean distance between the habitat core or protected areas was used as the edge of the graph for the connectivity analysis for both cases. As the connectivity analysis requires a threshold distance for the connectivity, a distance of 8 km-the threshold based on the recorded migration distance of a sympatric pheasant, Satyr Tragopan (*Tragopan satyra*, Norbu et al., 2013) was used.

3 | Results

3.1 | Model performance and influencing variables

All the model runs (n=20) performed very well (AUC>0.8) to predict the distribution. The average AUC of the model was found to be 0.83 (SD=0.016), while the average TSS was 0.56 (SD=0.03). Because all the models present a very good fit for the prediction and did not present a large difference in the prediction ability, all the models were used for the ensemble. The relative variable importance for the distribution is given in Fig. 2. The measure of variable importance showed the climatic variable temperature of the coldest quarter to be the most important variable to determine the

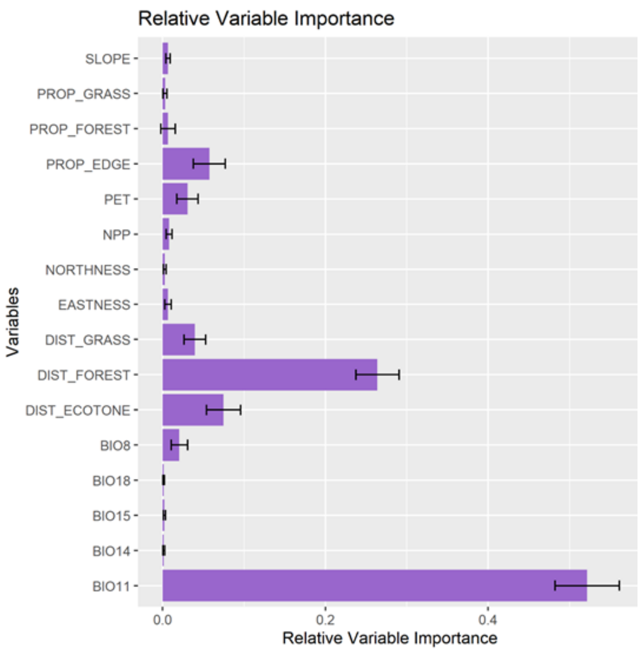

Figure 2. Relative variable importance of all the modelled candidate set of predictors to define the distribution of *L. impejanus.*

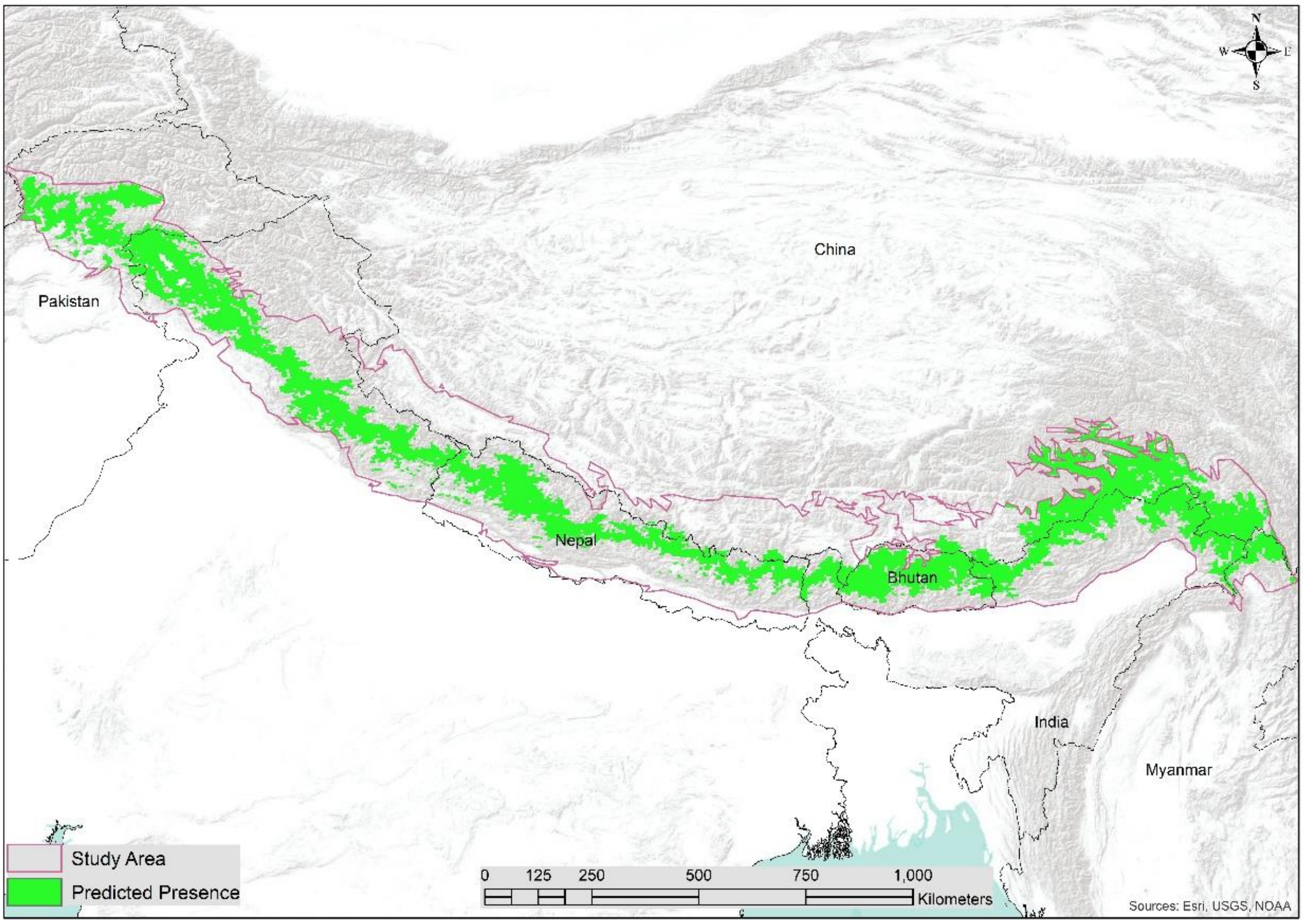

Figure 3. The habitat suitability model of *Lophophorus impejanus* as predicted by the ensemble model. The predicted presence only is shown in the model after using the threshold to maximize the TSS.

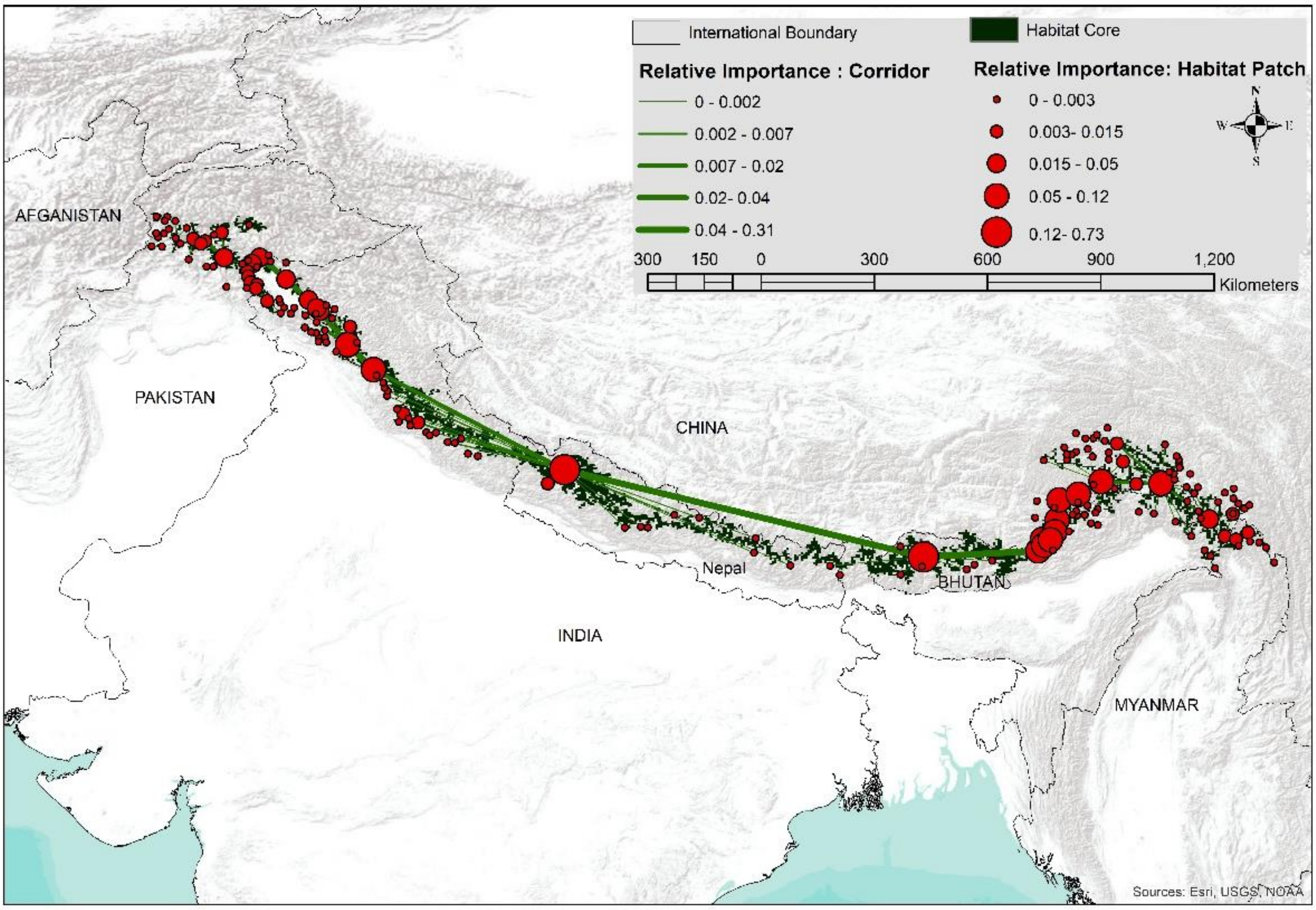

Figure 4. Topological map of the relative importance of habitat core and corridors for connectivity

distribution across the range with a 52% contribution to the model. The major variables that contributed to the distribution came under the habitat variables category with distance to the forest (26.4%), Distance to the edge (7.5%), and proportion of the distance to edge (5.7%) occupying the next top three positions in the model. All of the topographic variables, however, had only very little contribution (Fig. 2).

Of the total suitable habitat available, India constituted the largest suitable habitat followed by China and Nepal. All three countries jointly contributed to approximately 79% of the total habitat available in the Himalayas (Table 2, Fig. 3). On the contrary, Myanmar had the least suitable area. Within a country, Bhutan had the highest proportion of suitable habitat with 56% of its total area suitable. Nepal followed next with 27% of its area classified as suitable. China held the largest area suitable within the protected area network followed by Nepal and Bhutan. Pakistan had the least representation of suitable habitat within the protected area network (Table 2).

3.2 | Landscape and protected area connectivity

The connectivity analysis showed the presence of multiple components (24) for the habitat core (Fig. 4). The independent components for the habitat core were concentrated towards the eastern and western limit of the distribution with a single component forming the central region of the core habitat. The connectivity analysis also showed that the central region had a higher contribution for the overall connectivity for both habitat patches and corridors while the patches and corridors at the extreme showed relatively low importance. The existing network of the protected area also showed the presence of multiple components (42) with only a few protected areas in China, Bhutan, and Nepal showing high connectivity (Fig. 5).

4 | Discussion

The study presents the first regional assessment of the distribution of the HM across the Himalayas. Although earlier attempts to model the regional habitat suitability has been done (Dunn et al. 2015, Dunn et al. 2016), these studies were either used as a proxy for other species

Table 2. Country-wise distribution of predicted suitable habitat estimated by the ensemble model

Country	% suitable habitat in study area (in the country)	% suitable habitat in protected area network
Bhutan	9 (58)	20
China	22 (0.5)	31
India	39 (3)	17
Myanmar	2 (0.7)	12
Nepal	18 (27)	21
Pakistan	10 (3)	0.1

(Dunn et al. 2015) or not directly used to inform the distributional status in the Himalaya (Dunn et al. 2016). Still, other modeling exercises performed were performed on a small spatial scale (Rai et al. 2020, Chettri et al. 2021). This study presents the regional habitat connectivity and quantifies the connectivity between protected area networks for the first time for HM. Since connectivity for the species has not yet been modeled in other parts of the range, this study presents a novel finding which can serve as an important decision-making tool in the conservation as well as protected area management.

The model presented the temperature of the coldest quarter as the most important variable to determine its distribution in the region. Indeed, the Himalayan region is characterized by the abrupt change in altitude causing the climate to vary within a short distance (Bach & Price 2013). This variation in climatic conditions has made the region one of the major biodiversity hotspots in the world (Myers et al. 2000). The HM as a mountainous species (DNPWC & DFSC 2018) might be limited by the temperature extremes prevalent across the North-South direction of the region. Although the birds can tolerate a range of climatic extremes with the help of physiological processes (Ruskannen et al. 2021, Root 1988), the processes gradually diminish as the physiological threshold is reached (Root 1988) above which the species cannot exist. This study found that the HM is mainly limited by the extremes in temperature. Shrinivasan et al. (2018) found that the temperature

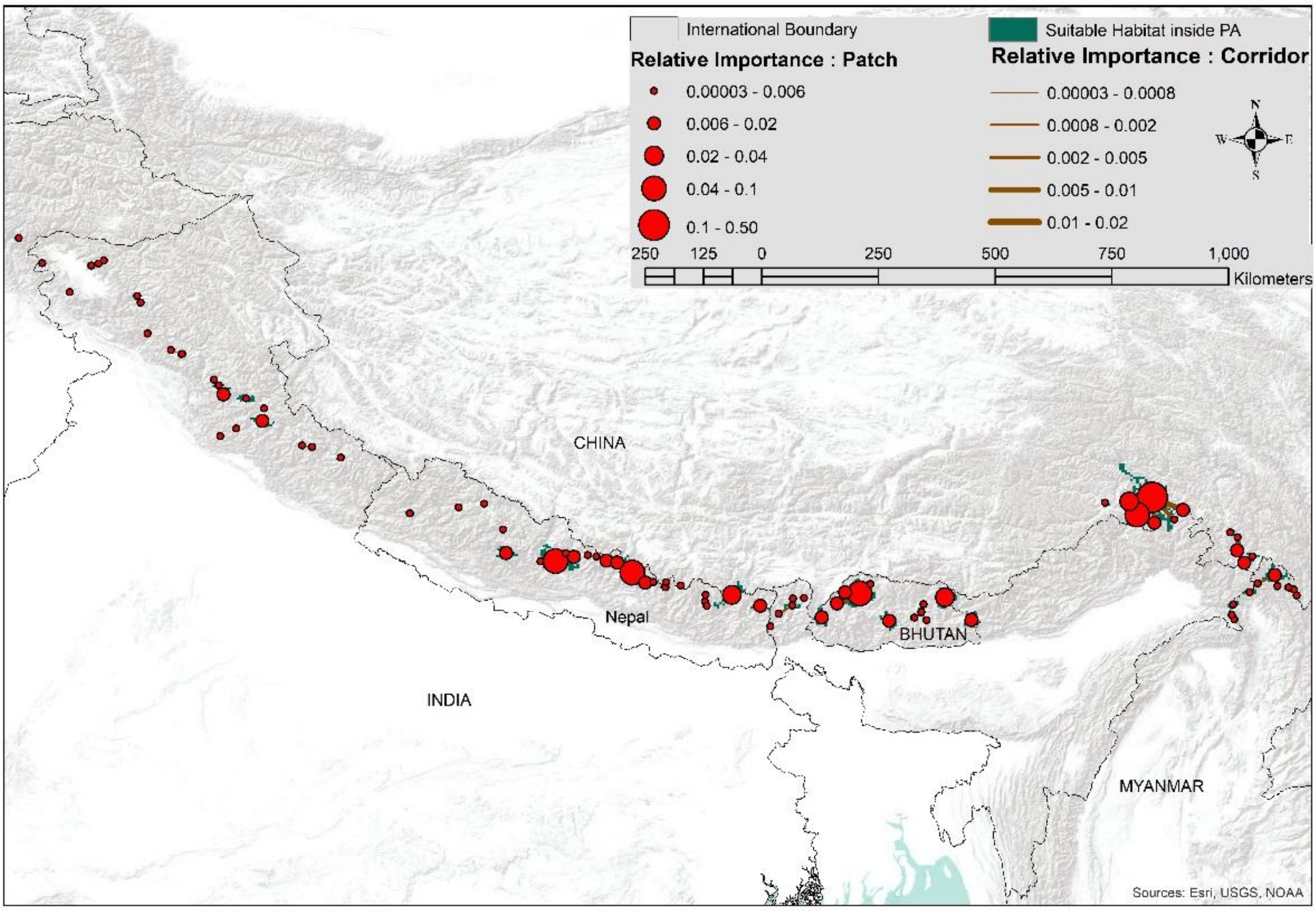

Figure 5. Topological map of the relative importance of protected area and corridors for connectivity

variability in the Himalayan region was one of the major reasons to limit the range of birds. Similarly, Root (1988) found that the extreme climate influences the metabolism in passerine birds in their northern boundaries which consequently limited the distribution of the passerines. HM might experience similar physiological distress due to the extreme temperatures which might have limited the distribution of the species. The altitudinal migration of the HM (DNPWC & DFSC 2018) can also be considered as proof that it uses behavioral mechanisms to escape the temperature extremes.

The vegetation or habitat-related variables were also found to have a significant impact on the distribution. Particularly the importance of distance to forest, distance to forest-grassland mosaic indicates the preference of the species around the forest-grassland edge. Bird diversity is shown to be higher in areas with higher spatial heterogeneity (Maskell et al. 2019). Moreover, HM requires both the habitat types as it feeds on open grassland (Soldatini et al. 2009) and shelters in forests (DNPWC & DFSC 2018). These reasons might explain the preference of grassland and forest mosaics by HM.

The habitat connectivity analysis showed that most of the habitat is presently connected for HM but the greater number of components suggest the existence of metapopulation (Minor & Urban 2008) in these regions. The visual analysis implies the naturally fragmented habitat in the range extremes with very little to no connectivity according to the current knowledge on the dispersal of the species. While the naturally fragmented habitats may reduce the risk of disease spread (McCallum & Dobson 2002), the cost of reduced gene flow is much higher for the persistence of the population. Likely, the range limits of the HM are determined by the effects of reduced gene flow rather than the climatic variables. To persist the genetic diversity of these metapopulations, human aided dispersal and careful planning on infrastructure development need to be done so as not to further increase the already fragmented habitat. China, Nepal, India, and Bhutan can be considered as the core area for the distribution of the HM. Therefore, these countries will have the most important role in determining it's the fate. While the current status of the habitat might be undisturbed at most of the parts (Das et al. 2017), encroachment of the habitat might soon be seen as the human population increases and so does the need for food to feed the growing population (Xu et al. 2019).

The connectivity analysis of the protected area network shows that only a little part of the total suitable area is represented in the network. Also, the network will not be able to connect across the region thus creating a dire future for the species if only protected areas are considered. Thus, the conservation planning well before the driving forces of habitat fragmentation takes a toll on the species might be much more successful. For the coexistence of humans and wildlife in these frontiers, a nature-friendly adaptation to the settlement and agriculture might need to be planned. These nature-friendly ways of living have proven to be successful for the conservation of wildlife as evidenced from across the world (Batáry et al. 2015; Jokimaki et al. 2018). The population of the HM along with other species with similar habitat requirements can be connected using these nature-friendly means of agriculture or urban planning.

Although the core area might be important as a source to the peripheral population, the peripheral areas within China, Myanmar, Pakistan, and Afghanistan still will have the challenge to conserve the HM in the face of ongoing global warming. The peripheral populations are adapted to living at the physiological extremes of the species and can cope with climate change (MacDonald et al. 2017). These countries will have an important role to ensure that these populations are well connected to the core population as well as preparing for the potential habitat that the species can move to.

Despite the potential a rapid assessment has on the conservation of a low threat risk species, the model expressed here is not without flaws and the responsible stakeholders must be prepared for adaptive conservation practices as the information builds up. The current study showed the habitat hugely impacts the distribution of the species. However, the mountainous regions are considered to be very sensitive to global warming (Xu et al. 2019). Along with the global climate change, the vegetation assemblages of the habitat are also expected to change (Salick et al. 2019). However, no particular study on the impact of climate change on the vegetation and its effect on the species is known. This might hinder the course of action for its conservation and warrants further study on the impact of climate change on the species and its habitat. The presence of locations with higher positional accuracy for the species was found to be limited across the region which required the use of coarse-resolution environmental predictors despite the availability of much finer data (Hijmans et al. 2005). Therefore, the studies aiming to determine the presence or absence of the species across the range might also contribute to building more accurate, fine-scale habitat suitability models. With the availability of demographics and population parameters, mechanistic models of habitat suitability or population viability analyses will further help to strengthen the information required for robust conservation planning. Furthermore, modelling the season distribution of the species and possible pathways, which is yet lacking, might also help to adopt suitable conservation measures.

5 | Conclusions

Although the present study may be a rapid assessment of a relatively less-studied species and does not possess a significant human-induced threat currently, it is concluded that the species across its range is exposed to various threats like fragmentation and climate change. The study presented the potential distribution of the species, status across the Himalayas, the current status of human-induced threats, and possible areas and ways of intervention. However, the study can be considered as a rapid assessment based on the best available data and additional data on the presence or absence, demographic and population parameters might help provide robust data to ensure the species is conserved before it's too late and hopefully the species is never listed in the species with high threat risk.

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Conflicts of interest

Author declares no conflict of interest.

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