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Vegetation Composition and Habitat Suitability Analysis of Common Mega Faunal Species in Biological Corridor 5, Southeast Bhutan

**Yenten Phuntsho, Ugyen Dorji, Sangay Dorjee, Choni Dorji, Lha Tshering, Dhan Bahadur Gurung,
Karma Lhundup, Yejay, Phuntsho Wangmo**

Ministry of Energy and Natural Resources, Department of Forests and Park Services, Thimphu, Bhutan College of
Natural Resources, Lobesa, Bhutan

ABSTRACT: The study on vegetation composition and habitat suitability in Biological Corridor 5, spanning 212 km² between Pemagatshel and Samdrup Jongkhar, aimed to assess vegetation and map habitats for key mega faunal species: Tiger, Gaur, and Elephant. This corridor links Royal Manas National Park (RMNP) and Jomotsangkha Wildlife Sanctuary (JWS). Using systematic sampling, 3 km x 3 km grids were established with 20 m x 20 m plots for trees and shrubs, and 2 m x 2 m plots for ground cover. A total of 181 plant species from 83 families were recorded, with tropical evergreen trees dominating (79.2%). Lauraceae and Urticaceae were the most common tree families. Ground cover included 49 species, mainly perennial herbs (44.76%). Canonical Correspondence Analysis indicated weak species-environment associations. Habitat suitability modelling showed high suitability for tiger (96.39%), elephant (98.94%), and gaur (98.34%). The findings suggest that this area is suitable to be part of Bhutan's protected area network.

KEYWORDS: Corridor, Elephant, Gaur, Habitat, Suitability modelling, Tiger.

I. INTRODUCTION

Forests are fundamental to life on Earth, offering vital ecosystem services such as air purification, climate regulation, water supply, and raw materials like timber, while also providing essential habitats for diverse wildlife species (Saara et al., 2003). The habitat serves as a place for animals to live and reproduce, and the availability of suitable habitat areas directly influences the survival and population continuity of species (Yarrow, 2009). Evaluating vegetation composition is a critical method for assessing habitat quality and identifying the impacts of both natural and anthropogenic disturbances (Rajpar & Zakaria, 2011). Even minor shifts in vegetation structure can significantly affect wildlife populations, highlighting the importance of habitat management in sustaining biodiversity (Janean et al., 1997).

Habitat Suitability Modelling (HSM) has gained prominence as a tool to predict suitable habitats for species of conservation concern, particularly as increasing human activities have led to habitat fragmentation and species decline (Morrison et al., 2006). In response, conservation measures such as protected areas and biological corridors have been implemented to preserve biodiversity and promote gene flow (Chape et al., 2005). Bhutan initiated the concept of biological corridors in 1999 to connect protected areas and facilitate wildlife movement (Nature Conservation Division, 2007). Reducing habitat loss and identifying suitable areas for wildlife are critical for conservation, especially as habitat structure and vegetation composition directly influence species abundance and distribution. Despite Bhutan's progress in establishing a network of biological corridors, detailed data on habitat suitability within these areas remain lacking. This study addresses that gap by analysing vegetation composition and modelling habitat suitability for key megafaunal species using GIS. The resulting maps, based on species-specific environmental preferences and verified through GPS-based field sightings, provide a scientific basis for future conservation planning and decision-making. This study specifically focuses on Biological Corridor 5 to evaluate its vegetation structure and map the habitat suitability for key megafaunal species.

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Biological corridors play a vital role in wildlife conservation by enabling species migration, interbreeding, and adaptation to changing environmental conditions. They serve as essential connectors between fragmented habitats, promoting gene flow, population movement, and the survival of threatened species (Walker & Craighead, 1997; Gilpin & Soule, 1991). The primary ecological function of these corridors is to maintain population persistence through connectivity, especially in landscapes fragmented by human or natural disturbances (Rosenberg et al., 1997). In Bhutan, twelve biological corridors were established in 1999 to connect protected areas, covering a total of 3,640 km². These corridors are part of the national protected area system and aim to reduce the risk of species extinction by enhancing wildlife mobility and diversity (Nature Conservation Division, 2007). Studies have shown that smaller patches linked to larger gene pools via corridors often support higher species richness than isolated larger areas (Harris & Scheck, 1991). Despite such initiatives, habitat fragmentation and loss continue to pose major global threats to biodiversity (Henle et al., 2004; Fahrig, 2003).

Habitat Suitability Modelling (HSM) has emerged as an important scientific tool for evaluating habitat quality and predicting species distribution based on environmental factors. HSM assigns suitability scores ranging from 0 (unsuitable) to 1 (optimal) and uses spatial and ecological data to model species–habitat relationships (Guisan et al., 2000; Eastman, 2006). As natural habitats face increasing pressure from climate change and human activity, HSM provides valuable insights for identifying potential habitat loss, prioritising conservation areas, and guiding ecological restoration efforts (Guisan & Zimmermann, 2000). In Bhutan, integrating HSM into conservation planning enhances the management of biological corridors and supports long-term strategies for biodiversity protection.

II. METHODOLOGY

The entire area of the biological corridor (figure 1) was divided into 3 x 3 km² using QGIS. In each grid, separate plots were laid out for vegetation survey and GPS coordinates of mega faunal species were recorded based on their evidence sighted. There were 22 grids laid out covering the entire corridor area, from which the vegetation cover of the area has been enumerated. Systematic sampling was used for collecting the data. Vegetation data in Biological Corridor 5 were collected between December 2019 and January 2020. Tree species with DBH ≥ 10 cm and height ≥ 1.3 m were measured in major plots, while saplings and herbaceous species were recorded in minor plots. Topographic variables such as altitude, aspect, and slope were documented using field instruments, and climatic factors like temperature and precipitation were derived using models by Dorji et al. (2016). A geospatial model using a fuzzy/weighted overlay technique was used to generate habitat suitability maps for common megafaunal species. Key variables such as land use, slope, aspect, and buffer zones were integrated, with ground truthing used to validate the maps by comparing them with GPS-recorded field evidence.

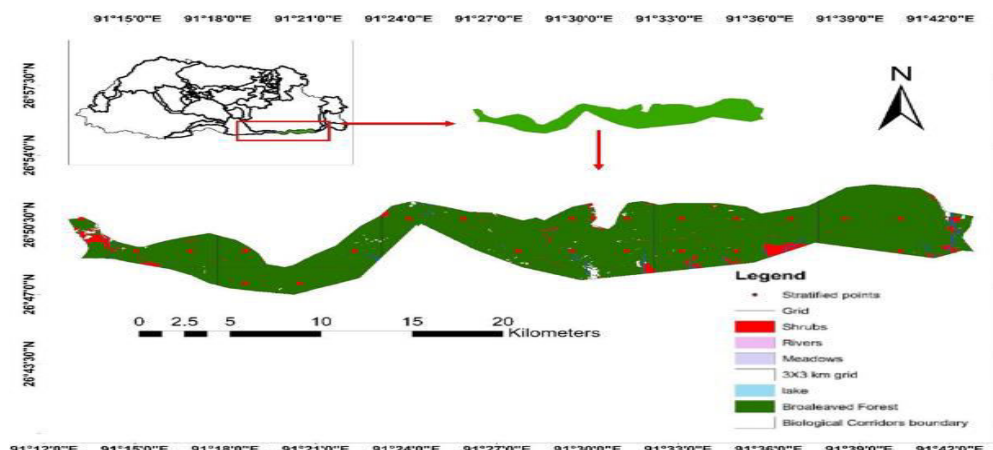


Figure 1. Study area map showing the grid stratification

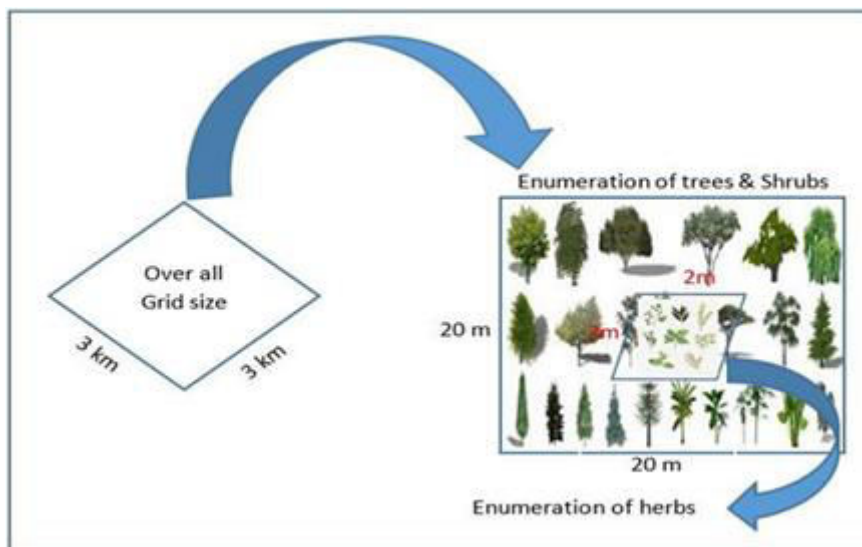


Figure 2. Survey Plots design

III. RESULT

A total of 181 plant species from 83 families were recorded in Biological Corridor 5 across 22 sampling plots (figure 2), comprising trees, shrubs, and ground herbs. Among these, 132 species belonged to 57 families of trees and shrubs, with the majority (79.2%) being tropical evergreen trees, followed by deciduous trees (13.8%), evergreen shrubs (5.2%), and deciduous shrubs (1.7%). Evergreen trees dominated most gewogs, except in Phuntshothang, which had a notable presence of deciduous trees. Dominant plant families included Lauraceae, Urticaceae, Euphorbiaceae, Leguminosae, Araliaceae, Anacardiaceae, and Apocynaceae. Additionally, four invasive species, *Chromolaena odorata*, *Ageratum conyzoides*, *Mikania micrantha*, and *Sida acuta*, were present, with *Chromolaena odorata* being the most prevalent.

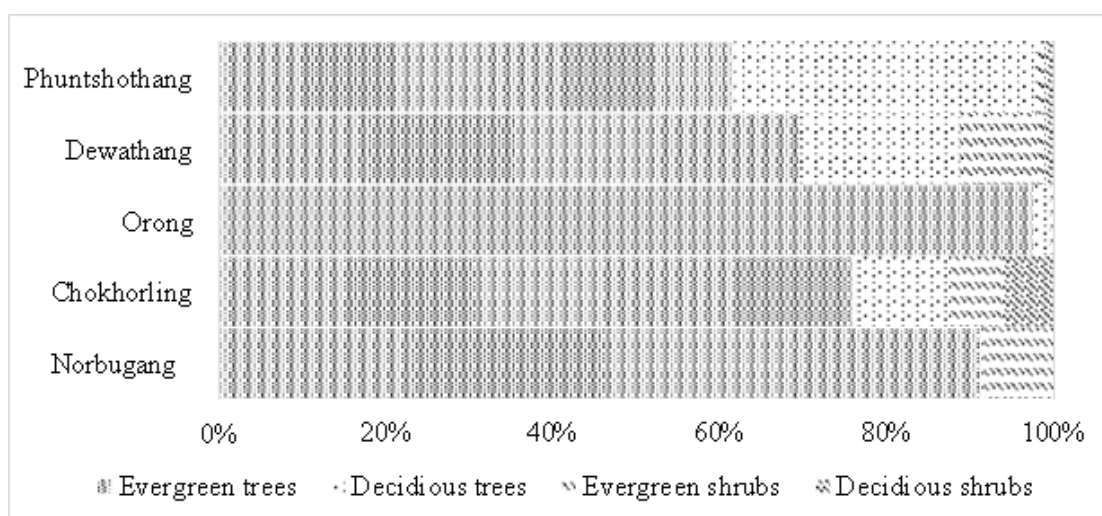


Figure 3. lifeform trees and shrubs composition using relative basal area (%)

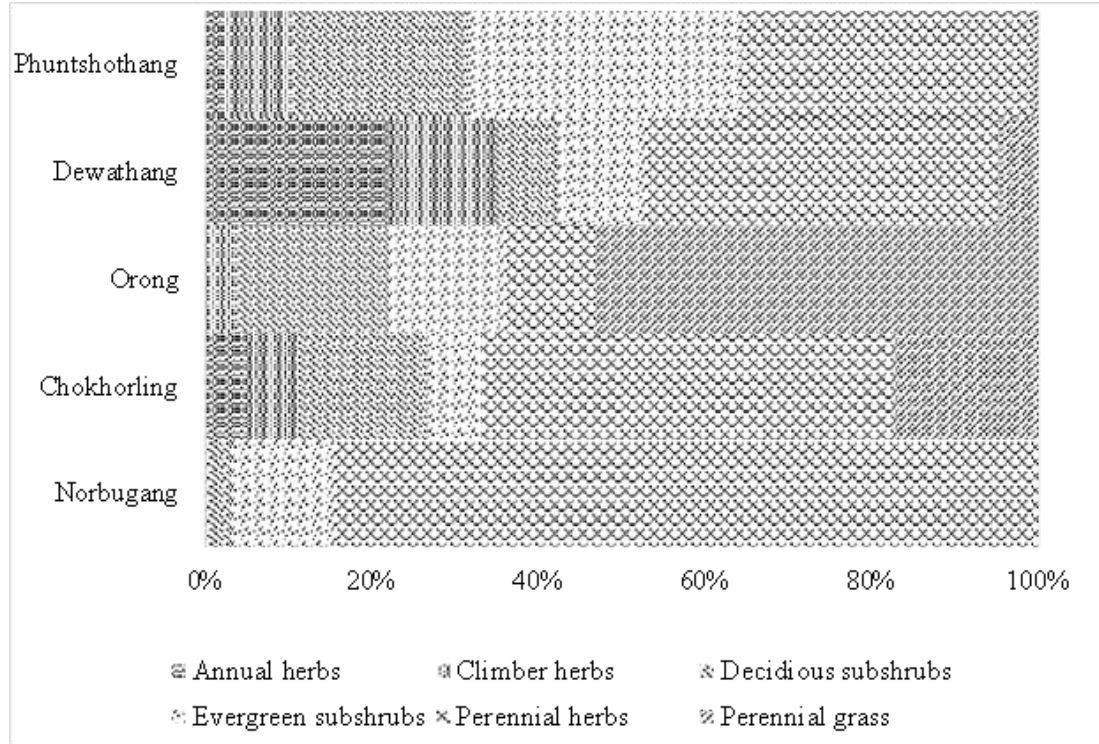


Figure 4. Lifeform understory composition using relative density (%)

The groundcover vegetation (figure 3) in Biological Corridor 5 includes 49 species from 26 families, with Compositae, Piperaceae, and Urticaceae among the most represented. Perennial herbs dominate the ground layer, accounting for 44.76% of the composition, while annual herbs are the least represented at 5.77%. These perennial herbs and ferns form the primary undergrowth in the broadleaved forest, consistent with patterns observed in similar ecosystems (Paoli et al., 2001).

Habitat suitability mapping using ArcGIS revealed a high potential for supporting mega faunal species within Biological Corridor 5, as most of the area shows minimal land use variation and is protected from human encroachment. The models, developed using species-specific habitat parameters and expert input, were validated through field GPS data. For tigers, 96.39% of the area was identified as highly suitable, with slope, forest type, and topography being key contributing factors. Moderate, least, and unsuitable zones accounted for only 1.11%, 0.32%, and 2.19% respectively. These findings align with results from similar GIS-based studies, though further research is needed on prey density for tigers (Karwariya et al., 2017).

The habitat suitability analysis (figure 5) for elephants categorised the corridor into suitable (98.94%) and unsuitable (1.05%) zones, with suitable habitats being those near water sources, far from roads, and rich in vegetation (Areendran et al., 2011). Similarly, for gaur, 98.34% of the area was found to be suitable, with preferences for regions abundant in tender leaves, grasses, and shrubs. Gaur also favours low-lying, less rugged terrain that facilitates movement (Imam & Kushwaha, 2013). These findings underscore the corridor's critical role in supporting large mammal species and highlight its value in conservation planning.

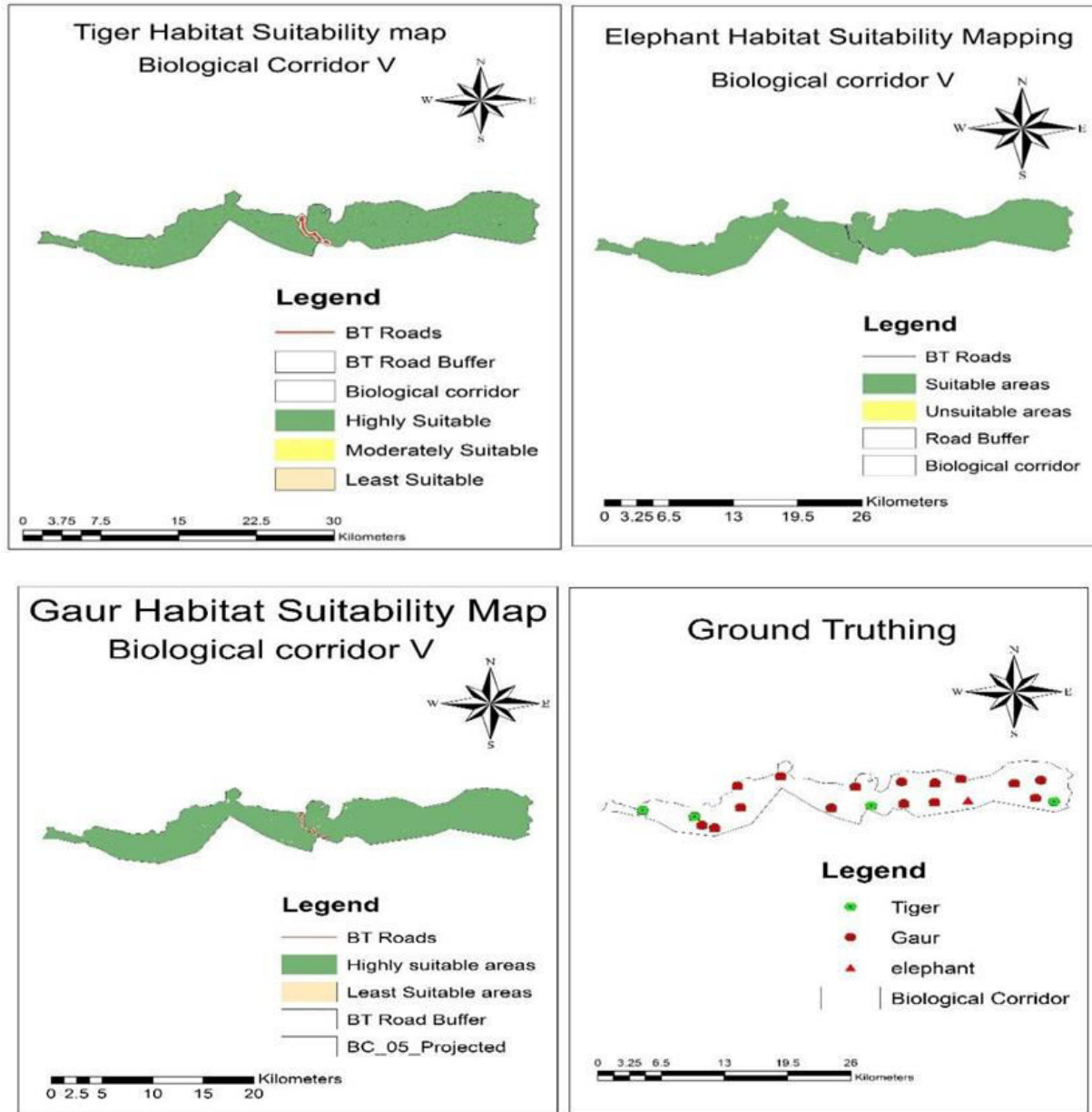


Figure 5. Habitat Suitability Mapping and Ground-Truthing of Mega-Faunal Species

IV. CONCLUSION

The study assessed the vegetation composition and diversity within Biological Corridor 5 through 22 sampling plots, recording 181 plant species from 71 families. Among these, 132 species of trees and shrubs were identified, predominantly tropical evergreen trees (79.2%), along with 49 groundcover species, where perennial herbs were most dominant. Lauraceae and Urticaceae emerged as the most common tree families. Canonical Correspondence Analysis indicated a weak relationship between species distribution and environmental variables.

Habitat suitability maps for tiger, elephant, and gaur were generated using ArcGIS, integrating species-specific habitat parameters. The analysis revealed that 96.39% of the area was highly suitable for tigers, 98.94% for elephants, and 98.34% for gaur. While the maps show strong potential for conservation, their accuracy may be limited by variable

selection. The findings support designating the corridor as part of the protected area network, with recommendations for future research on prey density to enhance habitat modelling precision.

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