A Geospatial informed Conservation Strategy for Sustainable Management of Dalbergia sissoo (Roxb.) Population in India amidst Climate Change and Pathogen Induced Mortality Stress

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Abstract

The natural population of *Dalbergia sissoo*, is declining due to biotic and abiotic stressors. Existing studies focus on pathogen-induced mortality in *D. sissoo*, but the impact of climate on habitat loss and population decline is limited. This study fills this gap by integrating climate change impacts and pathogen outbreaks to assess their combined influence on the distribution and survival of *D. sissoo*. Field assessments identified *Neofusicoccum solani* and *Ganoderma lucidum* as the predominant pathogens contributing to widespread mortality. Using MaxEnt, we evaluated habitat suitability across the Indian subcontinent under climate models IPSL-6A_LR and MIROC6A proxied through Shared Socioeconomic Pathways; SSP-126, 245, 370, 585. Presently, ~ 19% of the study area was found suitable for *D. sissoo* distribution, primarily concentrated in northern and eastern India. However, depending upon the climate scenario, projections for 2050 suggest a substantial reduction in habitat, limiting the current suitable range to ~5–16%, with a northward shift. Among bioclimatic variables, Bio_9 (mean temperature of driest quarter) contributed most to limiting the distribution of *D. sissoo*. We recommend a collaborative approach to assess pathogen risk and climate resilience into restoration planning and advocates for a combined *in-situ* and *ex-situ* conservation and sustainable management of *D. sissoo* population.

Keywords: Plant pathogen, Plant disease, Climate Change, Habitat Model, Climate resilient strategy

1. Introduction

The natural population of *Dalbergia sissoo* is declining across its native range and leading towards the verge of extinction (Shah et al., 2021; Ghazali et al., 2022). The existing body of literature points to this decline in *D. sissoo* population due to the dieback from fungal pathogen attacks (Mukhtar et al., 2015). The soil borne pathogens are major causative factors for plant diseases and losses (Mehta et al., 2014). A study by Wang et al. (2021) notes that soil born pathogens significantly compromise tree health.

Climate change has also been noted in recent studies as one of the major factors exacerbating forest fragmentation, range shifts and biodiversity loss (Smith et al., 2019; McNutt, 2013). The abrupt variation in the bioclimatic conditions has been associated with this habitat fragmentation, and species migration (Gan et al., 2024; Zindros et al., 2020). Anthropogenic stresses coupled with climate change have been deteriorating the long-term susceptibility of the *D. sissoo* population (Boisvert et al., 2022; Srivastava & Bharti, 2023).

Understanding species-specific habitat response to climate change is essential to plan its conservation and management strategies (Wilkening et al., 2019; Garamvölgyi & Hufnagel, 2013). However, a review of existing literature reveals the outbreaks of the pathogens in the decline of *D. sissoo* are over-debated (Dangwal et al., 2014), but the climate change impacts are not much concerned (Durrani et al., 2024). The current scenario calls for adopting an integrated approach that accounts for both biotic and abiotic stressors.

In this context, the present study offers a comprehensive assessment of *D. sissoo* distribution and mortality by integrating field-based pathogen examination with habitat modelling. We examined the spatial distribution, disease prevalence and regeneration condition of the *D. sissoo* population. Using MaxEnt, we simulated the future and present climatic scenarios of *D. sissoo* with regard to habitat suitability and determined the major bioclimatic constraints. The study aims at a climate-resilient conservation framework through three key objectives: 1. Study the current distribution range of the *D. sissoo* population. 2. Examine the occurrence of diseases in the *D.sissoo* population and their major causative factors, and 3. To model and investigate the potential suitable habitat range of *D. sissoo* population for the current and future climate change scenarios.

The findings of this study offer updated insights into the population status, health condition, and pathogen-induced mortality of *D. sissoo*, alongside projections of habitat suitability amidst climate change scenarios. The combination of ecological and climatic aspects helps the study to complement the existing knowledge of *D. sissoo* distribution patterns, as well as identify possible ecosystem service disturbances associated with the habitat fragmentation. These findings offer a strong background of evidence-based insights on the part of the forest managers and policy makers to design region-specific conservation and management strategies for the *D. sissoo* population.

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2. MATERIALS AND METHODS

2.1 Study Area

The study area exhibits remarkable diversity in climatic zones, topography, and socio-economic conditions (Fig. 1). The northern region, encompassing Jammu & Kashmir, Himachal Pradesh, and Uttarakhand, is dominated by the Himalayan ranges and serves as the source of major rivers. The Indo-Gangetic plains, ranging Uttar Pradesh, Bihar, and West Bengal, are enriched by the Ganges and its tributaries, supporting intensive agriculture. The western part encompassing Rajasthan features the Thar Desert and the Aravali ranges. Central India, including Madhya Pradesh, is marked by the Vindhya and Satpura ranges, while the Chotanagpur Plateau across Jharkhand and parts of Bihar and West Bengal is rich in minerals and forest cover. The deltaic zones of West Bengal, including the Sundarbans, a UNESCO World Heritage Site are biodiversity hotspots. Assam in the northeast is shaped by the Brahmaputra River system and flanked by the Eastern Himalayas and Meghalaya Plateau. This varied physiography significantly influences regional climate, biodiversity, and development patterns, making it ideal for comprehensive environmental research.

INSERT FIG 1 HERE

2.2. Species occurrence data and major factors causing disease in *D. sissoo* population

An extensive field survey was carried out across the entire study area to record the occurrence of *D. sissoo* distribution alongwith pathogens and other causative factors affecting *D. sissoo* population. Region-wise institutional teams were formed to collect the field data prevalence of *D. sissoo* population. To ensure uniformity in data collection, a structured data form was developed and disseminated across the research team.

2.3 Environmental variables

Bioclimatic variables (Bio1–Bio19) at a 30-arc second resolution for the present period were acquired from the WorldClim database (Fick and Hijmans, 2017). The dataset was pre-processed in QGIS, ensuring uniform spatial extent and resolution for analysis with Maxent 3.4.4 (Phillips et al., 2021). To ensure model accuracy and prevent overfitting, 11 bioclimatic variables were selected after eliminating highly correlated ones using the Pearson correlation coefficient, with a threshold of $r \geq 0.8$ (Tiwari et al., 2022).

2.4 **Modelling potential suitable habitat range of *D. sissoo***

We employed Maxent 3.4.4 to model the potential suitable habitat range of *D. sissoo* for the current and future climate change scenarios. Maxent due to ease of use, robustness, and accuracy is considered the most effective machine learning tool to study species habitat response to climate change (Kaky et al., 2020). Global climate models for IPSL-CM6A-LR and MIROC6 were used to simulate climate scenarios for 2050 proxied through the shared socio-economic pathways SSP 126, 245, 370 and 585 and were sourced from the Climate Change, Agriculture, and Food Security (CCAFS) platform (Navarro-Racines et al., 2020) and WorldClim. SSPs are key inputs in climate models, offering a structured framework to assess how socioeconomic trends and policy choices shape future climate scenarios (Meinshausen et al., 2020). IPSL-CM6A-LR, developed by the Institute Pierre-Simon Laplace, features a low-resolution grid of 2.5° × 1.3° with 79 vertical layers (Dufresne et al., 2013). The MIROC models have a consistent horizontal resolution of 1.4° × 1.4° (Tatebe et al., 2019). These models screened based on their relevance to the study region (Sanderson et al., 2015).

2.5 Model performance and accuracy assessment

Occurrence data for *D. sissoo* were combined with 10 non-collinear bioclimatic variables. The dataset was split, with 75% used for training and 25% for testing (Phillips, 2017). The model ran 10 iterations using a subsample approach. Performance was assessed using the Area Under the Receiver Operator Characteristic Curve (AUC), where values below 0.5 indicate unsuitability and above 0.5 indicate suitability. The Jackknife test evaluated predictor variable contributions. The average test AUC for *D. sissoo* was 0.893 confirming strong model performance.

Alongside AUC, the True Skill Statistic (TSS) is a widely used metric for evaluating model accuracy, ranging from –1 (indicating random performance) to +1 (indicating perfect prediction). TSS was calculated using MaxEnt model outputs, based on the equation incorporating true positive rate (TPR) and true negative rate (TNR) (Allouche et al.,2006). Upon averaging the empirical results of 10 replicates the TSS for was 0.60 denoting good model fit.

2.6 Predictor variable analysis and response curve

The Jackknife test analysis to determine the most significant bioclimatic contributing variable in limiting species distribution showed that Bio_9 contributed most to limiting the distribution of *D. sissoo* (Fig. S1).

The response curve for the preferred suitable range of Bio_9 shows that the value ranging ~ 30 is most suitable for the distribution of *D. sissoo* (Fig.S2). The value initially rises from 29 and attains optimal range between ~30 to 31.

3. Results

The results presented herein provide a comprehensive assessment of *D. sissoo* population across its native range, integrating field-based observations with predictive modelling. The results described the spatial distribution and expansion nature of the current populations, a study of the disease prevalence and identification of pathogens. Lastly, we assessed habitats in the present and future climate scenarios to explain possible changes in species range and stability.

3.1 Distribution of *D. sissoo* population

The spatial distribution of *D. sissoo* across study areas revealed distinct patterns as depicted in Fig S3. Data were classified into four categories based on Diameter at Breast Height (DBH): woody shoots (<10 cm), established individuals (10–20 cm), mature trees (>20 cm), and areas with no available data. A notable concentration of established and mature tree patches was observed in the eastern and northern part of the study area, implying that there would be successful regeneration in these areas. Northern and west regions of the country, in contrast, had a larger number of sites with no data indicating the absence of regeneration or missing field evaluation. The regeneration at the early stages was sparser, which demonstrates localised production of the woody shoots. These spatial patterns depict the differences in regeneration on a regional scale and point to areas that need special attention for targeted regeneration and monitoring.

3.2 Occurrence of disease in *D. sissoo* population and major causative factors

It was found that most of the diseased D. sissoo trees were mainly infested by *Fusarium solani* (current name: *Neocosmospora solani*), a soil-borne pathogen and *Ganoderma lucidum*, a decay-causing fungus on wood (Fig. 2). The study exhibited distinct regional patterns in pathogen prevalence. Northern and eastern parts show a predominance of *N. solani*, while central-eastern parts exhibit mixed occurrences involving *G. lucidum, N. solani,* and unidentified pathogens. In several sites, especially in central India, there are reports of co-occurrence of the multiple pathogens and this indicates that there are complex disease dynamics and may be interactive. The finding underlines the heterogeneity of the distribution of pathogens and gives a basis to specific disease management procedures.

INSERT FIGURE 2 HERE

3.3 Potential distribution range of *D. sissoo* for the current and future climate scenario

Spatial analysis revealed that ~ 19% of the total study area exhibited suitable habitat conditions for the potential distribution of *D. sissoo*. These suitable zones are predominantly concentrated along the northern plains, extending eastward into the sub-Himalayan foothills and further into the northeastern part (Fig. 3). In central India, there were also instances of scattered high suitability especially along the plateau-plain boundary areas. These areas are largely characterized by alluvial soils, moderate elevations, and sub-humid climatic conditions, which collectively support optimal habitat conditions. The eastern region emerged as particularly conducive for species establishment. The bioclimatic factors such as temperature, rainfall, and soil composition in these eastern parts likely provide optimal conditions for the species' growth and survival especially for those patches of distribution where the plant growth is complimenting the survival. Also, some appropriate patches were found in the isolated locations in the southern extremes of the central highlands, which indicated ecological flexibility outside the primary distribution zone.

Moreover, the map shows that the habitat suitability gradually diminishes towards the west suggesting that a certain restriction might be imposed by the evolving climatic parameters. This data can play a key role in the conservation and sustainable management of *D. sissoo*, emphasizing the need to focus on maintaining and promoting the favourable conditions within its existing optimal habitat range.

INSERT FIGURE 3 HERE

The future potential habitat sites of *D. sissoo* distribution range were modelled for the two climate scenarios; IPSL-CM6A-LR (Fig. 4), and MIROC6 (Fig. 5) and were proxied through SSP 126, 245, 370, and 585. For IPSL-CM6A-LR, under SSP126, *D. sissoo* exhibits a broad and contiguous distribution in the northern and eastern part of India, particularly concentrated along the Indo-Gangetic plains and Himalayan foothills. As emissions intensify in SSP245 and 370, the suitable habitat range begins to fragment and contract, indicating increasing ecological stress. In the worst case,

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SSP585, which relies on fossil fuel utilisation and high emission levels, the areas of suitable habitats become significantly smaller, and the suitability of the habitats is reduced to isolated spots.

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Fig. 5 demonstrates the projected suitable habitat distribution for *D.sissoo* under climate scenarios MIROC6A proxied SSP126, 245, 370, and 585. Under SSP126, which represents a low-emission, sustainable development pathway, the model predicted a broad and continuous suitable habitat range for *D. sissoo*, particularly along the Indo-Gangetic plains and the Himalayan foothills. This scenario suggests minimal disruption to the species' ecological niche. The suitable habitat remains largely similar for SSP 245, but shows slight fragmentation, especially in the eastern regions, indicating emerging potential climatic pressures.

Under SSP370, the suitable habitat appears more restricted, with noticeable contraction in the central and eastern zones; further intensification for SSP585 with most pronounced reduction and fragmentation of suitable habitat. The species' range becomes increasingly confined to northern and northeastern pockets, indicating significant vulnerability to intensified climate stress.

Overall, the maps show a clear trend: as emissions and climate change severity increase across SSPs, the higher the level of emissions and the severity of climate change in the SSPs, the smaller and less sustainable is the habitat of *D. sissoo*, emphasising the importance of mitigation efforts to preserve ecological resilience.

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The graph presents the percentage of area under current and projected climate scenarios based on two climate models: IPSL-CM6A-LR and MIROC6A, each evaluated across three Shared Socioeconomic Pathways (SSPs) 126, 245, 370, and 585. The current scenario exhibits the highest area coverage at approximately 19%. Under the IPSL-CM6A-LR model, area percentages decline progressively from SSP126 (~16%) to SSP585 (~12%), indicating a moderate reduction in area with increasing climate severity. In contrast, the MIROC6A model projects a steeper decline, with area percentages dropping from ~10% under SSP126 to ~5% under SSP585.

Overall, the results suggested a consistent decline in area coverage of *D. sissoo* distribution by 2050. This highlights the vulnerability of potentially suitable habitat range of *D. sissoo* distribution to climate change, particularly under high-emission pathways.

4. Discussion

The current study was an effort to examine the complex interaction between habitat suitability, growth performance, and disease prevalence in the *D. sissoo* population. The combination of field observations and the disease incidence data with species distribution modelling provide critical insights on the ecological resilience and vulnerability of *D. sissoo*. The noticed trends on mortalities caused by the pathogens, as well as the irregular regeneration, indicate emerging threats to *D. sissoo* population.

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Furthermore, the shifts in potential habitat under future climate scenarios indicate the necessity of adaptive management practices. The implications of findings have been discussed with existing literature as well as how these findings can be used to develop conservation and management strategies. We further identified key directions for future research and conservation action.

One of the aims of this study was to assess the current distribution of *D. sissoo.* The results demonstrated a wide distribution of *D. sissoo* in the northern and eastern region. The findings suggest eastern and northern Indian parts as the promising regions for *D. sissoo* population. Notably, the modelled potential suitable sites for *D. sissoo* not only align with its known ecological preferences but also reflect areas that offer favourable conditions for its growth, regeneration, and long-term establishment. Similar findings were reported by (Mehrotra et al. 2023), who used fuzzy-based spatio-temporal modelling in the Doon Valley to demonstrate that *D. sissoo* thrives along riparian zones, particularly where NDVI values indicate healthy vegetation and moisture availability.

The second objective of the study was to examine the occurrence of disease in *D. sissoo* trees and their causative factors. The primary causative agents were identified as *N. solani* and *G. lucidum*. These pathogens were confirmed through detailed morphological characterization and molecular analysis. *N. solani*, a soil-borne fungus, is primarily associated with wilt, whereas *G. lucidum*, a root- and wood-decaying fungus, contributes to dieback symptoms (Harsh, 2025). Together, they act as the principal causative factors leading to severe wilt and dieback of *D. sissoo* trees.

The third objective of the study was to model the potential distribution range of *D. sissoo* for the current and future climate change scenarios. Findings revealed that under the current climatic conditions, the northern and eastern regions of the study area exhibited potentially suitable habitats for *D. sissoo*. The results indicate that these parts are characterized by favourable temperature regimes, precipitation patterns, and topographic features that align with the species' known ecological preferences (Abdullah and Rafey, 2021).

On the question of how the *D. sissoo* distribution will respond to future climate change scenarios, this study found a constant declining pattern in suitable habitat range of *D. sissoo* with northward shift. These results corroborate a substantial body of previous research indicating that suitable habitats of a number of ecologically important species are likely to decline and shift northward (Dyderski et al., 2018; Burley et al., 2019). Given these projections, intervention strategies must be formulated to conserve *D. sissoo* populations, especially for the sites vulnerable to climate change induced habitat loss.

Overlaying the suitable habitat map onto the natural regeneration status map revealed a strong spatial agreement between the simulated habitat sites and areas exhibiting active regeneration. This spatial overlap suggests that the modelled habitat suitability aligns well with field-based indicators of species growth, affirming the ecological validity of the predictive model (Gallerani et al., 2023). The convergence of modelled suitability areas and observed regeneration data endorsed the potential and efficacy of machine

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learning tools to provide greater insights into species' conducive ecological regime to support sustainable management strategies under prevailing and future climatic conditions (Tehrany et al., 2019; Nabiollahi, 2024).

Recent studies further validate this approach. A study by Ennakri et al. (2025), introduced "habitat intelligence," emphasizing how machine learning and deep learning models can uncover species preferences and ecological thresholds across diverse landscapes. The study affirms the rising impact of AI-driven species distribution models in conservation planning, particularly when integrated with remote sensing and citizen science inputs. Similarly, Rew et al. (2020) demonstrated the effectiveness of a two-stage ensemble modelling approach that combines deep neural networks with traditional habitat suitability methods.

Although the modelled sites exhibit ecologically suitable conditions for *D. sissoo*, a paradox emerges in the form of widespread disease occurrence, particularly dieback and wilt, which significantly impede restoration efforts. These diseases, primarily caused by *N. solani* and *G. lucidum*, have been increasingly reported across riparian zones and floodplains traditionally considered optimal for *D. sissoo* (Haq et al., 2021). However, flooding promotes *N. solani* proliferation by creating anaerobic soils that enable spore dispersal and rapid colonization of stressed *D. sissoo* roots, leading to wilt and dieback (Neupane & Ghimire, 2020; Muhammad et al., 2024). Simultaneously, *G. lucidum* targets the basal stem and lignified roots of old *D. sissoo* trees, compromising their structural integrity and often leading to tree failure (Bhansali et al., 2011). A study by Bhatia et al. (2015), noted the co-existence of *N. solani* and *G. lucidum* in the same *D.sissoo* host synergistically and may lead to severe decaying symptoms individually and jointly.

This paradox implies that habitat appropriateness and intense growth do not necessarily provide resistance to pathological risks. These pathogens exploit host susceptibility under stress conditions, but their occurrence in thriving populations suggests intrinsic genetic vulnerability in existing *D. sissoo* genotypes. This necessitates a paradigm shift in conservation strategy from habitat-centric approach to genotype-specific disease resistance breeding programs especially in regions where pathogen stress coincides with high habitat suitability.

Contemporary studies advocate combining *in-situ* and *ex-situ* approaches for robust conservation outcomes of plantation initiatives (Naruka & Reddy, 2023). In-situ conservation is critical for conserving *D. sissoo*, emphasizing the protection of populations within their native ecological settings. Key measures include establishing and managing climate-resilient protected areas, promoting assisted natural regeneration in regions experiencing habitat shifts, and developing habitat corridors to support species dispersal and long-term viability (Ramola et al., 2024, Pakhira et al., 2024). Adaptive management practices such as monitoring phenological shifts and soil-moisture dynamics can further support *in-situ* resilience (Duarte & Hernandez,2024). Complementing this, *ex-situ* conservation offers a buffer against habitat loss and genetic erosion. Establishing seed banks, germplasm reserves, and disease-resistant

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propagation programs of *D. sissoo* can be instrumental to preserve genetic diversity and supporting future reintroduction efforts (Volis & Blecher 2010).

Overall, the study supports the credibility of machine learning-based tools for restoration ecology. The study not only validates field observations but also offers scalable pathways for climate-resilient species management and policy integration. The presence of pathogens in ecologically favourable zones necessitates a more integrated approach to species selection, site assessment, and applying long-term monitoring protocols. This calls for a need to also consider biotic stressors within the restoration paradigm. Restoration initiatives must incorporate genetic diversity in planting stock to reduce monoculture vulnerability and enhance resilience for threats such as pathogen outbreaks (Engelhardt, et al. 2014). Moreover, hydrological assessments should be integrated into restoration planning to identify flood prone sites, which are likely to support spread of invasive species and pathogen persistence (Richardson et al. 2007). Evidence-based restoration frameworks should also include pathogen surveillance protocols to enable early detection and adaptive management (Mammola et al., 2022).

Taken together, this study offers a comprehensive approach, combining pathogen occurrence data, habitat modelling, and regeneration assessments to gain better insights to *D. sissoo* distribution and mortality amidst climate change. However, a key caveat is the limited temporal resolution of pathogen data and potential underrepresentation of microclimatic variables, which may affect predictive accuracy. Including micro-site conditions such as soil, and water-stagnant site analysis could offer a more realistic picture for the region-specific intervention initiatives, which was another caveat of the current study. Even so, the findings have important implications for sustainable forest management highlighting the need for climate-responsive afforestation strategies, early disease surveillance, and targeted conservation planning to conserve and promote *D. sissoo* across vulnerable landscapes.

5. Conclusion

The findings revealed *N. solani* and *G. lucidum* as the dominant pathogens responsible for disease outbreaks in *D. sissoo* populations. Habitat suitability simulations for the present climatic conditions showed eastern and northern regions as suitable zones for *D. sissoo* distribution. However, the coexistence of suitable habitat, vigorous growth, and disease prevalence in *D. sissoo* populations points to the inadequacy of habitat modelling alone for conservation initiatives. The future projections indicate a significant contraction and northward shift in suitable habitat of *D. sissoo* by 2050. The study advocates for a restoration framework that integrates habitat suitability assessments with pathogen presence and risk analysis, and genotypic selection to develop disease-resistant varieties and ensure long-term sustainability of *D. sissoo* in agroforestry and restoration programs.

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The authors report there are no competing interests to declare

Data Availability

Data The datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request. Spatial layers used for species distribution modeling were derived from publicly accessible sources including WorldClim (climate data). Relevant species occurrence and pathogen incidence records were received from different institutes which were the part of this investigation. All processed data, modeling outputs, and analytical scripts can be shared for academic and non-commercial use upon request, in accordance with institutional and journal policies.

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Figures

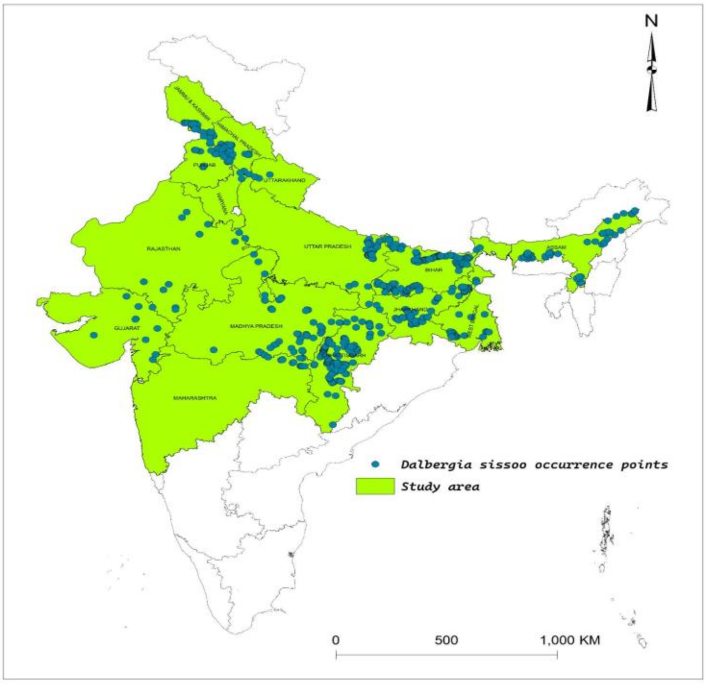


Fig. 1

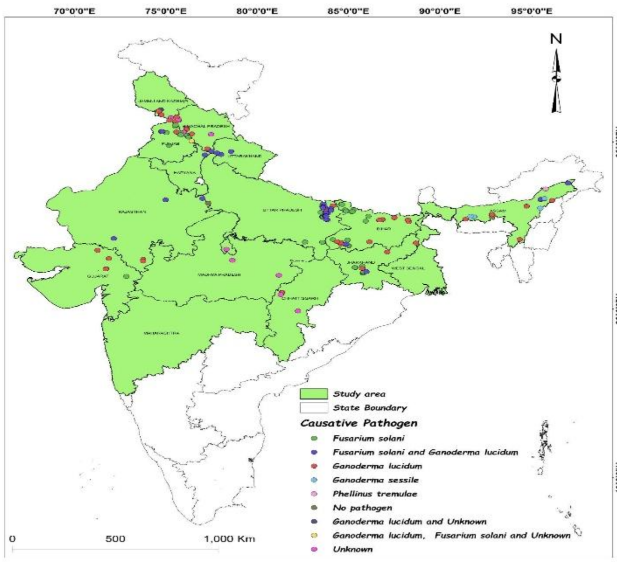


Fig. 2

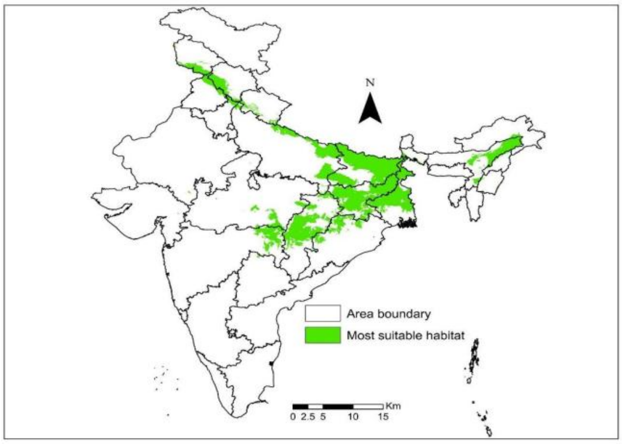

N
Area boundary
Most suitable habitat
0 2.5 5 10 15
Km

Fig. 3

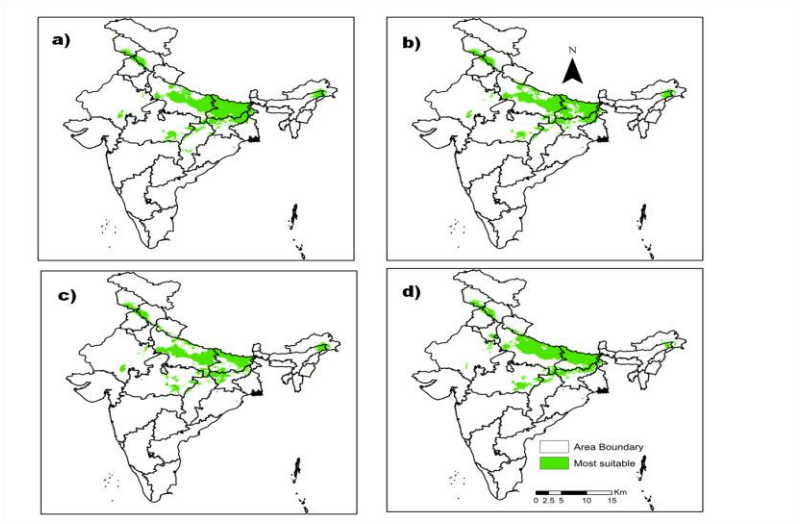
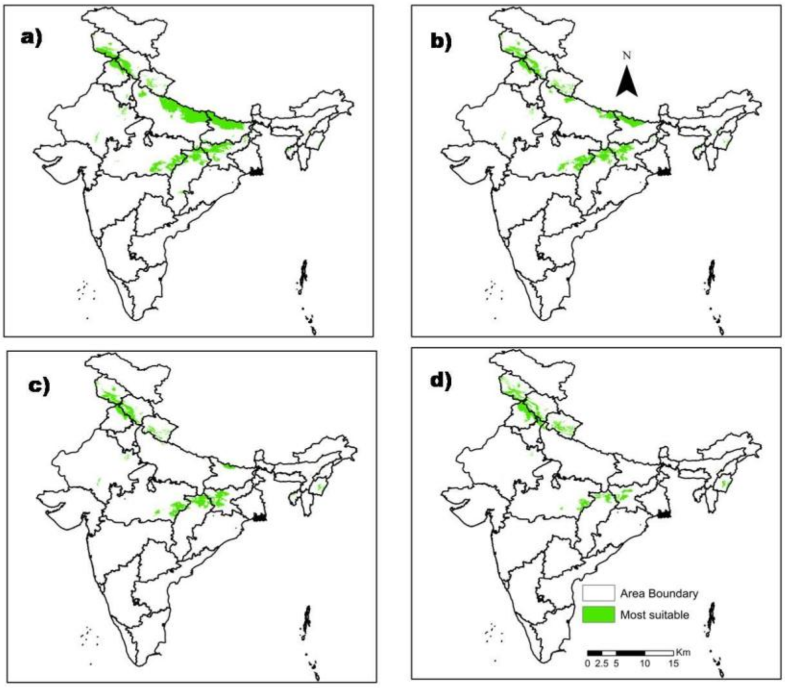

a)
b)
N
c)
d)
Area Boundary
Most suitable
0 2.5 5 10 15
Km

FIG. 4


a)
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c)
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Area Boundary
Most suitable
0 2.5 5 10 15
Km

FIG. 5

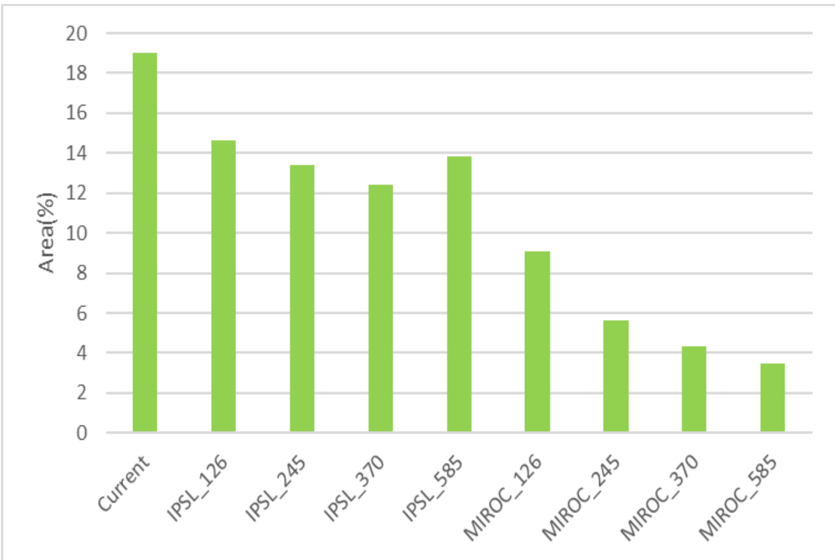

20
18
16
14
12
10
8
6
4
2
0
Area(%)
Current
IPSL_126
IPSL_245
IPSL_370
IPSL_585
MIROC_126
MIROC_245
MIROC_370
MIROC_585

FIG 6

Captions

Fig.1 Location map of the study area. The parts highlighted with green colour, shows the area covered in the current study. The blue points refer to the locations where the occurrence data of *D. sissoo* distribution were recorded.

Fig.2. Map showing distribution of major causative factors for the *D. sissoo* across the study area. The study area is shaded in green colours, while the locations of the causative factors are shown through different coloured dots. Visual interpretation showed *F. solani* as the major causative pathogen of disease in the *D.sissoo* population across the study area.

Fig.3 Potential suitable habitat range of *D. sissoo* for the current climate scenario. High suitability zones for *D. sissoo* ranged across the northern plains, extending eastward into the sub-Himalayan foothills and the northeastern region. Distribution pockets also appear concentrated along plateaus-plain transition zones of the central-eastern region**.**

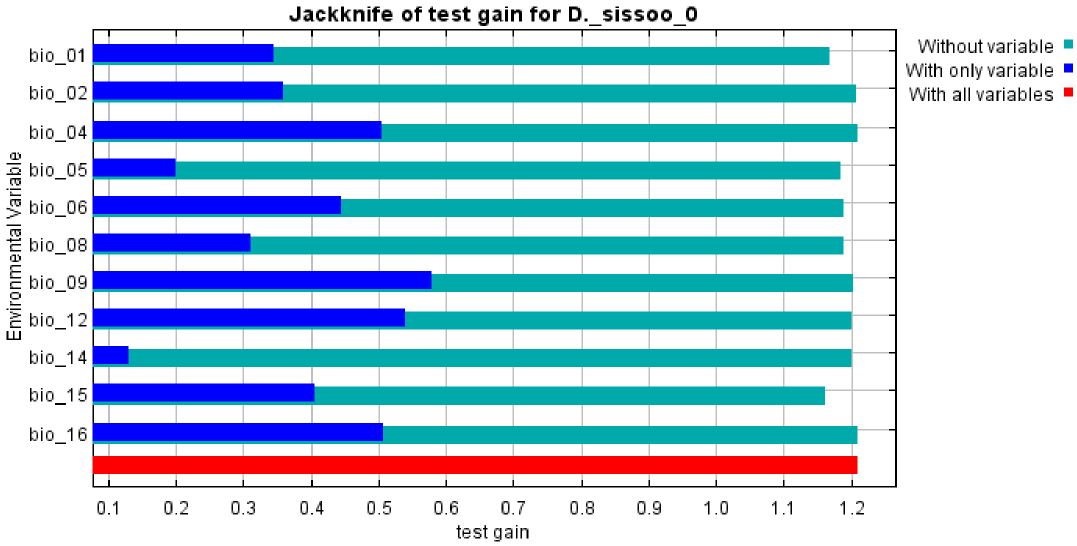
Fig. 4 Maps illustrate the future habitat suitability of *D. sissoo* for the IPSL-CM6A-LR climate proxied through different SSPs a) 126, b) 245, c) 370 and d) 585.

Fig. 5 Maps depicting the potential suitable habitat distribution range of *D. sissoo* by 2050 for MIROC6A climate scenario proxied through SSPs a) 126, b) 245, c) 370 and d)585.

Fig. 6 Graph illustrates the percentage of area for the potential suitable habitat range of *D. sissoo* under different climate scenarios, comparing the current condition with projections from two climate models: IPSL_6A_LR and MIROC6A . The future climate models simulating the potential climate scenarios for 2050 are proxied through different SSPs126, 245, 370, and 585. It can be seen from the graph that the potential suitable habitat range of *D. sissoo* will decline across all the probable scenarios in future. Currently ~19% of the study area is potentially suitable for the distribution of *D. sissoo.* But by 2050, depending upon the scenario this suitable habitat area might limit only to ~3-14% range.

Supplementary Figures with Captions

Supplementary File



ig. S1 The Jackknife of test AUC for *D. sissoo* shows Bioclimatic variable Bio_09 contributed most in limiting the distribution of *D. sissoo*. The environmental variable with highest gain when used in isolation was Bio_09.

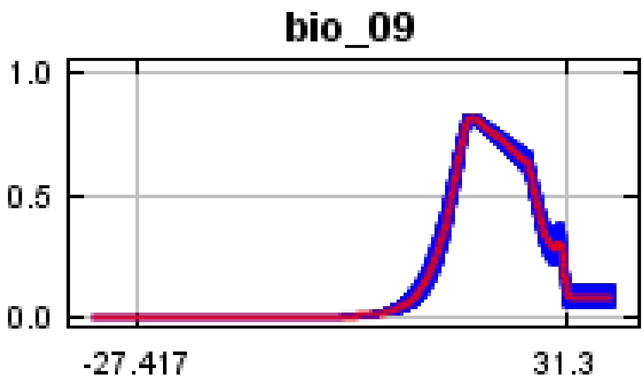


Fig. S2 The ROC curve for Bio_09, the most influential variable in restricting the distribution of *D. sissoo*. The graph demonstrates that, value ranging ~ 30 is most suitable for the distribution of *D. sissoo*. The value initially rises from 29 and gains the optimal range between ~30 to 31 before beginning to decline.

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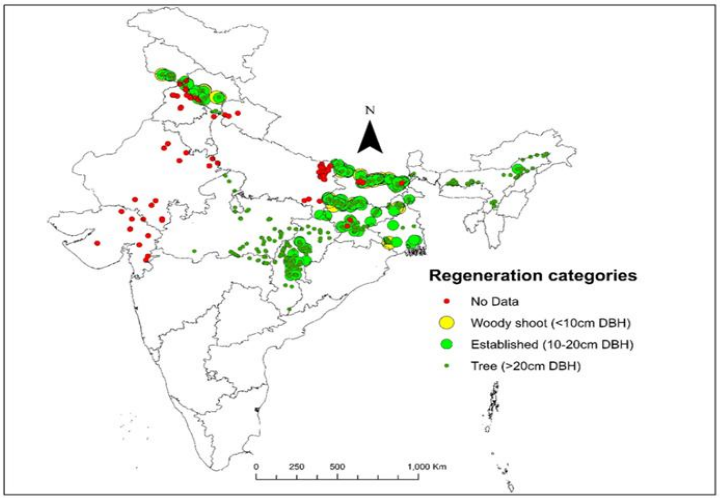

Fig. S3. Growth-wise population distribution of *D. sissoo* based on diameter at breast height (DBH) classes. The map illustrates spatial variation in *D. sissoo* individuals categorized into three DBH classes: <10 cm (saplings), 10–20 cm (juvenile trees), and >20 cm (mature trees), highlighting regeneration status and structural composition across the study area.