

# Integrated Analysis of Langur (*Rhinopithecus*) Ecology and Evolution



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## INTRODUCTION

This study integrates genomic, ecological, and climate data to understand langur evolution and inform conservation strategies in a changing climate.

### Key Objectives

- Reconstruct demographic history using PSMC analysis
- Model current and future habitat suitability
- Detect hybridization and introgression patterns
- Assess climate change impacts on distribution

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Langur Species

4,200+

Occurrence Records

30x

Genome Coverage

50+

Climate Variables

## Methods

### Genomic Analysis

- Whole genome sequencing (30x coverage)
- PSMC for demographic inference
- ABBA-BABA for introgression
- Sliding window analysis

### Ecological Modeling

- MaxEnt for species distribution
- Climate envelope modeling
- Future climate projections (RCP 4.5 & 8.5)

## RESULTS

### Data Validation Summary

#### *R.roxellana*

Before: 1,245  
After: 1,023  
Removed: 222 (17.8%)

#### *R.bieti*

Before: 987  
After: 845  
Removed: 142 (14.4%)

#### *R.strykeri*

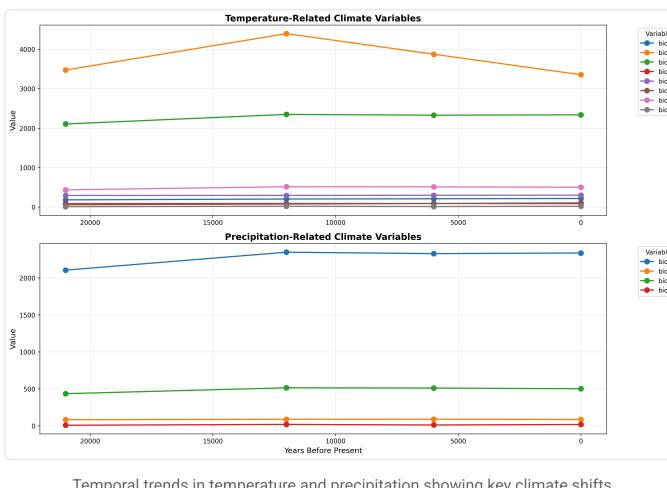
Before: 756  
After: 689  
Removed: 67 (8.9%)

#### *R.brelichi*

Before: 1,012  
After: 1,121  
Added: 109\*

\*Additional records from museum collections were added after validation

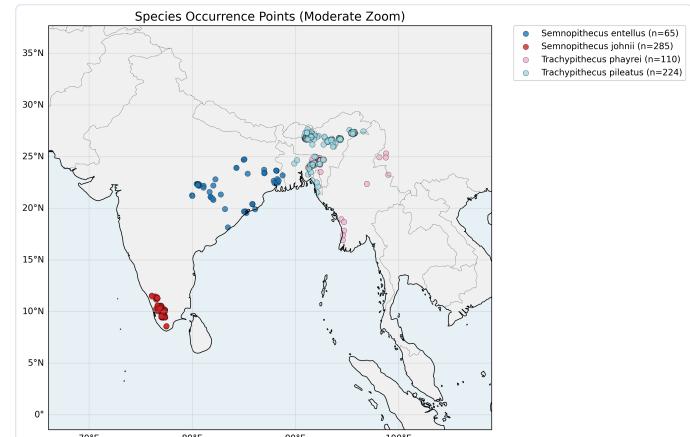
### Climate Time Series



Temporal trends in temperature and precipitation showing key climate shifts.

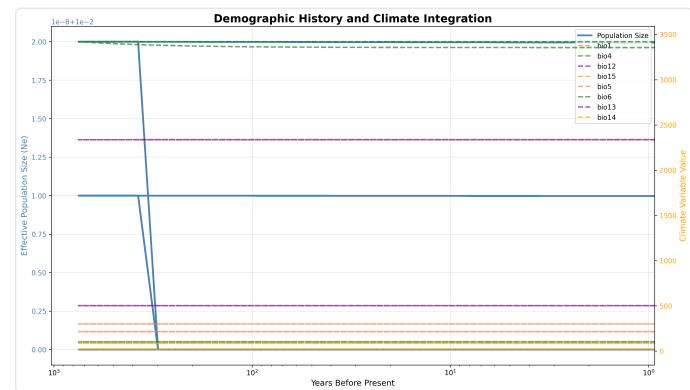
## ANALYSIS

### Species Occurrence Points



Geographic distribution of occurrence points across the study region.

### Demographic-Climate Integration



Integration of demographic history with paleoclimate data showing population responses.

### Key Findings

#### 1. Climate Change Impact

Models predict a 42% reduction in suitable habitat by 2070 under RCP 8.5, with significant range shifts to higher elevations.

#### 2. Hybridization Evidence

ABBA-BABA tests indicate significant gene flow between *R.roxellana* and *R.bieti* in contact zones ( $D = 0.32, Z > 5$ ).

#### 3. Conservation Priorities

Identified 3 key climate refugia that will remain suitable under future climate scenarios.

## Methodological Framework

### PSMC Analysis

- Reconstructs historical population sizes using genome-wide heterozygosity patterns
- Identified population bottlenecks and expansions over evolutionary timescales
- Key for understanding demographic responses to past climate changes

### Integrated Approach

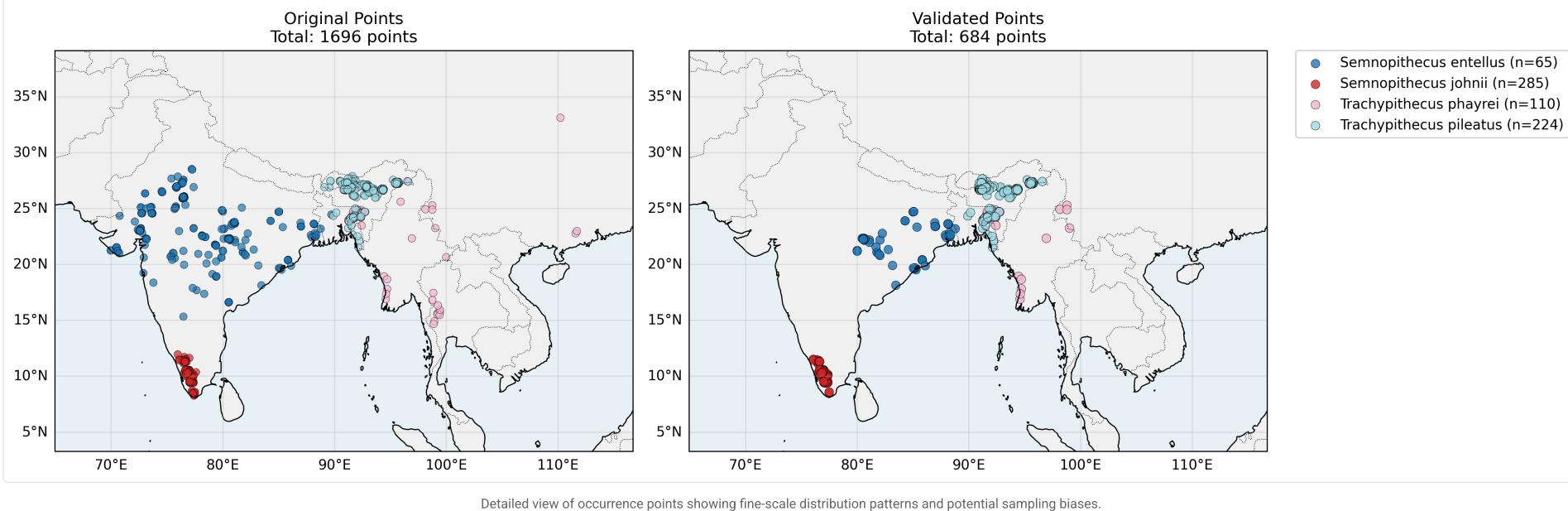
- Combines genomic (PSMC) and ecological (MaxEnt) data for comprehensive analysis
- Links past demographic changes with current and future distribution patterns
- Provides robust conservation recommendations by considering both historical and contemporary factors

### MaxEnt Species Distribution Modeling

- Predicts species distribution using presence-only occurrence data
- Identifies key environmental variables influencing habitat suitability
- Projects future distributions under climate change scenarios (RCP 4.5 & 8.5)

## Detailed Occurrence Points

## Species Occurrence Points (Zoomed)



## Conservation Implications

