Vegetation and Microbial Composition in the Grassland Meadows of TATR

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1. Executive Summary

Our study evaluates the successional trajectory of five grassland sites within the Tadoba-Andhari Tiger Reserve (TATR). We documented 95 species across 50 quadrats, and we assessed how soil physical properties and biomass allocation strategies influence vegetation assembly in a chronosequence of relocated village sites (Navegaon, Jamni, Panderpauni, Kolsa) and a natural baseline (Alizanza).

Furthermore, we documented the diversity of microbial communities between forest and grassland sites of Jamni, Panderpauni, and Kolsa. In these three sites we evaluated the functional differentiation among microbial communities. This was complemented by a comparative profile of their predicted metabolic pathways to identify border community-level functional shifts.

Key Findings

Soil Carbon and Restoration Age

The amount of total carbon (organic and inorganic) in the restored meadows was relatively low, averaging at 1.7 tons/ha. One of the sites sampled, Panderpauni, had the lowest carbon despite being relocated and restored since 1973. Jamni, relocated and restored in 2013, had the highest soil carbon.

Edaphic Drivers of Community Structure

Soil bulk density emerged as a primary environmental filter. Higher density soils in the non-restored site support specialised, stress-tolerant communities (*Cyperaceae/Acanthaceae*). In contrast, the lower bulk density of recently restored sites facilitates rapid aboveground productivity.

Biomass Allocation Trade-offs

A distinct functional shift was observed across the restoration timeline. Early successional sites (Navegaon) prioritise aboveground biomass, while older, more stable sites (Jamni/Panderpauni) prioritise belowground root biomass. This shift indicates a transition from rapid site occupancy to long-term ecosystem stability and carbon storage.

Vegetation Diversity and Taxonomic Resilience

While Shannon diversity peaked in Kolsa, Taxonomic Distinctness (TD) remained relatively stable across all sites. This suggests that the restoration process successfully preserves the evolutionary breadth of the region's flora, preventing the formation of taxonomically impoverished monocultures.

Successional Convergence in Vegetation

Ordination and similarity analysis revealed that older restored sites are converging (50% similarity between Jamni and Panderpauni), forming a cohesive mature meadow matrix that differs significantly from the pioneer state of Navegaon and the hard-soil state of Alizanza.

Functional Guilds Within Grassland Microbial Communities

Five functional guilds were analysed, namely, nitrogen fixers, growth promoters, bacterial decomposers, bacterial bioremediators, and nutrient cyclers. In general, Pandherpauni grassland showed more evenness, i.e. presence of multiple moderate abundance of genera in the functional guild, compared to the other two grasslands; except in the case of nitrogen fixers where the Kolsa grassland showed marginally higher evenness. Furthermore, nitrogen fixers guild showed the least abundance among all the five functional guild – underscoring the need for legumes that might be getting removed as unpalatables. Largely, the nitrogen-fixing community consists of symbiotic rhizobia associated with leguminous shrubs.

Microbial Diversity

Alpha diversity indices and taxonomic intersections corroborate in identifying Pandharpauni grassland supporting the highest microbial diversity among the grassland sites. The presence of a waterbody closeby creates an ecotone (a transition zone) subjected to seasonal or periodic water-level fluctuations creates shifting ecological niches that support a highly diverse community of aerobic, anaerobic, and facultative microbes, boosting overall microbial diversity. Furthermore, terrestrial plant species do not tolerate root hypoxia or fluctuating water tables to the extent microbes do – and therefore we see a decline in vegetation diversity.

Predictive Metabolic Pathways

Ecologically, the Kolsa grassland hosts metabolically streamlined microbial communities reflecting human-alteration-driven reductions and management filtering compared to Pandherpauni and Jamni grasslands.

2. Background

The Tadoba-Andhari Tiger Reserve (TATR), located in Maharashtra, is one of India's most important protected areas, safeguarding tigers, herbivores, and a rich forest ecosystem. Understanding the ecological interactions within this landscape is critical for effective conservation planning. Many villages inside the reserve have been relocated, and the agricultural fields are being restored to meadows by the forest department. Systematic assessment of vegetation change in these meadows and how much carbon is being sequestered is currently missing.

This study aims to characterise vegetation composition, diversity, and community structure in grassland meadows within the TATR. Vegetation sampling was conducted across five grassland sites: Alizanza, Jamni, Kolsa, Navegaon, and Panderpauni, using standardised quadrat-based surveys. Within each site, species identity and percentage cover were recorded for all vascular plants encountered. In addition to floristic data, soil bulk density, belowground biomass, aboveground biomass, soil carbon, nitrogen and plant height were measured to examine potential relationships between vegetation patterns and edaphic conditions. We wanted to understand the differences in the vegetation composition across the meadows of TATR, especially between the older and recently restored meadows. We did this by asking two questions:

1. **What is the grass and forb composition in the meadows, and does it change with the age of restoration?**
2. **How do the physical and chemical properties of soils vary relative to vegetation composition?**

3. Materials and Methods

3.1. Study Area

We sampled five grassland meadows inside TATR, Alizanza, Jamni, Kolsa, Navegaon, and Panderpauni *(Figure 1)*. In all sites, except Alizanza, the villages were relocated at various time points, and the agricultural land was converted to meadows.

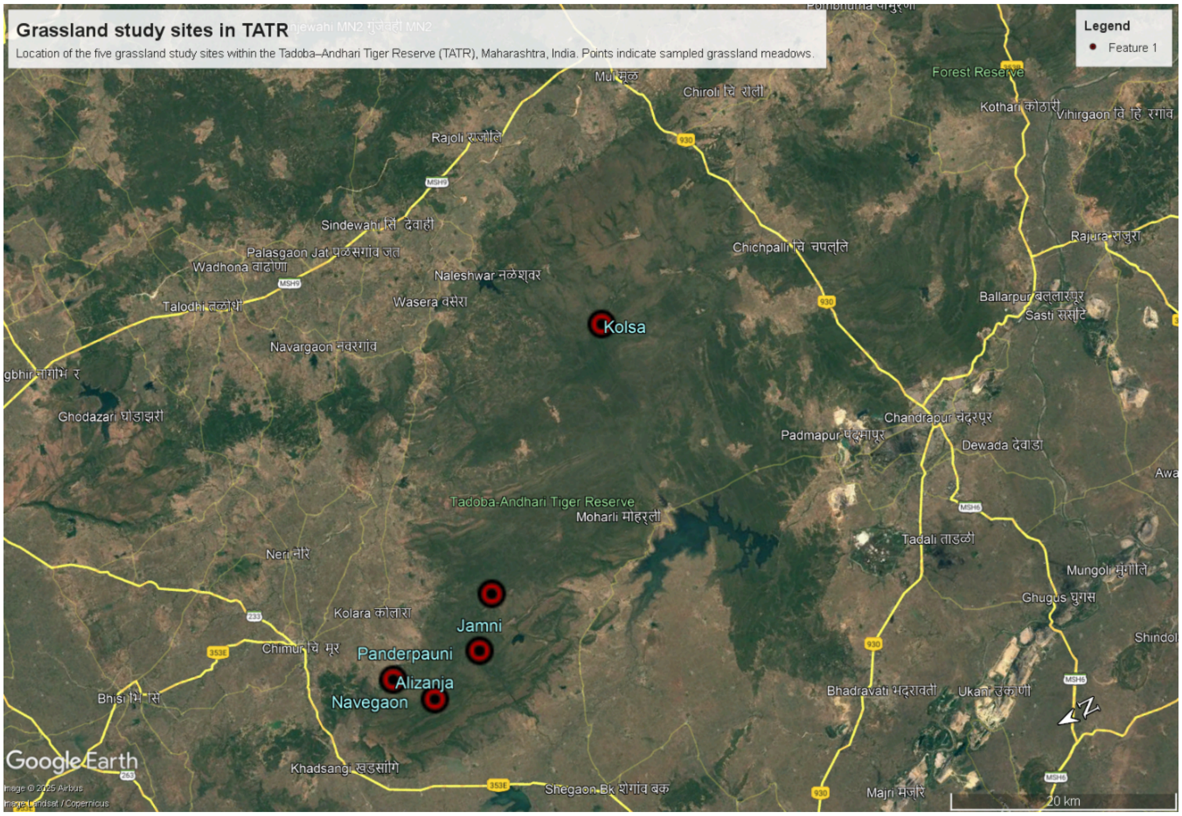

Figure 1: TATR grassland meadows (Alizanza, Jamni, Kolsa, Navegaon, Panderpauni)

3.2. Study Design

We followed a stratified random sampling approach *(Figure 2)*. We conducted 10 spatial replicates within each site to quantify vegetation composition and collect soil in the corresponding site. A minimum of 5–10 randomly distributed blocks, measuring 5 x 5 m grids, were established using GIS to ensure adequate replication and statistical robustness, while still capturing the variation in soil, climate, and management intensity across the reserve.

3.3. Vegetation Surveys

In each block, one 1 × 1 m quadrat was used to visually estimate the percentage cover of all vascular plant species present. Plants were identified using the grassland field guide, with the assistance of the forest department staff.

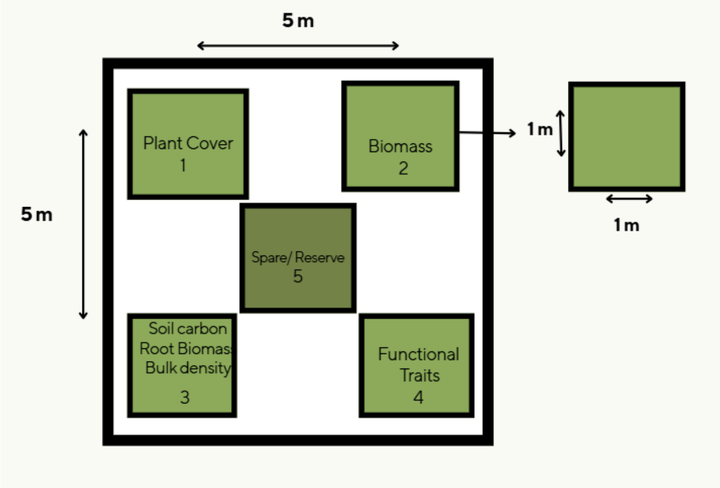

Figure 2. In each location, we sampled vegetation and soil in this plot design

3.4. Biomass Collection

Above and below-ground biomass was collected from a 0.25 m^2 sub-plot within a 1 x 1 m quadrat. This is a measure of productivity. The plants were clipped to the ground level and bagged separately for drying. Samples were dried in the lab at 60 °C for 72 hours (three consecutive days) to obtain dry mass, separately for the different functional groups. Belowground biomass was calculated from the soil samples collected at cm 15 cm depth, with a 3 cm diameter core. Roots were separated from soil by sieving with a 2 mm mesh, and the dry weight was measured after cleaning and drying.

3.5. Soil Sampling and Analysis

Two sets of soil samples were taken from an average depth of 15 cm using a 3 cm diameter soil corer. The soil samples were preserved separately for analysis in the laboratory. Bulk density of the soil was determined using the core-volume method, wherein the sample of known cylindrical volume was sun-dried for approximately three days (about 10–12 hours per day) until it reached a nearly constant weight. The samples were then further dried in a hot air oven at 40 °C to remove the remaining moisture. After complete drying, the soil was weighed using a precision balance to the nearest 0.01 g. Bulk density was calculated as the ratio of cylinder volume divided by the dry weight in g/cm^3. The carbon values were estimated using a 2 mg sample of sieved samples in an ElementAR machine in an external lab (Poornayu Labs, Bangalore).

Figure 3: Soil sample collection from Kolsa grasslands

3.6. Statistical Analysis

The statistical analyses were carried out using R (v5.1+) and PAST version 5.2. Species accumulation and rarefaction analyses were performed to assess sampling completeness across the five sites. Differences among sites were tested using the Kruskal–Wallis test. Functional group composition per site, frequency of occurrence of functional groups, and proportional vegetation cover across sites were analysed and visualised in R. Species diversity was assessed using alpha diversity indices, including Shannon's diversity index (H′), along with other diversity measures to compare community structure across sites. A diversity *t*-test was also performed between sites to examine differences in Shannon diversity values. Similarity in vegetation composition among sites was evaluated to understand patterns of community resemblance. Indicator species analysis was conducted to identify species strongly associated with particular sites. Biomass and soil properties across sites were summarised using mean and standard deviation, and differences were examined in R. Finally, Canonical Correspondence Analysis (CCA) was used to examine the relationship between vegetation composition and environmental variables across the study sites.

4. Results and Discussion

4.1. Species Composition and Functional Group Structure

Overall, we documented 95 species of plants, representing 72 genera and 21 families from 50 quadrats. Totally, we encountered 362 instances of these species being detected across all the plots, and the species accumulation curve began to reach an asymptote (*Figure 4*). However, the species accumulation curves did not reach an asymptote at any of the five sites, indicating a potentially greater vegetation diversity (*Figure 5*). While the overall species richness has been documented here, continued surveys across these sites with increased sampling effort would help detect a greater number of species. Alternatively, the lack of an asymptote could also be a consequence of the active grassland management, where certain non-palatable species have been removed.

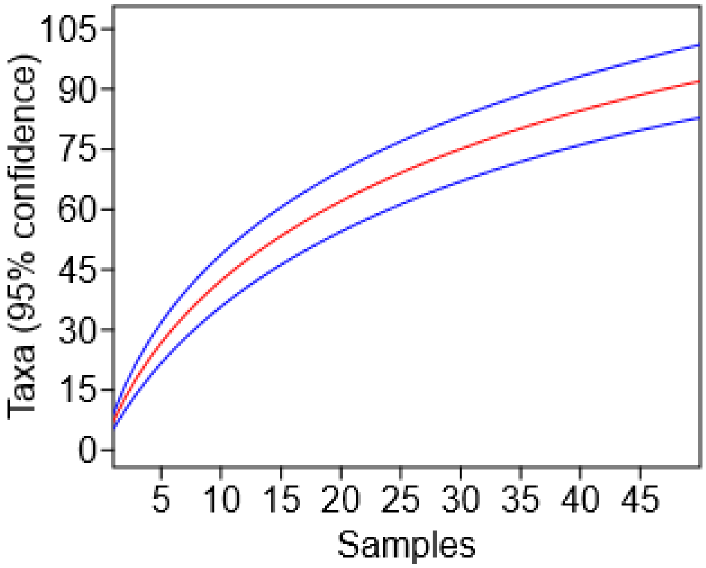

Figure 4: Overall species accumulation curve

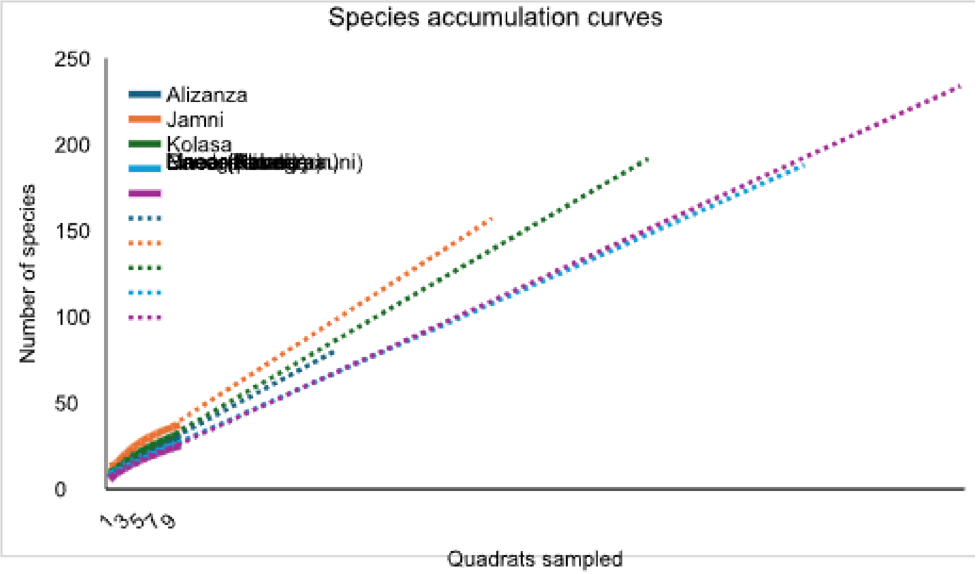

Figure 5: Species accumulation curves across the five sites

4.2. Functional Groups

The plants belonged to six functional groups, with the vegetation cover being dominated by grasses (*Figure 5)*. Vegetation was dominated by herbaceous functional groups, particularly grasses and forbs, accounting for 73 of the 96 recorded species, while woody species (shrubs and trees) contributed only 5 species. Forbs occurred more frequently in the quadrats, followed by grasses, with only one tree being detected (*Figure 5*). This difference in occurrence across functional groups was not statistically significant (Kruskal-Wallis = 2.784, p = 0.56).

Among the functional groups, highest species richness was observed among Forbs with 45 species belonging to 37 genera, and 16 families. These species were represented by families including Acanthaceae, Amaranthaceae, and Asteraceae, among others. Grasses (family Poaceae) formed the second most diverse functional group, comprising 28 species belonging to 18 genera within a single family. Grass represented a major structural component of the vegetation community. Legumes (family Fabaceae) accounted for 9 species belonging to 9 genera. Sedges (family Cyperaceae) also comprised 9 species belonging to 3 genera, primarily by the genus *Cyperus* and *Fimbristylis*, along with unidentified *Cyperaceae* morphospecies. We documented four species of shrubs, belonging to 4 genera and 4 families (Fabaceae, Malvaceae, Melastomataceae, and Rhamnaceae). In all our 50 plots, we only documented one tree species, *Butea monosperma* (*Table A1*). The functional group composition of the TATR meadows reflects a robust herbaceous-dominated state, typical of successfully maintained tropical grasslands. The high richness of forbs (45 species) relative to grasses (28 species) suggests that while grasses provide the physical matrix and biomass, forbs drive the taxonomic diversity of the system. This high forb-to-grass ratio is often an indicator of high-quality habitat for pollinators and small herbivores. The near-total absence of woody recruits indicates that these meadows are being maintained in an early-to-mid successional state, likely through a combination of herbivory and the Forest Department's management interventions. The presence of specialised functional groups, such as the Cyperaceae assembly in the high-density soils of Alizanza, further suggests that functional distribution is being filtered by edaphic conditions rather than random dispersal.

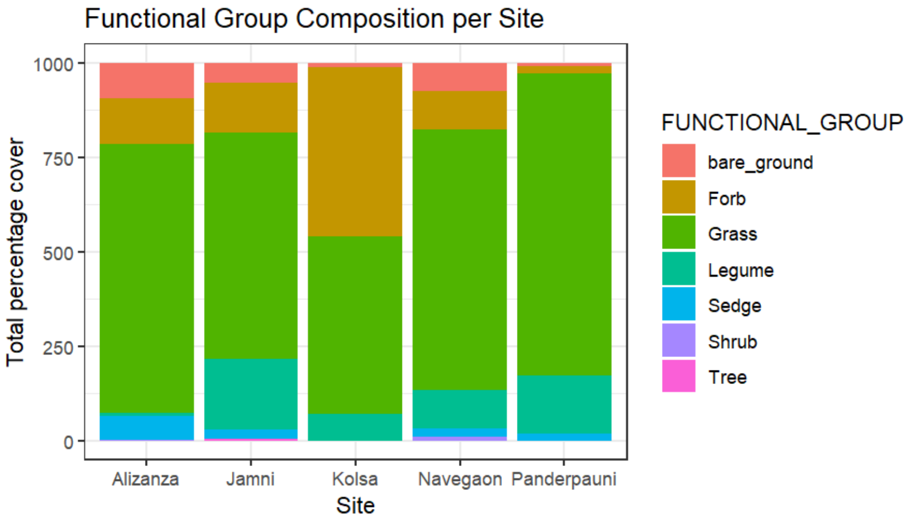

Figure 6: Functional group composition per site based on total percentage cover. Grasses dominate all sites; the relative contributions of forbs, legumes, and sedges vary with restoration age and site-specific conditions

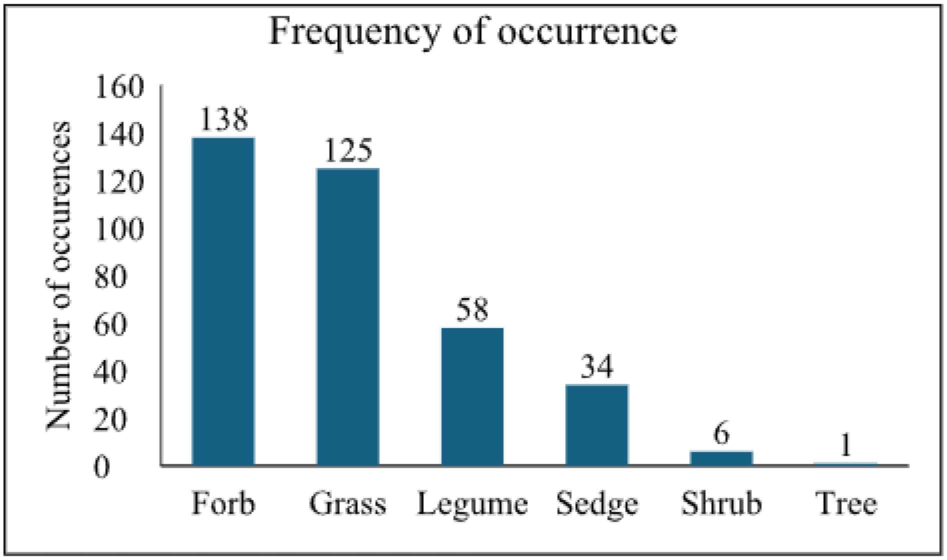

Figure 7: Frequency of occurrence of plants belonging to the five functional groups across all samples

4.3. Vegetation Cover

The sampled quadrats had a relatively high proportion of vegetation cover across all sites, with very little bare ground (*Figure 7*). The differences in the proportion of vegetation cover across sites were not statistically significant (Kruskal-Wallis H = 8.95, p = 0.06). The high proportion of vegetation cover recorded across all five study sites indicates a successful transition from agricultural land-use to established meadow communities. The absence of significant differences in cover between recently restored and older sites suggests that surface stabilisation occurs relatively rapidly post-relocation. From a management perspective, the minimal bare ground observed across the 50 quadrats is a critical indicator of restoration success, as it limits the niche availability for invasive opportunistic species and reduces the risk of topsoil erosion during monsoon events. However, the uniformity in cover underscores the necessity of using multivariate analyses (such as CCA and IndVal) to distinguish between sites; while they appear structurally similar in terms of 'greenness,' they remain ecologically distinct in terms of species assembly and biomass allocation strategies.

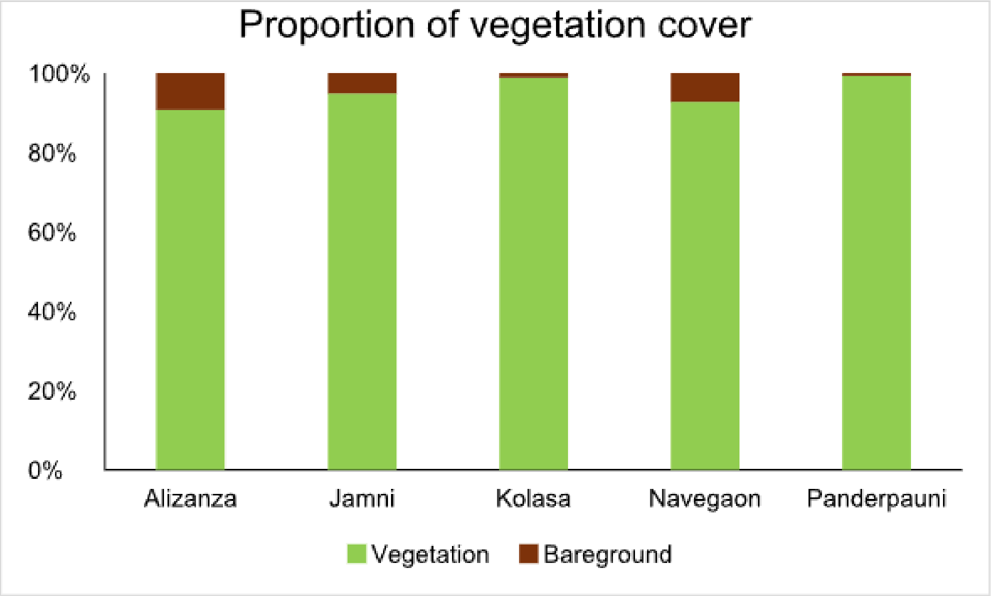

Figure 8: Proportion of vegetation cover across the five sites

4.4. Species Diversity

Species richness was the highest in Jamni (37) was followed by Kolsa (32 taxa), Alizanza (30 taxa), Navegaon (26 taxa), and Panderpauni (25 taxa). The diversity of the vegetation community was highest in Kolsa (H′ = 2.7), followed by Jamni (H′ = 2.4), Navegaon (H′ = 2.1), Alizanza (H′ = 2.1) and lowest in Panderpauni (H′ = 1.4). Conversely, Panderpauni had a high dominance (D = 0.44), followed by Alizanza (D = 0.22), Navegaon (D = 0.19), Jamni (D = 0.14), and Kolasa (D = 0.12). The difference in diversity of species was statistically significant across all sites (*Table 1*).

The significant variation in diversity indices across the five sites suggests that while all meadows have achieved high ground cover, their internal community structures are on divergent successional trajectories. The peak diversity observed in Kolsa is driven by high evenness, where the absence of a single dominant species allows for a complex coexistence of forbs and grasses. This contrasts sharply with Panderpauni, where high dominance suggests a 'specialist' community likely dominated by a few high-biomass perennial grasses. The high species richness in Jamni, despite its moderate diversity, indicates a transitional state where many species are present but have not yet reached an equilibrium in abundance. From a conservation perspective, the maintenance of a mosaic of high-diversity sites (like Kolsa) and high-dominance sites (like Panderpauni) is ideal, as it provides both nutritional variety for generalist herbivores and high-bulk forage for larger ungulates.

Table 1: Diversity 't' test between the sites. Shannon's H values are significantly different between all combinations of sites. 't' test values are in the top half of the diagonal, and 'df' values are in the bottom half. P values in bold represent statistical significance, of $p < 0.01$.

	Alizanza	Jamni	Kolsa	Navegaon	Panderpauni
Alizanza	1	**-6.9**	**-11.4**	**-1.79**	**8.95**
Jamni	1839.6	1	**-4.38**	**5.38**	**15.96**
Kolsa	1824.4	1914.5	1	**10.01**	**20.61**
Navegaon	1819.7	1875	1892.5	1	**11.01**
Panderpauni	1898.5	1917.8	1895.5	1898.3	1

4.5. Taxonomic Distinctness

The composition of the vegetation community was most taxonomically distinct in Alizanza (TD = 3.7) and Kolsa (TD = 3.69), Jamni (TD = 3.55) and Navegon (TD = 3.52), and lowest in Panderpauni (TD = 3.27). The differences, however, in the taxonomic distinctness index are similar at each site, suggesting a rather homogenous taxonomic representation of plants in the meadows. While Shannon diversity and dominance varied significantly across the chronosequence, the Taxonomic Distinctness (TD) remained relatively consistent across all five sites. This stability suggests that the taxonomic 'breadth' of the meadows is maintained regardless of the time since relocation or local dominance patterns. The consistently high TD values indicate that these meadows are not becoming taxonomically impoverished or dominated by a single evolutionary lineage (such as a few closely related Poaceae). Even in Panderpauni, which exhibited the lowest diversity and highest dominance, the taxonomic representation remains high, suggesting that the underlying evolutionary structure of the community is resilient. This 'taxonomic homogeneity' across sites provides evidence that the relocation process in TATR is successfully facilitating the assembly of phylogenetically diverse plant communities that mirror the natural baseline found in Alizanza.

4.6. Similarity in Vegetation Composition

The vegetation composition across the five sites within TATR was not homogeneous but structured into two groups. The first group comprised Panderpauni and Jamni, which shared 50% similarity, followed by Kolsa, having about 40% similarity to the former two sites. The second group comprised Navegon and Alizanza, which shared 30% similarity and ~20% similarity with the remaining three sites. The hierarchical clustering of the TATR meadows reveals a clear divide in community assembly, likely driven by the age of restoration and edaphic conditions. The 50% similarity between Jamni and Panderpauni suggests a convergence toward a stable 'mature meadow' state, characterised by significant investment in belowground biomass and a shared suite of perennial species. In contrast, the low similarity (20-30%) between the Navegaon-Alizanza group and the rest of the sites highlights two different forms of ecological distinctness. Navegaon’s divergence is likely a function of its early successional stage, where rapid aboveground productivity outpaces the establishment of 'stable-site' taxa. Alizanza’s distinctness, however, is more likely rooted in its unique soil profile; the high bulk density recorded there acts as a persistent environmental filter that maintains a community taxonomically distinct from the previously cultivated, softer-soiled relocation sites.

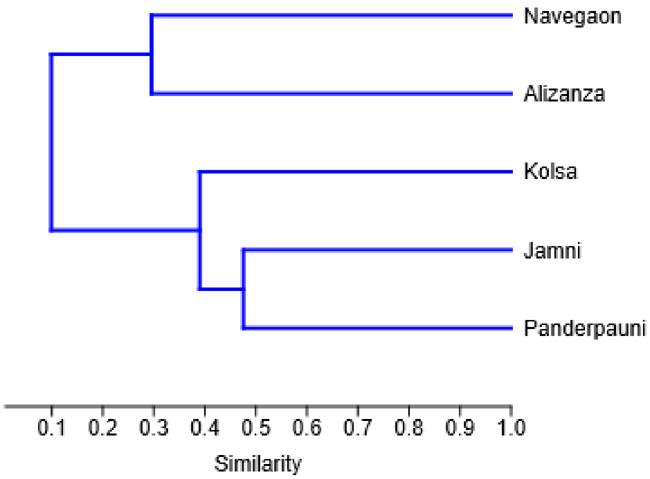

Figure 9: Bray-curtis similarity index of vegetation composition across sites

4.7. Indicator Species across Sites

The occurrence of plants across the five study sites varied substantially, and key species served as indicators of the site (*Figure 9*). In Alizanza, two taxa emerged as the primary indicators: *Acanthaceae* sp. 1 (IV = 60.0) and *Cyperaceae* sp. 3 (IV = 70.0). In Kolsa, *Cyanotis* sp. was the dominant significant indicator (IV = 70.0). In Navegaon, two species showed high indicator values: *Chloris* sp. 1 (IV = 70.0) and *Convolvulus* sp. 1 (IV = 55.53). No species achieved the same level of statistical distinctiveness as an indicator for either Jamni or Panderpauni, although several species, like *Ischaemum indicum* (IV = 51.6) and *Cyperus fuscus* (IV = 37.33), were frequent in Panderpauni.

The significant indicator species identified across the TATR meadows provide a biological signature of their respective successional and edaphic states. In Alizanza, the dominance of *Cyperaceae* and *Acanthaceae* as indicators (IV = 70.0 and 60.0) likely reflects an adaptation to the high soil bulk density characteristic of this non-relocated site. These taxa act as specialists for hard-soil conditions where more common meadow grasses may face recruitment limitations. Conversely, the indicator profile of Navegaon, dominated by *Chloris* sp. 1, is indicative of an early-successional 'pioneer' community. This aligns with the site's recent restoration history and its focus on high aboveground biomass production. The presence of *Cyanotis* sp. as the primary indicator for Kolsa serves as a marker for high taxonomic diversity, signalling a transition from grass-dominated monocultures to a more complex, herb-rich meadow structure. The absence of significant indicators in Jamni and Panderpauni, despite high species presence, suggests a high degree of ecological overlap, marking these sites as a unified, stable matrix within the larger Tadoba landscape.

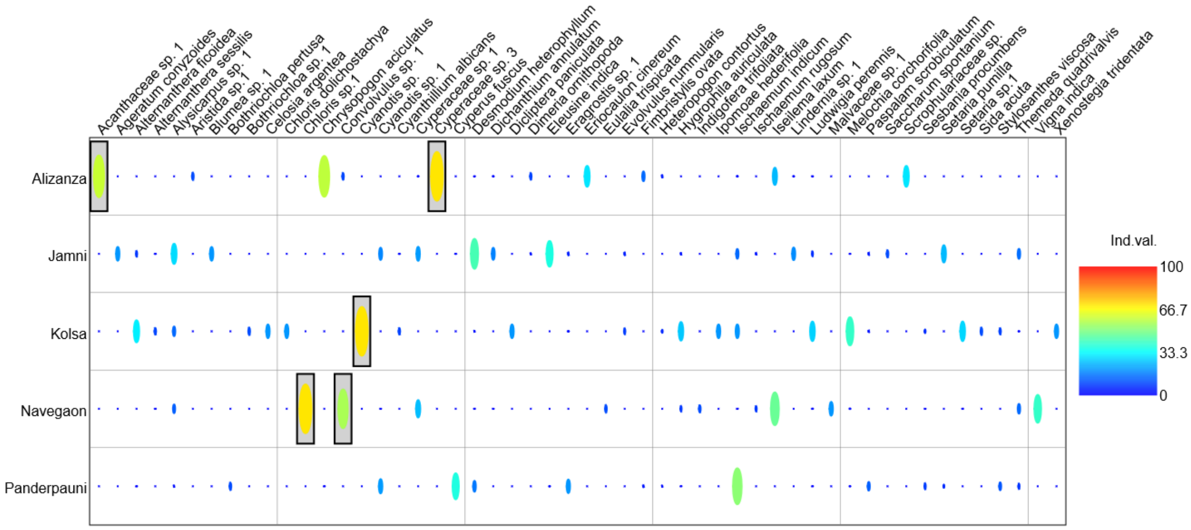

Figure 10: Indicator value of plants differed significantly across sites. Species with % cover > 10 were chosen

4.8. Biomass across Sites

The above and below-ground biomass varied significantly across the five sites that were sampled (*Figure 11*). Aboveground biomass was the highest in Navegaon (mean ± SD = 77.20 ± 119.85 g/m^2) and lowest in Alizanza (mean ± SD = 18.21 ± 9.11 g/m^2). In contrast, the root biomass showed a different pattern with Panderpauni (mean ± SD =0.19 ± 0.13) and Jamni (mean ± SD = 0.18 ± 0.10) being the highest, whereas Navegaon was the lowest (mean ± SD = 0.04 ± 0.02 g/m^2). This inverse relationship between aboveground and belowground biomass at Navegaon may reflect a grass species assemblage that allocates relatively more biomass above ground.

The observed variation in biomass allocation across the study sites suggests a shift in life-history strategies along the restoration chronosequence. The inverse relationship at Navegaon, characterised by the highest aboveground biomass and lowest root biomass, is typical of early-successional communities. Here, pioneer species prioritise rapid vertical growth and seed production to maximise site occupancy in the relatively soft, low-density soils post-relocation. In contrast, the significantly higher belowground biomass recorded in Panderpauni and Jamni indicates a transition toward a 'stability-oriented' community. In these older meadows, plants likely allocate more energy to root systems for nutrient storage and drought resilience, a trait common in mature perennial grasslands. This shift from surface-heavy to root-heavy biomass suggests that while recently restored sites like Navegaon provide immediate high-volume forage, older sites like Jamni and Panderpauni offer greater long-term ecosystem stability and carbon sequestration potential.

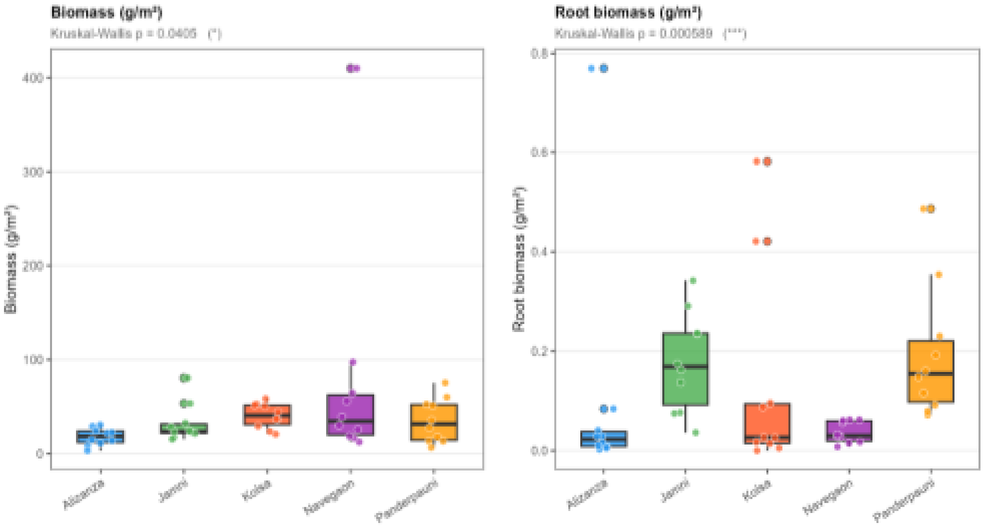

Figure 11: Aboveground and belowground biomass allocation across restoration sites.

4.9. Soil Properties

The Bulk density of the soil also differed significantly across the sites (*Figure 12*) was highest value at Alizanza (mean ± SD = 1.10 ± 0.31 g/cm^3) and Kolsa (mean ± SD = 1.01 ± 0.26

g/cm^3), and the lowest at Navegaon (mean ± SD = 0.63 ± 0.11 g/cm^3). The significant variation in soil bulk density across the sites suggests that the physical structure of the soil is a primary determinant of plant community assembly in the TATR meadows. The exceptionally low bulk density at Navegaon likely reflects the recent history of village land-use and soil disturbance, which has created a high-porosity environment conducive to rapid aboveground biomass production by pioneer species. The higher bulk density values recorded at Alizanza and Kolsa represent a more compacted, natural soil state. These higher densities act as an environmental filter, favouring stress-tolerant taxa such as *Cyperaceae* and *Acanthaceae,* which are capable of root penetration in resistant substrates. The moderate bulk density observed in the older relocated sites (Jamni and Panderpauni) suggests that over time, the 'soft' agricultural soils are gradually settling and compacting, moving toward the regional edaphic baseline seen in the non-relocated Alizanza site.

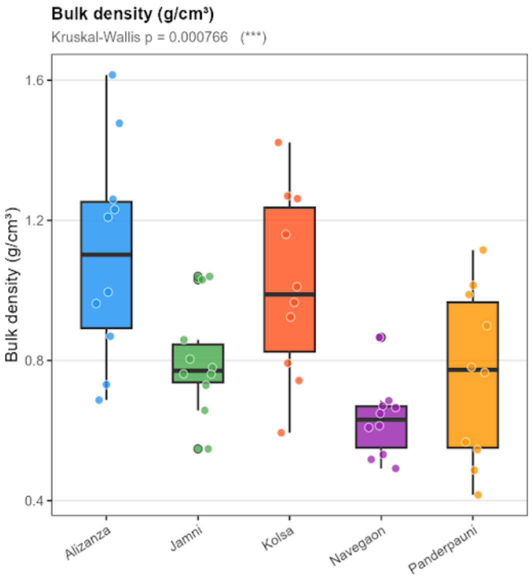

Figure 12: Soil hardness varied significantly across the five sites

4.10. Total Soil Carbon

The average total carbon in the restored grasslands in TATR was 1.7 t/ha (range = 0.6-4.8 t/ha) across the five sites sampled. Among the sites, the highest total carbon was found in Jamni, followed by Kolsa, Alizanza, Navegaon, and Panderpauni (Fig. 12). The total amount of carbon varied significantly across the five sites (Kruskal-Wallis test: H =25.95, $p < 0.001$). Jamni, which was relocated in 2014, had the highest carbon, followed by the most recently relocated site, Kolsa (2007). Alizanza, which likely represents the true savanna grassland habitats once found in TATR, ranked third in the amount of carbon, followed by Navegaon (2013) and Panderpauni (1973). The differences in total carbon were significantly different between Jamni and Navegaon (Dunns test: Bonferroni corrected $p = 0.004$) and between Jamni and Panderpauni ($p = 0.00001$) as well as between Kolsa and Panderpauni ($p = 0.005$). Generally, there is high variability in the total carbon across all sites, as visualised in the figure.

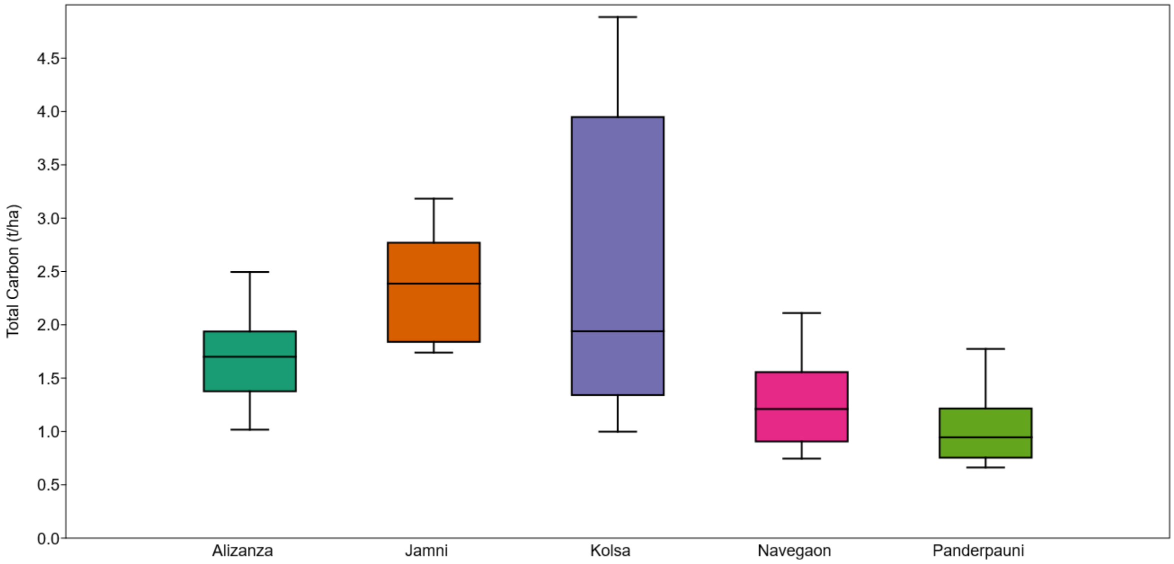

Figure 13: Total soil carbon across the five sites

4.11. Total Grassland Ecosystem Carbon

Across the five sites studied, the total carbon in the grassland ecosystem was the highest in Kolsa and Jamni, followed by Panderpauni and Navegaon, with the relatively lowest in Alizanza (*Table 2*). The total grassland ecosystem carbon is an additive estimate of the carbon stored in Above and Below ground biomass, as well as soil carbon in the top 15 cm layer. In

Navegaon, the above-ground biomass dominated the carbon storage, followed by soil and very little in the roots. Whereas Jamni and Panderpauni stored carbon in the roots compared to the other sites. Panderpauni has the highest physical root biomass on the entire landscape, but it holds the lowest soil carbon stock. This contrast suggests that the plants Navegaon are over-allocating energy into root architecture to forage for nutrients, but that carbon is not yet being transferred or stabilised into the root-free bulk soil matrix. The natural grasslands of Alizanza show a balanced, steady-state allocation of above and below-ground carbon, indicating an old-growth system that has settled into a stable, low-turnover equilibrium.

Table 2: Total grassland ecosystem carbon in the five sites that are sampled. The year when villages were shifted is shown in parentheses. Carbon stored in above- and below-ground biomass is calculated as per IPCC standard of assuming 50% biomass is carbon.

Site (Relocation year)	Aboveground Grass Carbon (tC/ha)	Belowground Root Carbon (tC/ha)	Total soil carbon (tC/ha)	Total Ecosystem Grassland Carbon (tC/ha)
1. Navegaon (2013)	1.54 ± 2.28	0.26 ± 0.14	1.24 ± 0.41	3.05 ± 2.14
2. Kolsa (2007)	0.82 ± 0.25	0.90 ± 1.37	2.53 ± 1.33	4.25 ± 1.85
3. Jamni (2014)	0.64 ± 0.38	1.25 ± 0.67	2.40 ± 0.49	4.29 ± 0.71
4. Panderpauni (1973)	0.71 ± 0.45	1.37 ± 0.90	1.03 ± 0.35	3.11 ± 0.87
5. Alizanza (Natural)	0.36 ± 0.17	0.70 ± 1.59	1.69 ± 0.43	2.75 ± 1.36

4.12. Vegetation Composition and Soil Density

The soil density was not homogeneous across the sites, and this can influence the vegetation composition. When examined, the vegetation composition of the five locations grouped in ordination space with two axes explaining nearly 99% of the variation (Axis 1 = 55%, Axis 2 =44%). The plants found in Alizanza were associated with Bulk Density, implying that the plants here were likely adapted to growing in hard soil. Plants in Navegaon have the highest above-ground biomass, indicating that the species were allocating greater in production of biomass above the ground. The vegetation in Jamni and Panderpauni was characterised by the greater production of root biomass, suggesting that these plants were storing biomass below the ground. The vegetation in Kolsa, which also had the greatest diversity, was not characterised strongly by either bulk density or both kinds of biomass. The vegetation here was ideal in comprising species which effectively store biomass in roots as well as above ground. This association, however, is only indicative of a trend as the analysis was not statistically significant (Canonical Correspondence Analysis: trace p = 0.4).

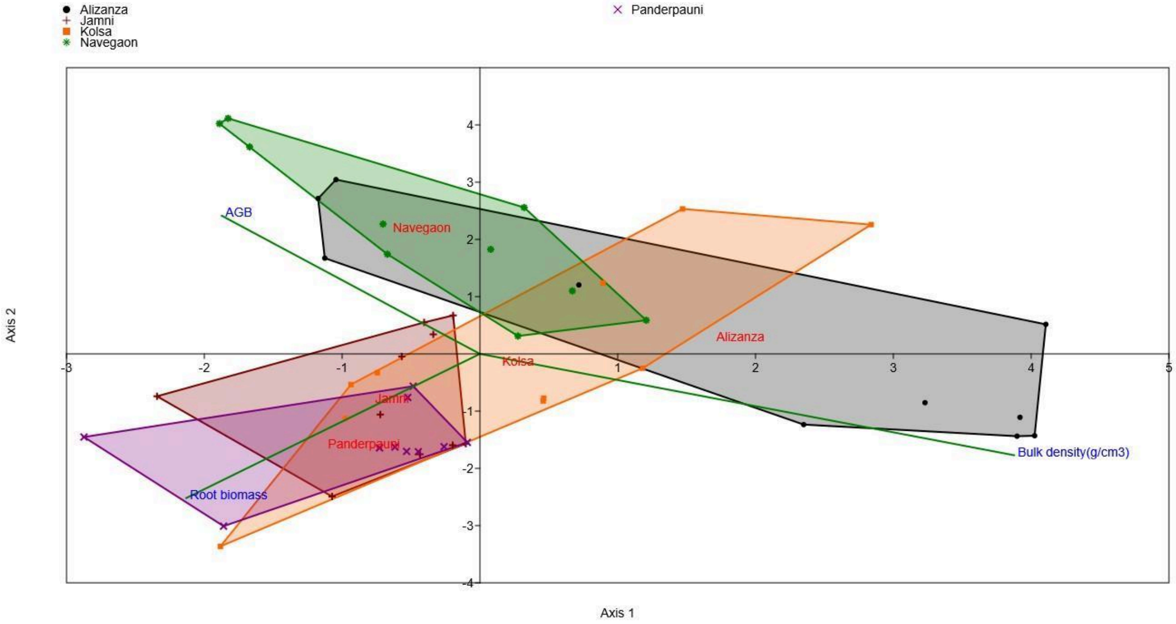

Figure 14: Canonical Correspondence analysis shows clear clustering of the five sites. Bulk density influenced composition in Alizanza, Jamni and Panderpauni comprising species that allocated greater resources to root biomass, and Navegaon comprised plants allocating to above ground biomass. Kolsa had a mix of species allocating both above and below ground, as well as variability in hard soil-tolerant species.

The lack of edaphic homogeneity across the study sites appeared to be a primary driver of vegetation structure. Our CCA results revealed that nearly 99% of the constrained variation was captured by two axes, effectively separating sites based on their 'life-history strategies. Navegaon represents a high-productivity state, where low bulk density likely facilitates maximum aboveground biomass allocation. In contrast, Jamni and Panderpauni represent a transition toward community stability, characterised by increased root biomass, a key trait for long-term persistence in seasonal tropical grasslands. The plant community at Alizanza is uniquely filtered by soil hardness, favouring taxa adapted to high bulk density. Interestingly, Kolsa's position in the ordination space is centralised and not dominated by a single environmental vector. This mirrors its status as the most diverse site, suggesting that a balance of edaphic conditions and biomass allocation promotes the highest levels of species coexistence. While these patterns reflect a strong biological trend (Axis 1), they highlight how the legacy of village relocation continues to shape the functional identity of TATR's meadows.

5. Conclusion - Vegetation Analysis

The relocation of human settlements within the Tadoba-Andhari Tiger Reserve (TATR) is an example of a successful assisted successional transformation, evolving former agricultural lands into functional meadow ecosystems. Our study demonstrates that while all study sites have achieved the primary restoration goal of high vegetation cover and soil stabilisation, they have diverged into distinct ecological habitat types, shaped by the legacy of land use and edaphic conditions.

Our findings reveal a clear successional trade-off between productivity and persistence. Recently restored sites, specifically Navegaon, represent an early-successional ‘pioneer’ stage characterised by low soil bulk density and an allocation strategy favoring high aboveground biomass. As the chronosequence progresses, sites like Jamni and Panderpauni converge toward a more stable state, characterised by increased investment in belowground (root) biomass and higher taxonomic similarity. Kolsa emerged as the ‘equilibrium’ site, where a balance of environmental factors supports the highest levels of species diversity and evenness. Furthermore, the comparison with the non-relocated site, Alizanza, highlights that natural meadows in this landscape may be fundamentally different from restored ones. The high soil bulk density at Alizanza acts as a physical filter that maintains a taxonomically distinct community of stress-tolerant specialists. This suggests that the soft-soil high-productivity state of restored meadows might be a temporary legacy of tillage that will eventually settle toward the regional baseline.

6. Microbial Diversity Assessment

6.1. Why Microbial Baselines Matter in Managed Grasslands

Grasslands within protected forest landscapes can play key roles in biodiversity and ecosystem functioning. This study establishes a baseline of soil's microbial diversity and its functional potential across the grassland and forest habitats in the Tadoba–Andhari Tiger Reserve. Our primary objective is to assess the microbial diversity within the grasslands to underline the complexities of the community to better inform ecosystem health monitoring, climate resilience, and restoration planning.

6.2. Forests and Grasslands Host Fundamentally Different Microbial Worlds

We first understand the diversity of microbial communities between forest and grassland sites. We analysed the between-samples community distances. Figure 15, here, is a PCoA, (Principal Coordinate Analysis), involving (Axis 1, and Axis 2, the two "principal coordinates" that capture the most significant patterns of variation in our data). The limited representation reveals a fairly clear compositional differentiation between grassland and forest microbiota.

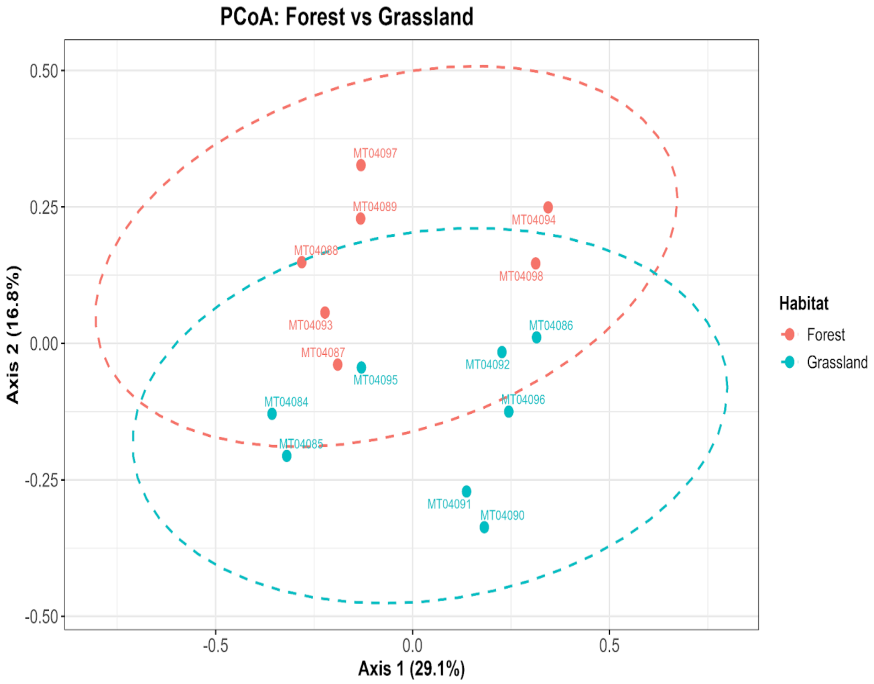

Figure 15: Principal Coordinate Analysis (PCoA) of soil microbial communities across forest and grassland habitats in the Tadoba–Andhari Tiger Reserve

Axis 1 explains 29.1% of the variation and largely separates the two habitats, with grassland samples clustering toward positive values and forest samples toward negative values, indicating habitat-specific community structure. Axis 2 accounts for another 16.8% of variation and captures within-habitat heterogeneity, both in forest and grassland samples.

Even in the light of the expected fair amount of overlap, the distinct clustering and separation of group centroids suggest that land-cover type strongly influences or determines the composition of the respective microbial community, likely reflecting differences in vegetation, soil properties, and resource availability between forest and grassland ecosystems.

Similar to the above, the three land-use types exhibit distinct microbial community structures shaped by contrasting environmental filters in tropical dry deciduous landscapes (*Figure 16*). **Grasslands, even when sampled post-monsoon**, are dominated by stress-tolerant taxa such as *Bacilli_A* and *Actinomycetes*, reflecting rapid wet–dry cycling, high temperatures, and fast-decomposing grass litter. The low representation of moisture- and stability-associated groups (e.g., Binatia) indicates that short-term moisture pulses do not override long-term abiotic constraints. **These grasslands are actively managed**, with manual removal of woody and nitrogen-fixing vegetation, likely reducing rhizosphere complexity and biologically mediated nitrogen inputs, further filtering microbial composition. Forests support more balanced communities enriched in *Alphaproteobacteria* and *Acidobacteria*, while forest fire-line soils show intermediate assemblages reflecting disturbance-driven reassembly.

Figure 16: Class-level taxonomic composition across forest, grassland, and fire-line soils

At the genus level too, perhaps more so, clear land-use–specific signatures are evident. Grasslands are characterised by a high contribution of *Bacillus*-affiliated taxa (*Bacillus_A, Bacillus_BD, Neobacillus, Peribacillus*), alongside *Bradyrhizobium* and actinobacterial genera such as *Streptomyces*, reflecting selection for spore-forming, fast-responding, and disturbance-tolerant microbes under recurrent drying and management. Forest soils show a comparatively lower dominance of Bacillus-related genera and a greater contribution from diverse, less stress-specialised taxa, consistent with more stable moisture and organic inputs. Fire-line soils display intermediate patterns, with elevated unclassified and generalist genera, again indicating community reassembly under episodic disturbance.

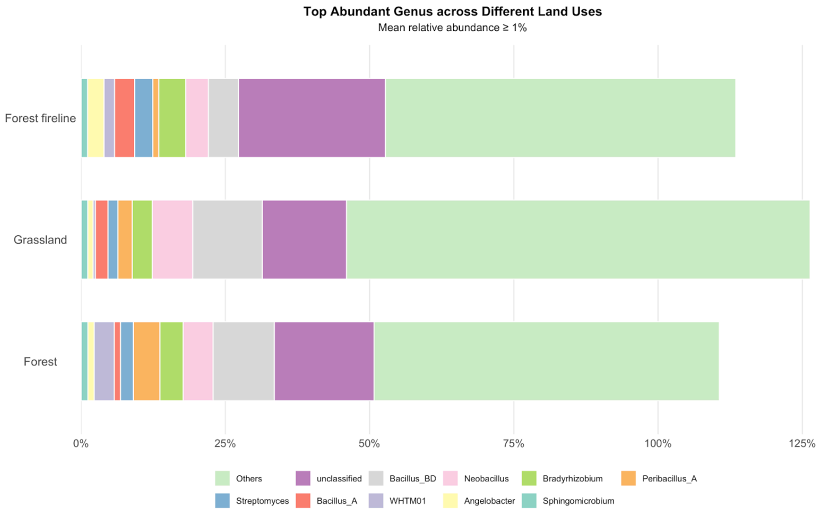

Figure 17: Genus-level microbial signatures across land-use types

Both alpha diversity indices and taxonomic intersections consistently identify Pandharpauni grassland as supporting the highest microbial diversity among the grassland sites.

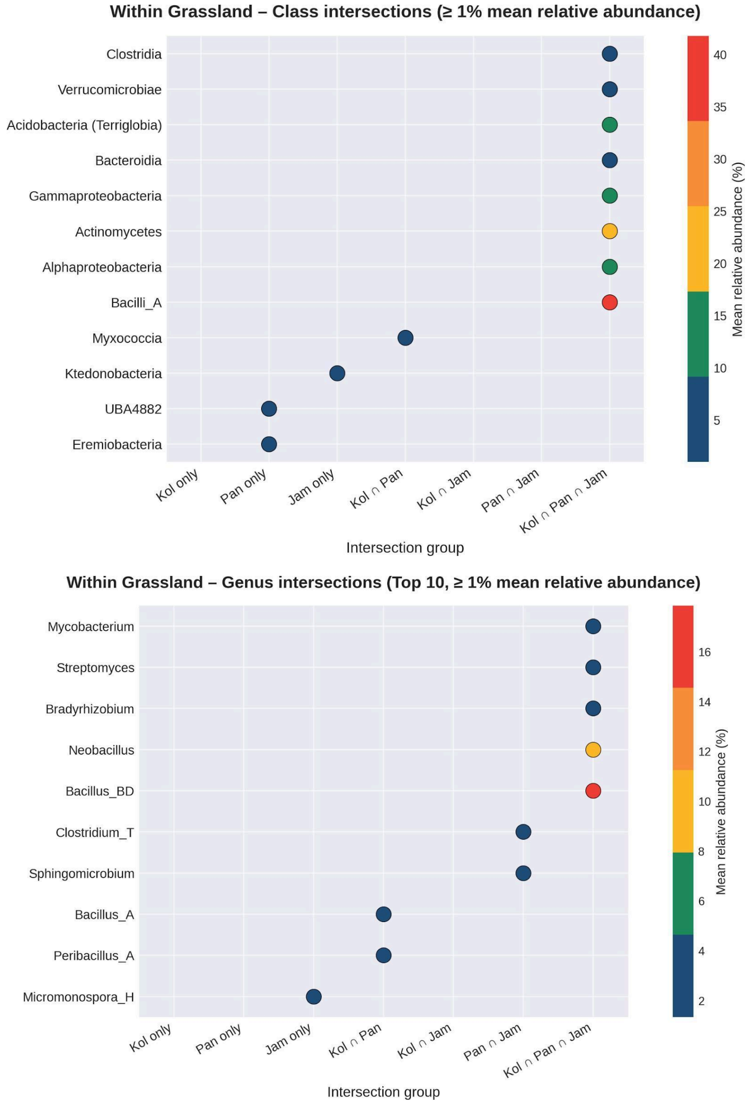

Figure 18: Alpha diversity indices across grassland sites

6.4. Not All Grasslands Are Equal

Alpha diversity indices and taxonomic composition together indicate that Pandharpauni grassland supports the highest microbial diversity among the three grassland sites. Pandharpauni grasslands exhibit the highest estimated richness (Chao1 up to ~976), higher Shannon diversity and Fisher's alpha, reflecting both greater richness and evenness. This is consistent with the broader and more balanced distribution of dominant bacterial classes in Pandharpauni, where *Bacilli, Actinomycetes, Alphaproteobacteria, Acidobacteria*, and *Gammaproteobacteria* contribute more evenly to community structure, rather than a single class dominating.

Figure 19: Class-level taxonomic composition among Jamni, Pandharpauni and Kolsa grasslands

At the genus level, Pandharpauni grasslands show a more even spread among Bacillus-related taxa (e.g. *Bacillus, Neobacillus, Peribacillus*), *Bradyrhizobium*, and actinobacterial genera such as *Streptomyces* and *Micromonospora*, alongside a substantial but not overwhelming "Others" fraction. In contrast, Kolsa grasslands, despite moderate Shannon diversity, show stronger dominance by fewer classes and a higher proportion of unclassified and "Others" at the genus level, consistent with lower Chao1 and Fisher's alpha. Jamni grasslands display intermediate patterns, with class-level diversity comparable to Pandharpauni but reduced genus-level richness, reflected in lower richness estimates. Overall, the stacked abundance profiles reinforce the alpha diversity results by showing that **Pandharpauni grassland diversity arises from both higher richness and a more even taxonomic structure**, whereas Kolsa and Jamni grasslands are characterised by comparatively greater dominance and reduced taxonomic breadth.

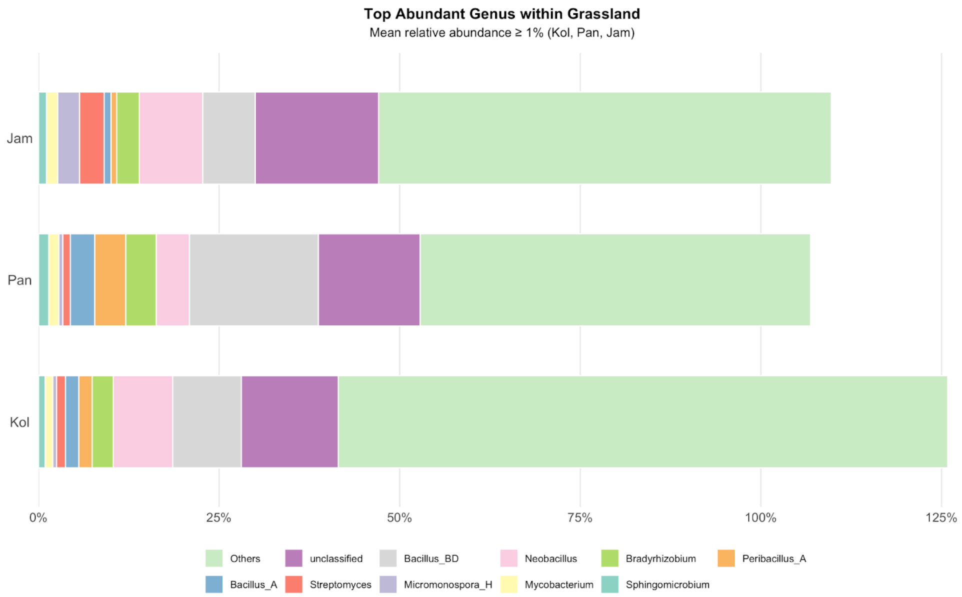

Figure 20: Genus-level composition across the three managed grasslands

6.5. How These Grasslands Function Belowground

The two graphs highlight clear functional differentiation among the three managed grasslands (Kolsa, Jamni, Pandharpauni) in terms of nitrogen-fixing bacteria (*Figure 21: Fig. A*) and plant growth–promoting rhizobacteria (*Figure 21: Fig. B*).

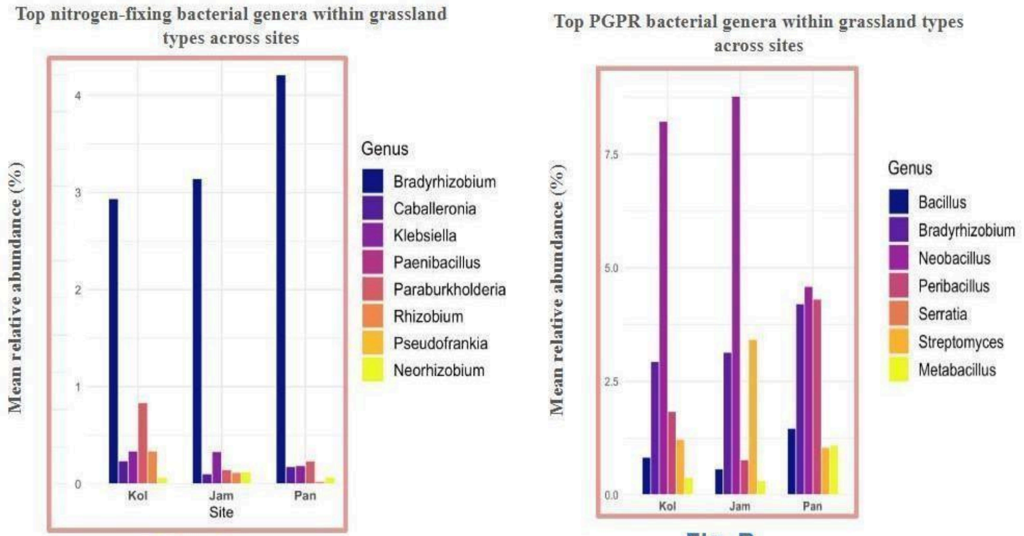

Fig. A.

Fig. B

Figure 21: Functional guild composition: nitrogen-fixing bacteria (A) and plant growth–promoting rhizobacteria (PGPR) (B) across grassland sites

Nitrogen-fixing genera (*Figure 21: Fig. A*) are dominated by *Bradyrhizobium* across all sites, with the highest relative abundance in Pandharpauni grassland, followed by Jamni and Kolsa. Minor contributions from *Caballeronia, Paenibacillus, Rhizobium*, and *Paraburkholderia* occur at all sites but remain consistently low, suggesting that symbiotic or free-living N fixation is largely driven by a single dominant genus. The relatively lower abundance of secondary N-fixers in these grasslands indicate stronger environmental or management filtering.

PGPR communities (*Figure 21: Fig. B*) show greater site-specific variation. Jamni grassland exhibits high relative abundance of *Neobacillus* and *Streptomyces*, taxa linked to stress tolerance and antimicrobial activity. Pandharpauni supports a more balanced PGPR assemblage, including *Bacillus, Bradyrhizobium,* and *Peribacillus*, indicating functional redundancy. Kolsa shows comparatively lower PGPR abundance, consistent with stronger abiotic stress and reduced rhizosphere complexity.

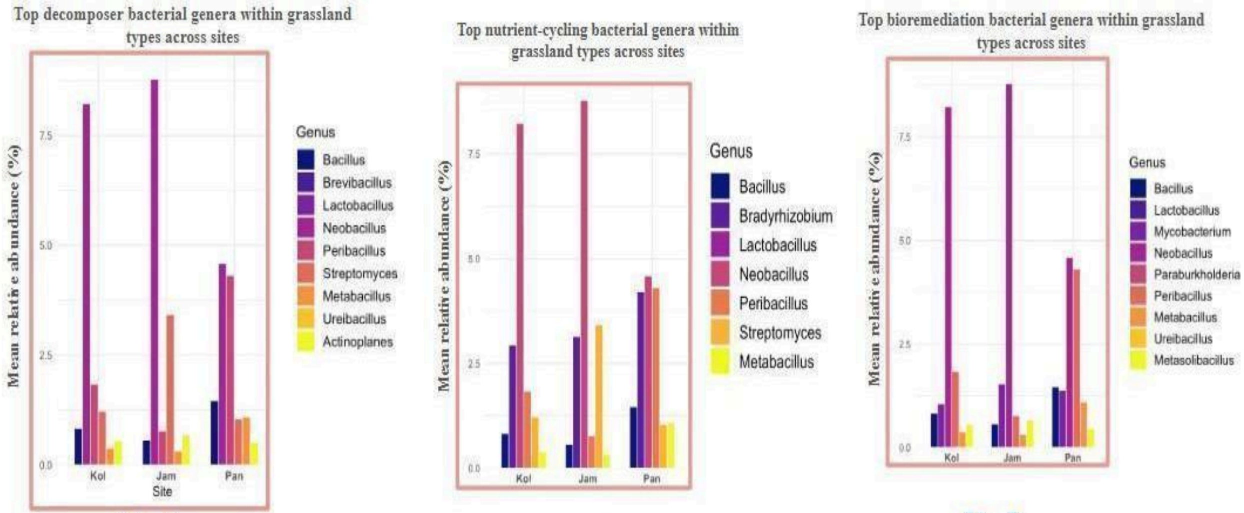

Fig. C Fig. D. Fig. E

Figure 22: Functional guild distribution: decomposers (C), nutrient cycling bacteria (D), and bioremediation-associated taxa (E) across grasslands

Decomposers (*Figure 22: Fig. C*) assemblages show dominance of fast-growing Bacillus-lineage taxa with moderate *Streptomyces* and limited actinobacterial diversity, indicating labile-carbon–oriented decomposition and comparatively lower capacity for sustained complex-carbon processing relative to forests. The presence of Actinoplanes exclusively in grasslands suggests active rhizosphere-driven decomposition and retained niche complexity, representing a positive ecological signal despite overall functional skewing.

Nutrient Cycling bacterial generic activity (*Figure 22: Fig. D*) in Kolsa, Jamni, and Pandherpauni is rapid and nitrogen-supported, driven largely by *Neobacillus* and *Bradyrhizobium*. Kolsa shows the strongest pulse-driven dynamics with high *Neobacillus* dominance and weaker stabilisation. Jamni exhibits moderate *Streptomyces* and slightly better functional balance, though still fast-cycling. Pandherpauni shows relatively greater evenness with *Streptomyces* and *Peribacillus*, but limited lignin-rich inputs and fewer specialist decomposers constrain long-term buffering. Overall, all three grasslands are productive but less structurally stabilised compared to the forest systems.

Bioremediation (*Figure 22: Fig. E*) associated communities in all three grasslands are metabolically active but functionally simplified. Kolsa and Jamni show strong dominance of the generalist *Neobacillus*, with comparatively low presence of *Mycobacterium* and minor degraders such as *Ureibacillus* and *Metabacillus*, indicating detoxification driven largely by fast-growing taxa. Pandharpauni exhibits relatively greater evenness with moderate *Mycobacterium* and *Peribacillus*, suggesting somewhat better functional balance. However, across all sites, reduced representation of specialist hydrocarbon degraders limits metabolic redundancy, resulting in moderate detoxification capacity but lower adaptive resilience compared to more structurally buffered systems.

6.6. Metabolic Activity: Streamlined vs Functionally Redundant Systems

Across the grassland microbial samples, **the top 20 metabolic pathways** show a strong and consistent emphasis on core carbon metabolism, cell maintenance, and stress adaptation, with variation in relative intensity among sites.

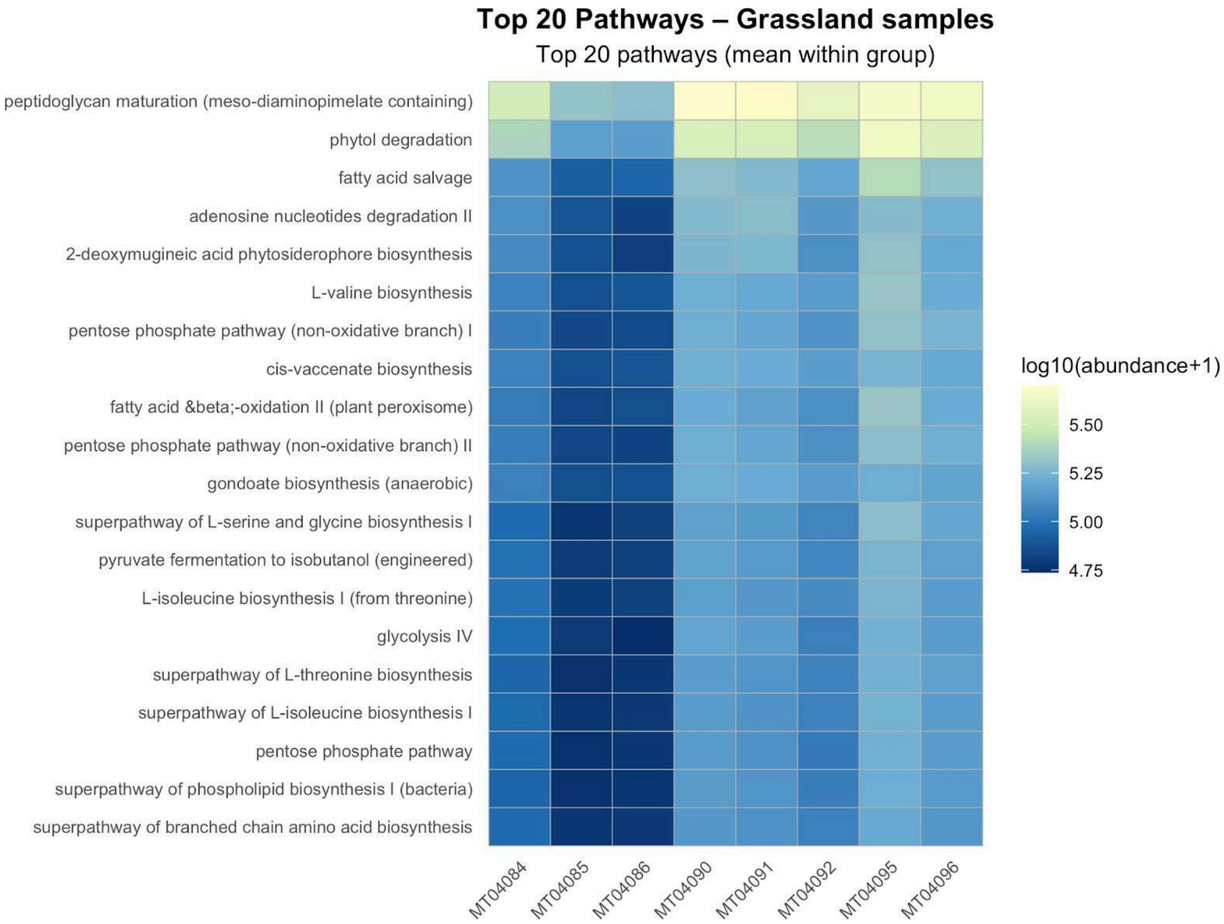

Figure 23: Heatmap of top 20 predicted metabolic pathways across grassland microbial communities

The Kolsa grassland samples (*Figure 23: first three columns*) show comparatively low log-abundance for many of the top 20 pathways, as indicated by darker blue shades. This suggests that, despite the presence of core metabolic functions, overall pathway representation is relatively constrained, likely reflecting strong environmental filtering in these open, managed grasslands.

In contrast, the Pandharpauni grassland samples (*Figure 23: middle three columns*) and Jamni grassland samples (*Figure 23: last two columns*) display lighter blue tones across multiple pathways, indicating higher relative pathway abundance and greater functional expression, consistent with higher microbial turnover and functional redundancy.

Ecologically, this pattern implies that Pandharpauni grassland is functionally more active, while Kolsa grassland hosts a metabolically streamlined community adapted to recurrent stress, rapid wet–dry cycling, and human-alteration-driven reductions in organic and rhizosphere complexity.

6.7. What This Means for Grassland Management

Structural and functional profiles of the respective microbial communities indicate that the three managed grasslands differ markedly in ecological condition and resilience, warranting site-specific management approaches.

1. **Pandharpauni grassland exhibits the highest taxonomic and functional diversity**, suggesting a well-buffered and resilient below-ground system; current management practices should therefore be maintained, avoiding further intensification or extensive vegetation removal.
2. In contrast, **Kolsa grassland is characterised by dominance of stress-tolerant microbial taxa and comparatively low functional pathway abundance**, indicating a constrained but stable system adapted to recurrent disturbance. Here, reducing the intensity or frequency of manual vegetation removal and allowing retention of native herbaceous legumes may enhance nutrient cycling without promoting woody encroachment.
3. **Jamni grassland shows intermediate diversity and functional redundancy**, suggesting greater vulnerability to environmental fluctuations; so, adopting rotational or mosaic management techniques could help stabilise microbial processes.

As sampling was conducted post-monsoon, seasonal monitoring—particularly during the late dry period—is recommended to assess temporal stability. Overall, grassland management in tropical dry deciduous landscapes should aim to sustain microbial functional redundancy to support long-term ecosystem resilience under erratic climatic variability.

6.8. Microbial Augmentation as a Restoration Tool

For more vulnerable or disturbance-prone grasslands, particularly Jamni and selected patches of Kolsa, **targeted application of native microbial consortia** could be explored as a supplementary restoration strategy. Consortia dominated by locally sourced ***Actinobacteria*, *Alphaproteobacteria*, and saprotrophic *Bacilli***, selected for drought tolerance, organic matter decomposition, and nutrient mobilisation, may help accelerate recovery of soil functions under recurrent stress. Such interventions should prioritise **autochthonous (site-derived) microbes** to avoid disrupting existing community structure or introducing invasive strains.

Microbial inoculation is most likely to be effective when combined with reduced disturbance intensity, organic matter retention, and post-monsoon application to maximise establishment success. Importantly, microbial amendments should be implemented through **small-scale pilot trials with long-term monitoring,** assessing effects on soil function, plant regeneration, and microbial stability. Used judiciously, microbial consortia can enhance functional redundancy and resilience, **but they should complement—not replace—habitat-based management, in tropical dry deciduous grasslands with their moderate complexity of environmental filtration.**

7. Management Implications and Proposed Interventions

These results offer actionable management insights for the TATR Forest Department and restoration practitioners, demonstrating that:

- Greenness or above-ground cover alone is an **insufficient metric for success**. Monitoring should include **Root: Shoot ratios, community composition, and species diversity measures** to track the ecosystem resilience and carbon sequestration potential.
- Grassland meadows are complex ecosystems. Kolsa could serve as a reference model for 'ideal' meadow restoration, where management aims for **high species evenness** and a **balance between grass and forb functional groups**.
- The TATR landscape is heterogeneous. The presence of both high-biomass pioneer meadows (for immediate forage) and high-diversity stable meadows (for long-term resilience) creates a valuable mosaic for the reserve's herbivores. **Management should focus on maintaining this diversity across the landscape** rather than forcing all meadows toward a single structural type.
- It is critical to recognise that these meadows are not merely high-yield pastures for ungulates, but complex plant communities. Our findings show that **forbs contribute the highest species richness across all sites**; while these taxa may appear "non-palatable" for large herbivores, they are essential for maintaining taxonomic distinctness and sustaining a broader range of biodiversity, including pollinators and soil micro-fauna.
- The current practice of selective plant removal risks simplifying the meadow into a functional monoculture, potentially reducing long-term ecosystem resilience. Any management intervention involving the removal of "non-target" species must be preceded by carefully designed, long-term experimental evaluations to ensure that the structural integrity and evolutionary depth of the TATR meadows are not compromised for short-term biomass gains.
- Distinct microbial profiles across the three grasslands require site-specific management:

  - **Pandharpauni:** Being close to the waterbody, it supports high microbial diversity and evenness. Current management should continue without intensification of vegetation clearing.
  - **Kolsa:** Dominated by stress-tolerant microbes, this system is stable but constrained by frequent disturbances. Reducing manual weeding and retaining native legumes will boost nutrient cycling without causing woody plant encroachment.
  - **Jamni:** Intermediate diversity makes this site vulnerable to environmental shifts and management filtering. Using rotational or mosaic management will help stabilize below-ground processes.

  Tailoring strategies to these unique microbial traits ensures long-term ecosystem resilience.

- Vulnerable grasslands with high environmental and management filtering, like Jamni or Kolsa, could benefit from application of native microbial consortia that can accelerate soil recovery under stress. Inoculants should feature locally sourced, drought-tolerant *Actinobacteria*, *Alphaproteobacteria*, and *Bacilli* to boost decomposition and nutrient mobilization without introducing invasive strains. To maximise success, **apply these site-derived microbes post-monsoon alongside reduced weeding and organic matter retention**. This strategy should start with small-scale pilot trials to monitor soil and plant impacts. Ultimately, bio-inoculation should complement habitat management to safely enhance functional redundancy and resilience in these dry deciduous landscapes.

8. Acknowledgements

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This report was authored by Harshin Meera Ambavarapu, Sanjukta Biswas, Eapsa Berry, Seshadri K. S., and Abi T. Vanak, and prepared by the Centre for Policy Design, ATREE.

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9. Appendix

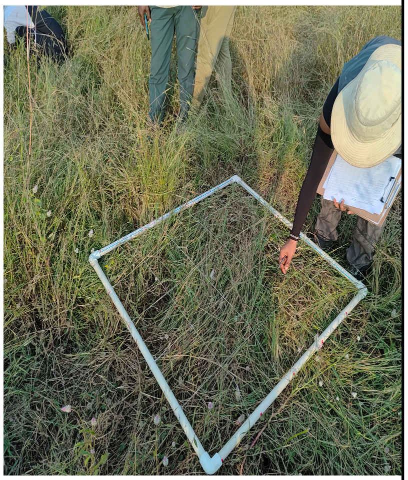
Table A1. List of species encountered and the mean % of cover across 50 quadrats across all sites.

Sl.no	Family	Genus	*Species*	Mean % cover	Range
1	Acanthaceae	Acanthaceae	*Acanthaceae sp. 1*	1.6	0 - 4
2	Acanthaceae	Acanthaceae	*Acanthaceae sp. 3 (small violet)*	0.1	0 - 1
3	Acanthaceae	Acanthaceae	*Acanthaceae sp.2 (blue)*	0.4	0 - 2
4	Acanthaceae	Dicliptera	*Dicliptera paniculata*	4.1	0 - 25
5	Acanthaceae	Hygrophila	*Hygrophila auriculata*	1.74	0 - 38
6	Acanthaceae	Justicia	*Justicia sp. 1*	0.2	0 - 2
7	Acanthaceae	Justicia	*Justicia sp. 2*	0.8	0 - 8
8	Acanthaceae	Rungia	*Rungia sp.*	0.2	0 - 2
9	Amaranthaceae	Alternanthera	*Alternanthera ficoidea*	3.03	0 - 40
10	Amaranthaceae	Alternanthera	*Alternanthera sessilis*	1.73	0 - 48
11	Amaranthaceae	Celosia	*Celosia argentea*	1.2	0 - 8
12	Asteraceae	Ageratum	*Ageratum conyzoides*	0.8	0 - 14
13	Asteraceae	Asteraceae	*Asteraceae sp. 1*	0.2	0 - 1
14	Asteraceae	Blumea	*Blumea sp. 1*	3.1	0 - 27
15	Asteraceae	Cyanthillium	*Cyanthillium albicans*	0.55	0 - 10
16	Asteraceae	Synedrella	*Synedrella nodiflora*	0.6	0 - 6
17	Asteraceae	Vicoa	*Vicoa cernua*	0.1	0 - 1
18	Commelinaceae	Cyanotis	*Cyanotis sp.*	4.9	0 - 30
19	Commelinaceae	Cyanotis	*Cyanotis sp. 1*	0.9	0 - 8
20	Convolvulaceae	Convolvulus	*Convolvulus sp. 1*	4.25	0 - 20
21	Convolvulaceae	Evolvulus	*Evolvulus alsinoides*	0.1	0 - 1
22	Convolvulaceae	Evolvulus	*Evolvulus nummularis*	1.25	0 - 20
23	Convolvulaceae	Ipomoea	*Ipomoea hederifolia*	1.1	0 - 12
24	Convolvulaceae	Xenostegia	*Xenostegia tridentata*	2.4	0 - 22
25	Cyperaceae	Cyperaceae	*Cyperaceae sp. 1*	1.1	0 - 12
26	Cyperaceae	Cyperaceae	*Cyperaceae sp. 2*	0.2	0 - 1
27	Cyperaceae	Cyperaceae	*Cyperaceae sp. 3*	4.9	0 - 12
28	Cyperaceae	Cyperus	*Cyperus brevifolius*	0.1	0 - 1
29	Cyperaceae	Cyperus	*Cyperus fuscus*	0.75	0 - 8
30	Cyperaceae	Cyperus	*Cyperus michelianus*	0.4	0 - 2

31	Cyperaceae	Cyperus	*Cyperus mindorensis*	0.1	0 - 1
32	Cyperaceae	Fimbristylis	*Fimbristylis cymosa*	0.1	0 - 1
33	Cyperaceae	Fimbristylis	*Fimbristylis ovata*	0.7	0 - 8
34	Eriocaulaceae	Eriocaulon	*Eriocaulon cinereum*	1	0 - 8
35	Fabaceae	Acacia	*Acacia sp.1*	0.8	0 - 6
36	Fabaceae	Alysicarpus	*Alysicarpus sp. 1*	2.65	0 - 16
37	Fabaceae	Butea	*Butea monosperma*	0.6	0 - 6
38	Fabaceae	Cassia	*Cassia tora*	0.05	0 - 1
39	Fabaceae	Desmodium	*Desmodium heterophyllum*	5.32	0 - 49
40	Fabaceae	Fabaceae	*Fabaceae sp. 1*	0.2	0 - 2
41	Fabaceae	Indigofera	*Indigofera trifoliata*	3.6	0 - 36
42	Fabaceae	Sesbania	*Sesbania procumbens*	2.33	0 - 56
43	Fabaceae	Stylosanthes	*Stylosanthes viscosa*	0.7	0 - 4
44	Fabaceae	Tephrosia	*Tephrosia purpurea*	0.1	0 - 1
45	Fabaceae	Vigna	*Vigna indica*	2.1	0 - 12
46	Gentianaceae	Canscora	*Canscora diffusa*	0	0 - 0
47	Gentianaceae	Enicostema	*Enicostema axillare*	0.1	0 - 1
48	Gentianaceae	Exacum	*Exacum pedunculatum*	0.4	0 - 4
49	Lamiaceae	Hyptis	*Hyptis suaveolens*	0.4	0 - 2
50	Lamiaceae	Lamiaceae	*Lamiaceae sp. 1*	0.1	0 - 1
51	Lamiaceae	Ocimum	*Ocimum canum*	0	0 - 0
52	Linderniaceae	Bonnaya	*Bonnaya ciliata*	0.4	0 - 4
53	Linderniaceae	Lindernia	*Lindernia sp. 1*	0.65	0 - 8
54	Lythraceae	Rotala	*Rotala sp.*	0.3	0 - 2
55	Malvaceae	Malvaceae	*Malvaceae sp. 1*	1	0 - 6
56	Malvaceae	Melochia	*Melochia corchorifolia*	0.525	0 - 8
57	Malvaceae	Sida	*Sida acuta*	1	0 - 10
58	Malvaceae	Sida	*Sida cordifolia*	0.1	0 - 1
59	Malvaceae	Sida	*Sida sp. 1*	0.8	0 - 8
60	Malvaceae	Urena	*Urena lobata*	0.2	0 - 2
61	Melastomataceae	Melastoma	*Melastoma sp. 1*	0.3	0 - 2
62	Onagraceae	Ludwigia	*Ludwigia perennis*	1.4	0 - 25
63	Orobanchaceae	Striga	*Striga angustifolia*	0.1	0 - 1
64	Phyllanthaceae	Phyllanthus	*Phyllanthus sp.*	0.5	0 - 2
65	Poaceae	Aristida	*Aristida sp.1*	0.6	0 - 6
66	Poaceae	Bothriochloa	*Bothriochloa pertusa*	1.6	0 - 16
67	Poaceae	Bothriochloa	*Bothriochloa sp. 1*	1.05	0 - 21
68	Poaceae	Chloris	*Chloris dolichostachya*	3.6	0 - 28
69	Poaceae	Chloris	*Chloris gayana*	0.3	0 - 4

70	Poaceae	Chloris	*Chloris sp.1*	22.1	0 - 74
71	Poaceae	Chrysopogon	*Chrysopogon aciculatus*	17.9	0 - 88
72	Poaceae	Dactyloctenium	*Dactyloctenium aegyptium*	0.1	0 - 1
73	Poaceae	Dichanthium	*Dichanthium annulatum*	3.23	0 - 45
74	Poaceae	Dichanthium	*Dichanthium caricosum*	0.1	0 - 1
75	Poaceae	Dimeria	*Dimeria ornithopoda*	4.1	0 - 74
76	Poaceae	Eleusine	*Eleusine indica*	0.65	0 - 4
77	Poaceae	Eragrostis	*Eragrostis sp. 1*	0.96	0 - 16
78	Poaceae	Eragrostis	*Eragrostis sp. 2*	0.2	0 - 1
79	Poaceae	Eragrostis	*Eragrostis tenella*	0.2	0 - 2
80	Poaceae	Eragrostis	*Eragrostis unioloides*	0.1	0 - 1
81	Poaceae	Eulalia	*Eulalia trispicata*	2	0 - 20
82	Poaceae	Heteropogon	*Heteropogon contortus*	0.8	0 - 12
83	Poaceae	Ischaemum	*Ischaemum indicum*	25	0 - 94
84	Poaceae	Ischaemum	*Ischaemum rugosum*	1.5	0 - 22
85	Poaceae	Iseilema	*Iseilema laxum*	27.55	0 - 88
86	Poaceae	Paspalum	*Paspalum scrobiculatum*	0.63	0 - 8
87	Poaceae	Paspalidium	*Paspalidium flavidum*	0	0 - 0
88	Poaceae	Saccharum	*Saccharum spontaneum*	2.2	0 - 22
89	Poaceae	Setaria	*Setaria pumilla*	0.85	0 - 8
90	Poaceae	Setaria	*Setaria sp. 2*	0.1	0 - 1
91	Poaceae	Setaria	*Setaria sp.1*	3.2	0 - 48
92	Poaceae	Themeda	*Themeda quadrivalvis*	9.325	0 - 89
93	Rhamnaceae	Ziziphus	*Ziziphus mauritiana*	0.1	0 - 1
94	Rubiaceae	Oldenlandia	*Oldenlandia herbacea*	0.5	0 - 2
95	Scrophulariaceae	Scrophulariaceae	*Scrophulariaceae sp.*	4	0 - 31

Soil Sample Collection (Kolsa Grasslands)

Soil Sample Collection (Kolsa Forest)

Soil Sample Collection (Panderpauni Grasslands)

Soil Sample Collection (Panderpauni Forest Core)



Soil Sample Collection (Jamni Grasslands)

Soil Sample Collection (Jamni Forest Core)