**Competition Cancels Out Phylogenetic Conservatism in Plant Response to Herbicide Spray in an Unmanaged Grass Lawn**

**Introduction**

Herbicides significantly shape plant community dynamics by selectively influencing their taxonomic and functional composition through their effects on survival, growth, and recovery. Some plant species demonstrate resilience and recover rapidly after herbicide exposure, while others fail to re-establish. Environmental conditions, resource availability, and species-specific traits may influence these differential responses. However, the extent to which evolutionary history shapes these responses remains unclear.

Closely related species often share phenotypic traits, which could result in similar levels of resilience or susceptibility to herbicides—a phenomenon known as phylogenetic conservatism. However, competition among closely related species may counteract this pattern. If related species experience stronger competition with one another than with more distantly related species, herbicide resilience within a closely knit clade could lead to intense intra-clade competition, ultimately favoring the persistence of more distantly related species. This means that competition could drive phylogenetic divergence in plant responses to herbicides, weakening the expected pattern of phylogenetic conservatism.

Despite extensive research on plant-herbicide interactions, the role of phylogenetic relatedness in shaping species’ responses to disturbances from herbicide application remains understudied. Understanding whether plant responses to herbicide application—either as survival or recovery—are phylogenetically conserved can provide valuable insights into community assembly and species coexistence in disturbed environments. Investigating these patterns is particularly relevant in unmanaged plant communities, where species interactions occur without human intervention, allowing for a clearer assessment of evolutionary constraints and competitive dynamics.

This study aims to assess the phylogenetic conservatism of plant responses to herbicide application in an unmanaged lawn. Specifically, we will determine whether closely related species exhibit similar survival and recovery patterns, as reflected in changes in ground cover over time. If phylogenetic conservatism influences herbicide resilience, we expect closely related species to exhibit similar responses immediately following herbicide application, leading to increased phylogenetic clustering among surviving species. However, as ground cover increases during post-spray recovery, competitive interactions may disrupt this pattern, leading to greater phylogenetic divergence over time.

By examining how phylogenetic relatedness influences plant survival and recovery in response to herbicide disturbance, this study will contribute to a broader understanding of species persistence in dynamic environments. Identifying the balance between evolutionary constraints and competitive interactions in shaping plant community responses can provide valuable insights for ecological management and conservation in both natural and human-influenced landscapes.

**Materials and Methods**

**Study site**

The study was conducted from January to April 2023 within an enclosed lawn behind Egborge Museum at the University of Benin, Benin City, Nigeria, located at a longitude of 6.39265 N and a latitude of 5.61343 E, as recorded using a handheld GPS device. The university is in southern Nigeria, which is characterized by a tropical rainforest environment. As shown in Figure 1, the study site is a pseudo-enclosed area, with three-quarters of its perimeter bordered by concrete structures, while the remaining side is open. The site measures 23.77 m by 11.58 m. During the survey, mean ambient temperatures ranged from 25 to 34 °C (Accuweather, 2023).

After a pre-spray sampling plant cover from the study site, the plot was treated with a non-selective systemic herbicide, Forceup™, containing glyphosate as the active ingredient. To assess the impact of glyphosate on the plant community, a recommended dose of 6L/ha was applied on ……… using a manually pressurized, two-liter, handheld sprayer to treat the entire study site with a 48 ml glyphosate solution per liter of water.

**Data collection and experimental plot**

The site would be divided into six plots (A-F; Figure 1) to allow for independent replication and to observe potential spatial autocorrelation in the data. Though each plot contained six subplots, data will be aggregated at the plot level to reduce random noise. Plant data would be collected over approximately 11 weeks, specifically at weeks 0 (pre-spray), 3, 6, 9, and 11.

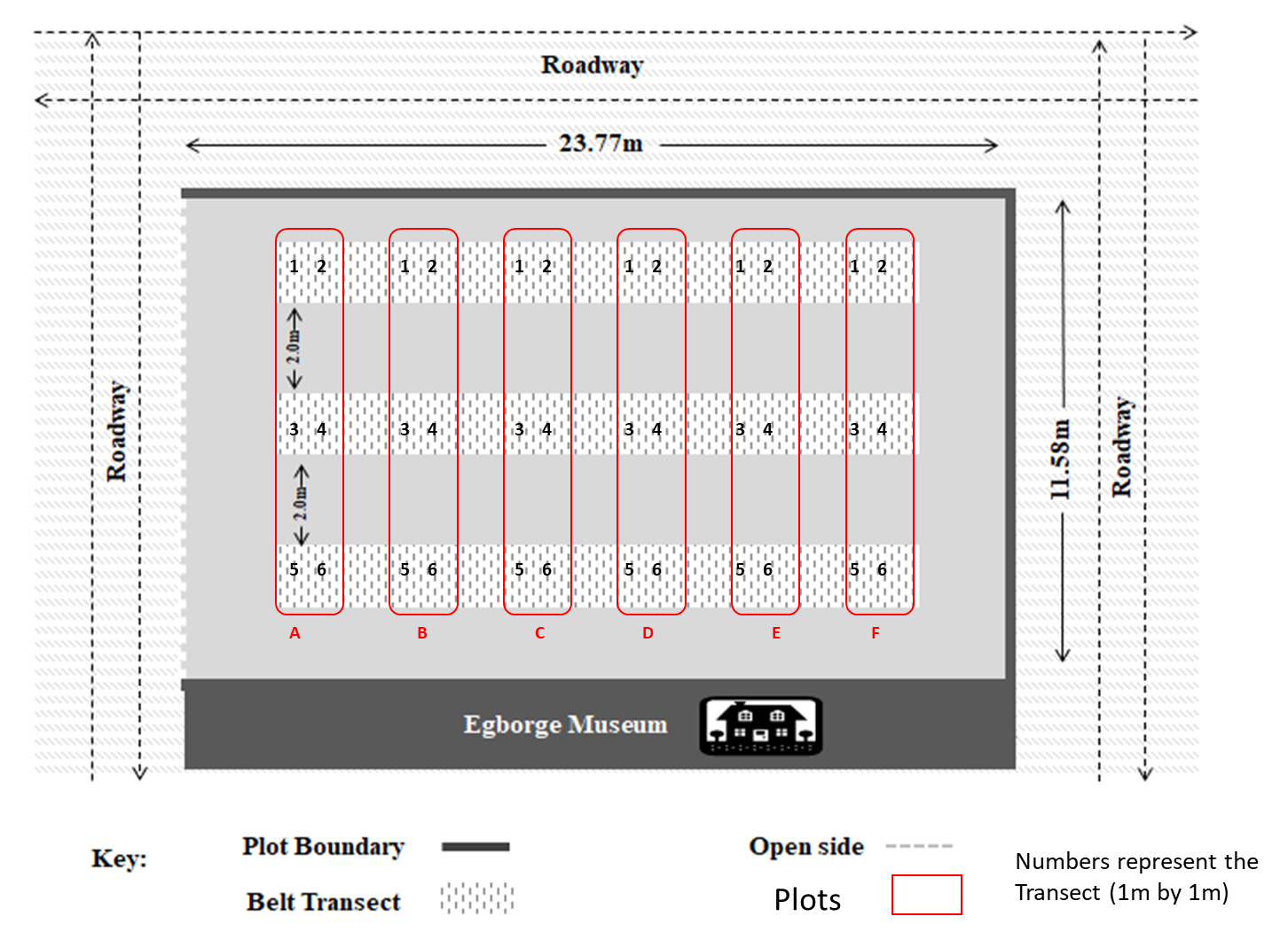


Figure 1: Experimental plot, adapted from Osawe N.E.'s undergraduate thesis (2023)

**Phylogenetic and statistical analysis**

Phylogenetic trees of plants in the lawn were assembled using the “V.PhyloMaker” R package, which matches the taxonomic names of our study plant species to a backbone phylogeny derived from the Global Backbone Of Tree for Biodiversity (GBOTB), with extended coverage. This approach allows for the inclusion of species that may not be present in the reference phylogeny by placing them within their most likely evolutionary position.

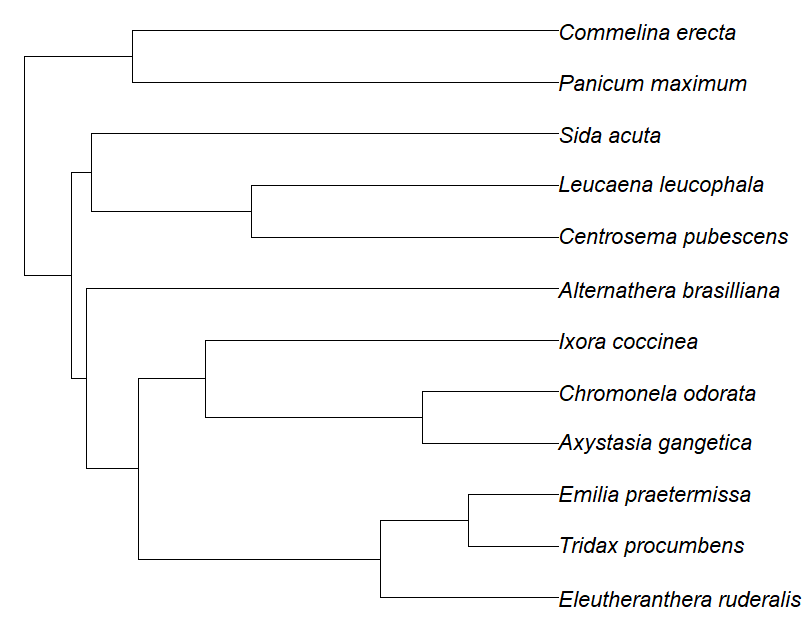
Phylogenetic distances were computed in R and matched with longitudinal percentage ground cover data. To estimate phylogenetic conservatism (or divergence), we will use Blomberg's K statistic. Blomberg’s K was used as a metric of phylogenetic signal, where K is calculated as the ratio of the observed phylogenetically correct mean-square error divided by the mean-square error of the data, standardized by the expectation under Brownian motion (Blomberg et al. 2003). K = 0 indicates no phylogenetic signal, 0 < K < 1 indicates that closely related species resemble each other less than expected under the BM model of trait evolution, K = 1 indicates phylogenetic signal as expected by BM evolution, and K > 1 indicates high phylogenetic signal, with closely related species resembling each other more than expected under BM (Blomberg et al., 2003).

We tested for significant phylogenetic signal, relative to a random distribution of the traits observed, given the topology and branch lengths of the ML phylogeny, with 999 replicates. A Welch’s t-test would be used to assess significant differences in the effect of spraying on Blomberg's K values and the percentage of plant ground cover before and after spraying. An orthogonal polynomial mixed-effects model would be used to examine the relationship between the percentage of plant ground cover and phylogenetic signal measured using Blomberg’s K. Analyses were conducted in R (version 4.4.0.1).

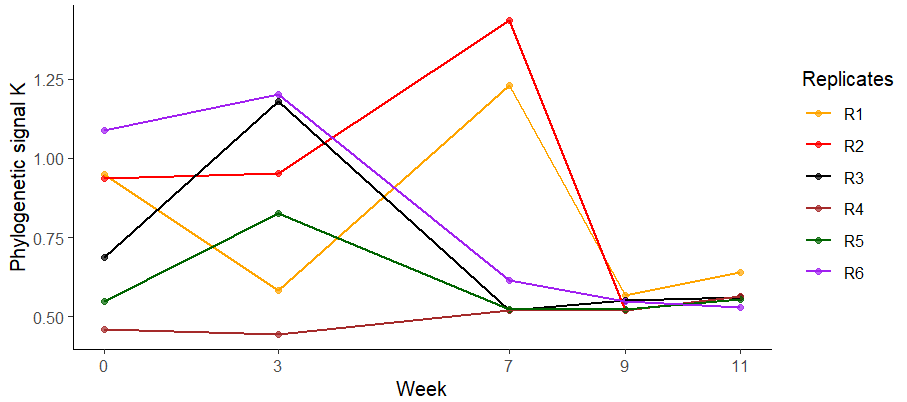
**RESULTS**

The phylogenetic tree is represented in Figure 1.

All plant species from our study belong to 12 distinct species. Their evolutionary tree is shown in Figure 1.



**Figure 1**: Phylogenetic tree showing the evolutionary relationships between the plants in the study.



**Figure 2**: Phylogenetic signal (Bloomberg K values) of plants at each survey week. Week 0 is a pre-spray, while weeks 3-11 are post-sprays.

Though plant cover was significantly reduced (t= 3.54, p<0.05) when compared to the immediate survey post-spray (week 3), there was no significant difference (t= -0.52, p>0.1) in the phylogenetic signal between week 0 and 3. This indicates that the spray of herbicide had no significant implication on the plant community structure, despite the high reduction (92.1%) in plant cover following the herbicide spray.

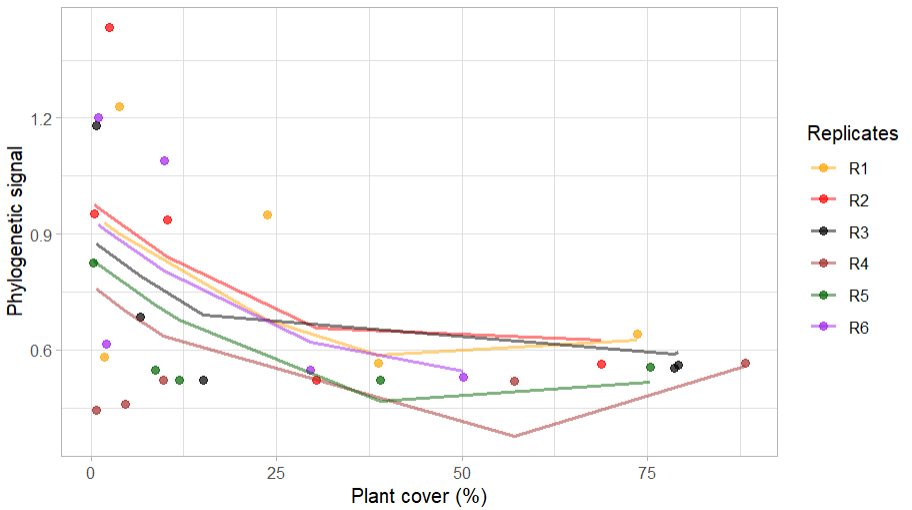


Figure \_: Relationship between (strength of) phylogenetic signal and plant cover (%). Each line indicates a different replicate.