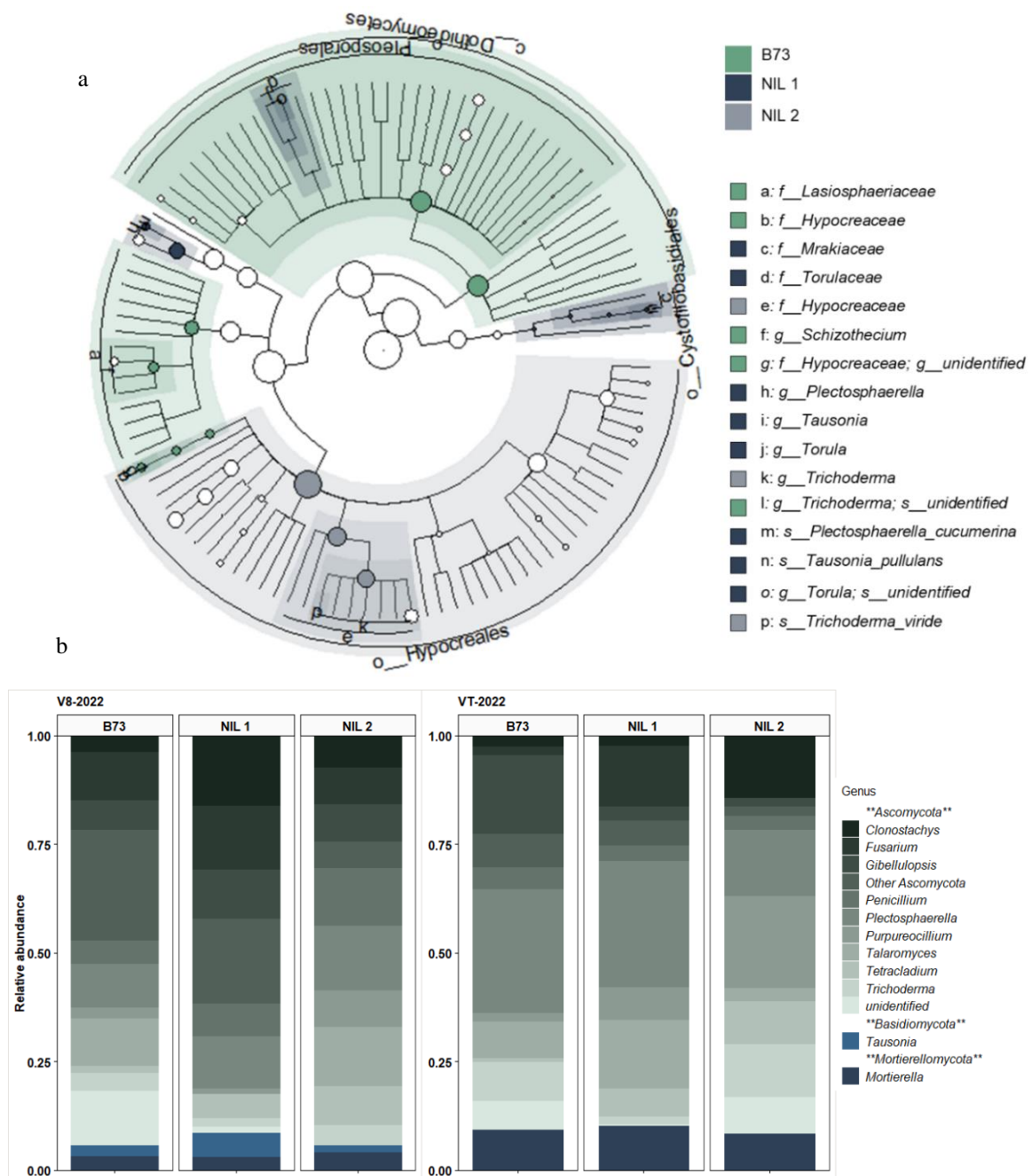
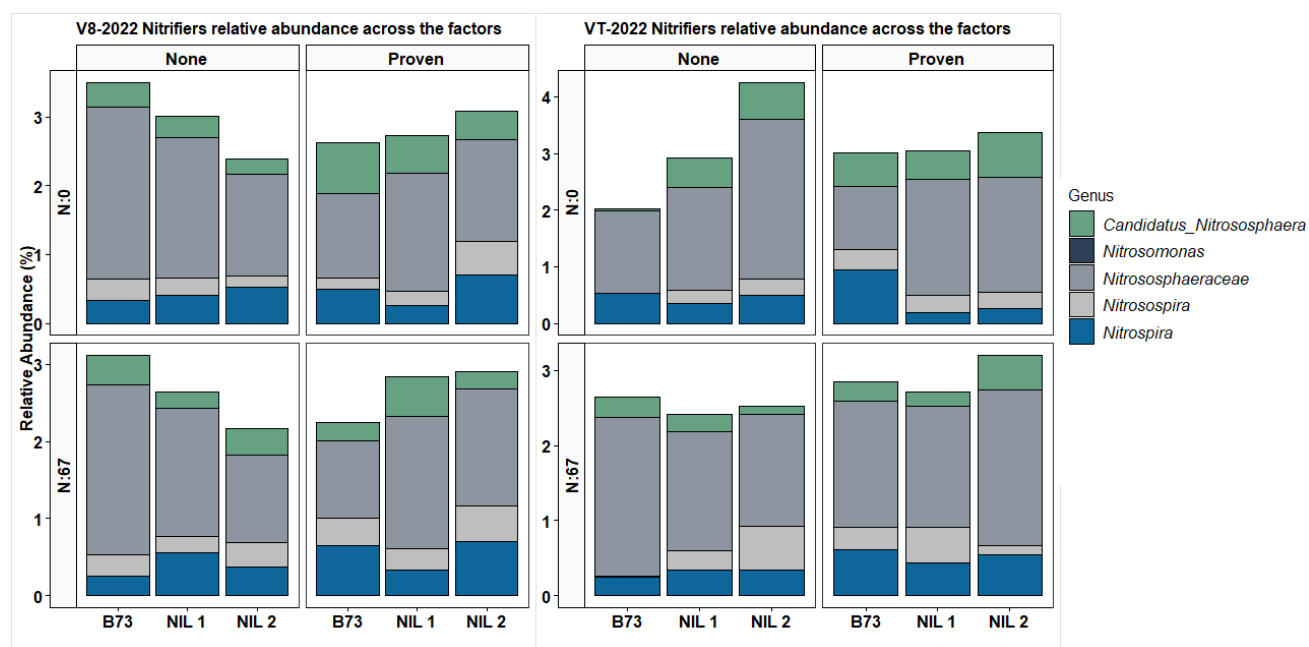


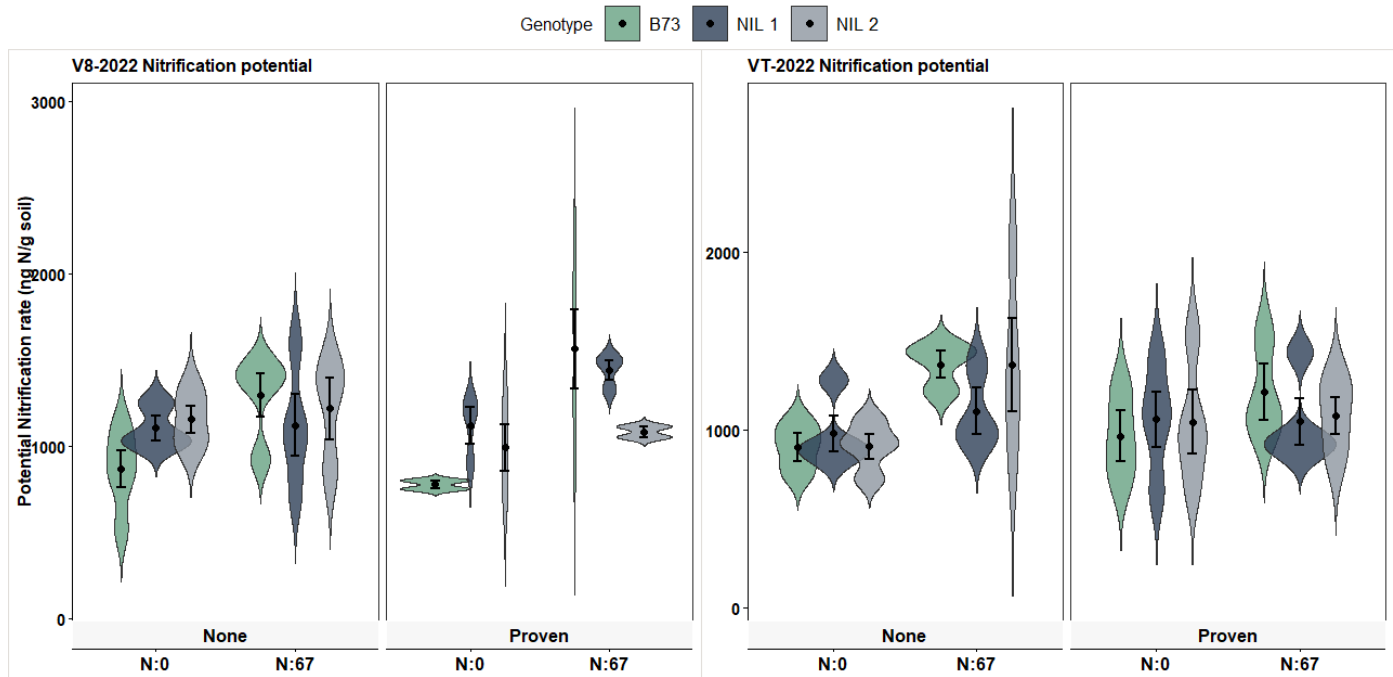
## 1 Main tables and figures



**Figure 1a-b** Cladogram of fungal taxa that significantly contributed to the variation of community composition (a) and abundance of dominant 10 genera for each top 3 phyla across genotypes (B73, NIL 1, and NIL 2) at V8 and VT stages of growth (b), irrespective of management are shown.

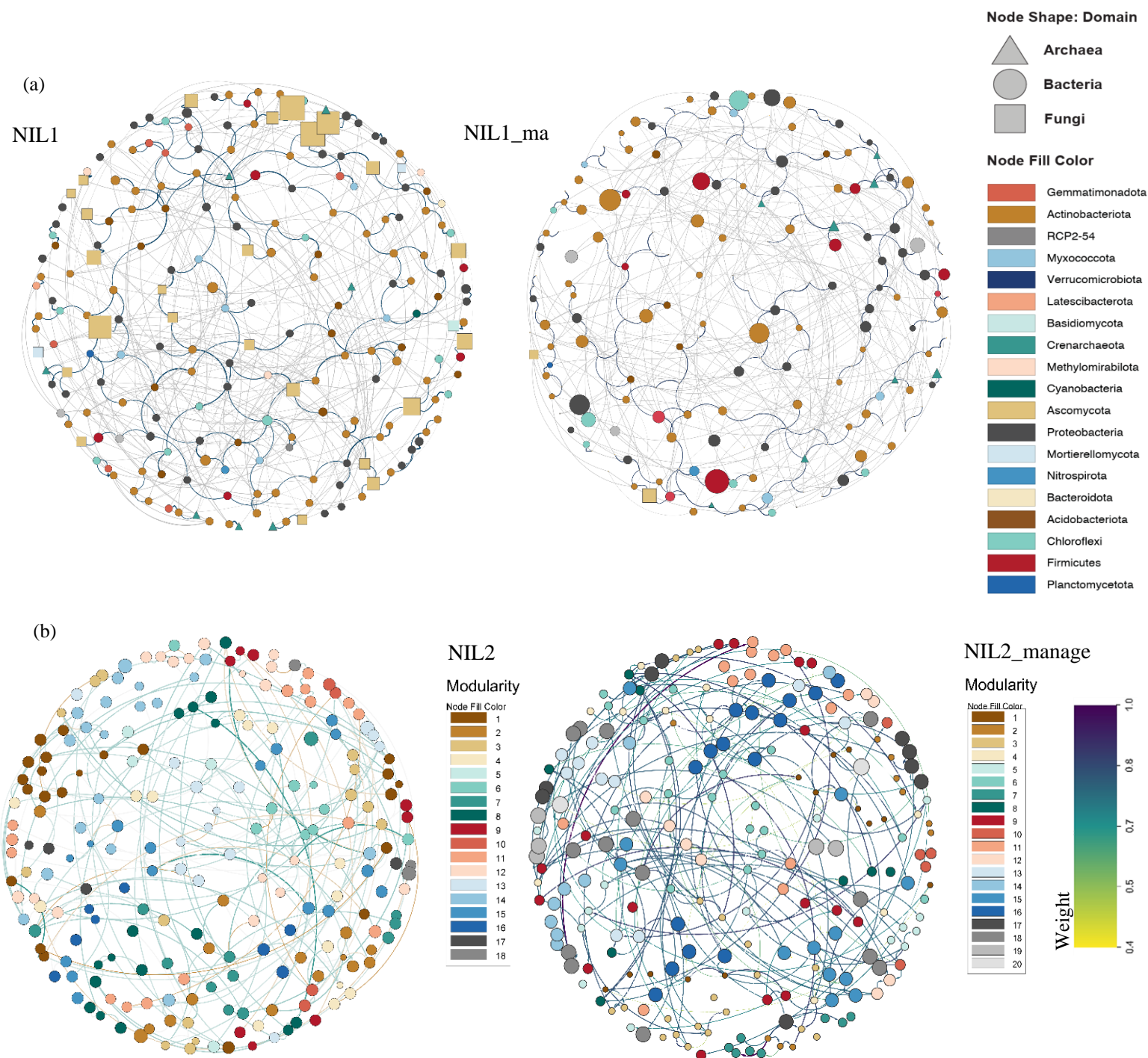


**Figure 2** Comparing nitrifiers' relative abundance at genus levels across the genotypes and fertility management with and without an N-fixing inoculant and N:67 kg ha<sup>-1</sup> amendment in 2022 at V8 and VT growth stages of maize. NIL= near-isogenic line. Genotype (B73, NIL 1, and NIL 2), management (Inoculant (Proven, None), mineral N fertilizer (N:0 kg ha<sup>-1</sup>, N:67 kg ha<sup>-1</sup>)).

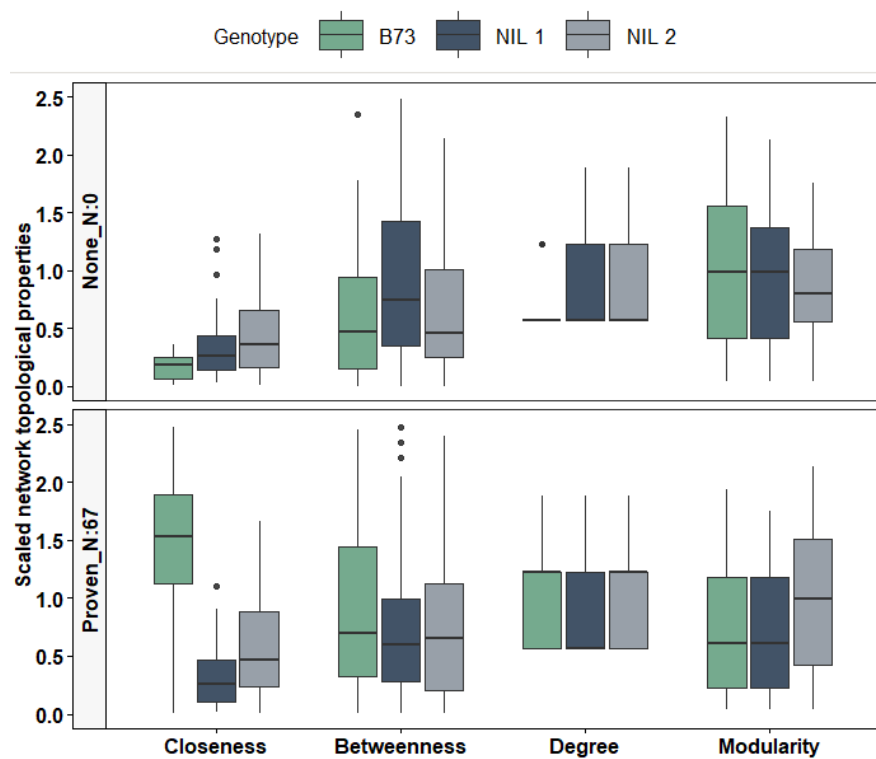


**Figure 3** Potential nitrification rate induced by genotype (B73, NIL 1, and NIL 2) and genotype × management interactive effects across V8, VT growth stages of maize during 2022. Facets grouping the nitrification rate based on management with Inoculant (Proven (with an N-fixing inoculant), None (without an N-fixing inoculant)), and mineral N fertilizer (N:0 kg ha<sup>-1</sup>, N:67 kg ha<sup>-1</sup>). In 2022 the vegetative growth stages of V8 and VT (tasseling), were considered. Detailed information on the significance of factors on potential nitrification is shown in Table S10.

NIL= near-isogenic line.

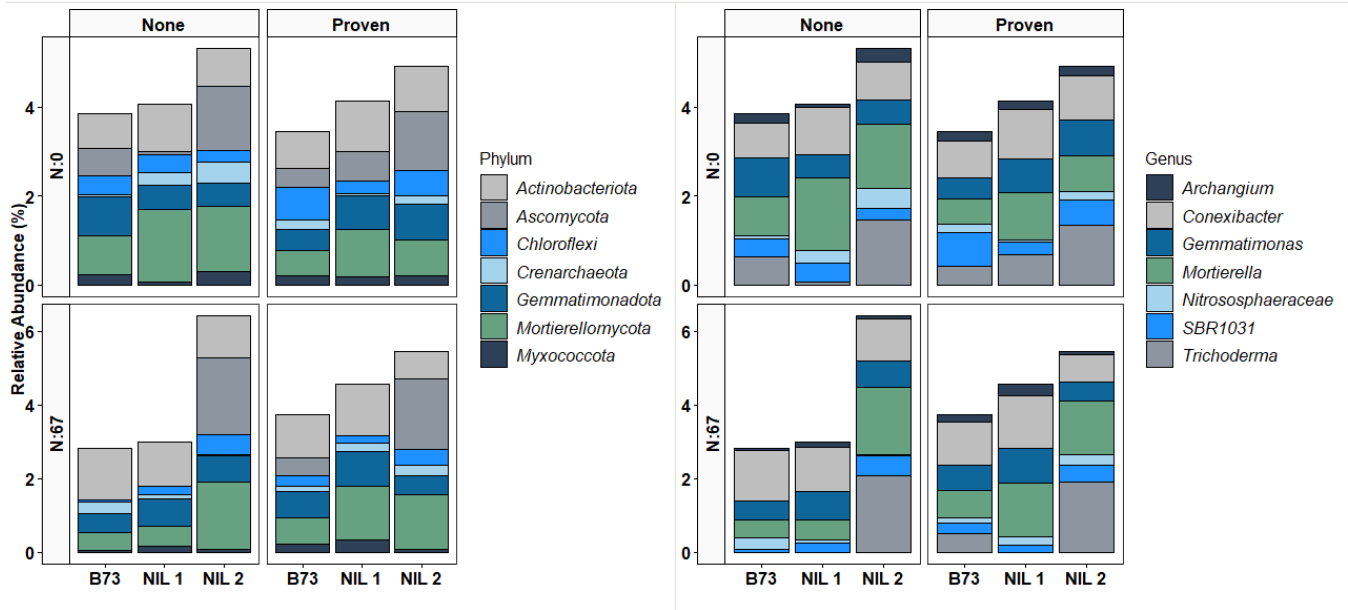


**Figure 4a-b** The nodes are color-coded to indicate ASVs relevant to phyla present in the co-occurrence network of NIL 1. The node size is relative to phyla relative abundance. The node shape shows domains, circle=Bacteria, square=Fungi, and triangle=Archaea. Edge colors indicate weight and positive (navy) and negative (gray) microbial associations (a). In modularity networks nodes (ASVs) with similar color are in one module (b), the number of modules and among modules connectivity are shown by edges, and edge thickness indicates weight. The presence and size of edges represent among-modules-connectivity. The nodes sizes are proportional to modularity. Networks were influenced by genotype (NIL 1, and NIL 2) and genotype: management (with an N-fixing inoculant (Proven) and mineral N fertilizer (N:67 kg ha<sup>-1</sup>) interactions. Networks' properties and details of their ecological relevance.

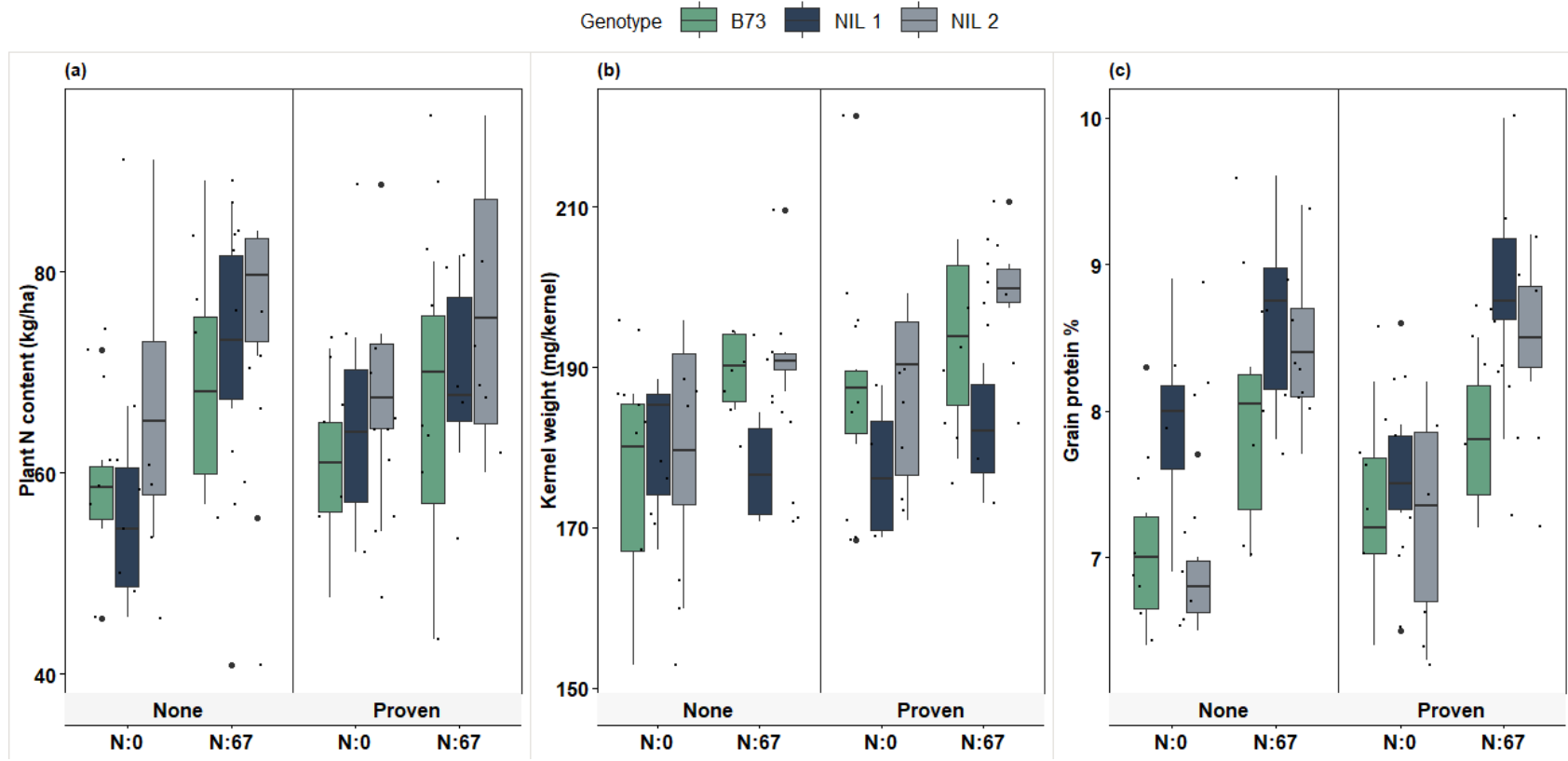


**Figure 5** Network topological properties influenced by genotype (B73, NIL 1, and NIL 2) with (Proven\_N:67 kg ha<sup>-1</sup>) or without management (None\_N:0 kg ha<sup>-1</sup>) are shown.

VT-2022 Network hub taxa relative abundance across the factors

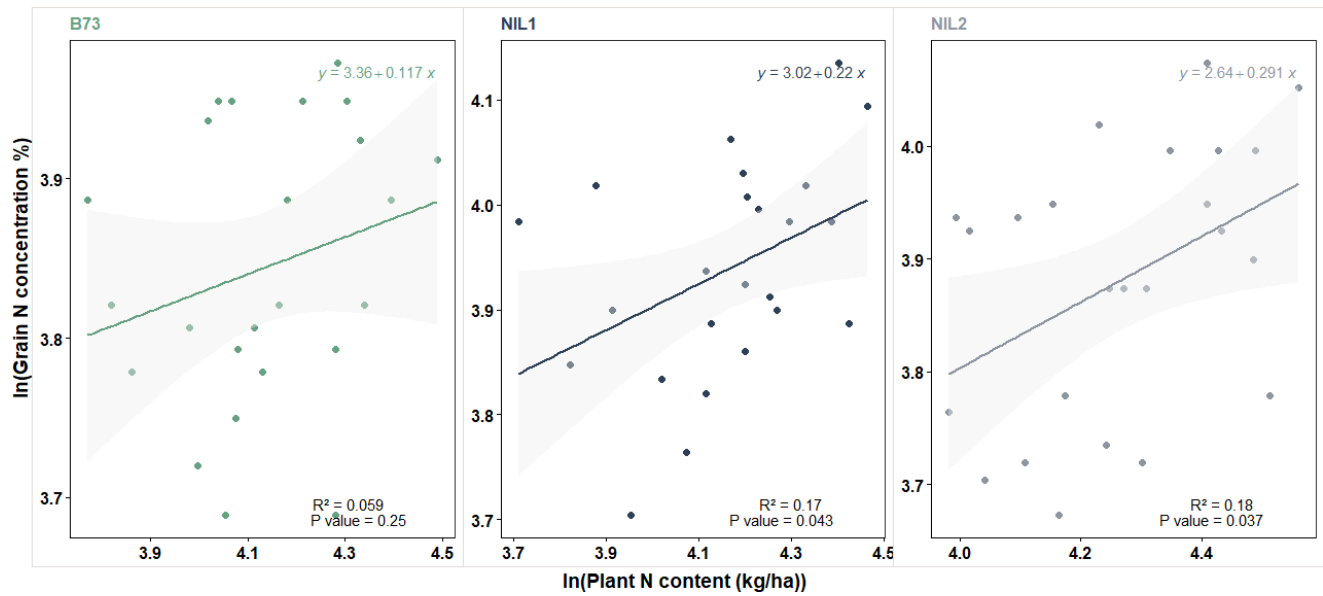


**Figure 6** Relative abundance of taxa representing network hubs across the genotypes and the genotype: management are shown. Facets grouping taxa based on treatments: field management: Inoculant (Proven, None), mineral N fertilizer (N:0 kg ha<sup>-1</sup>, N:67 kg ha<sup>-1</sup>). Similar color-coding has been used to trace the genus belonging to each phylum.

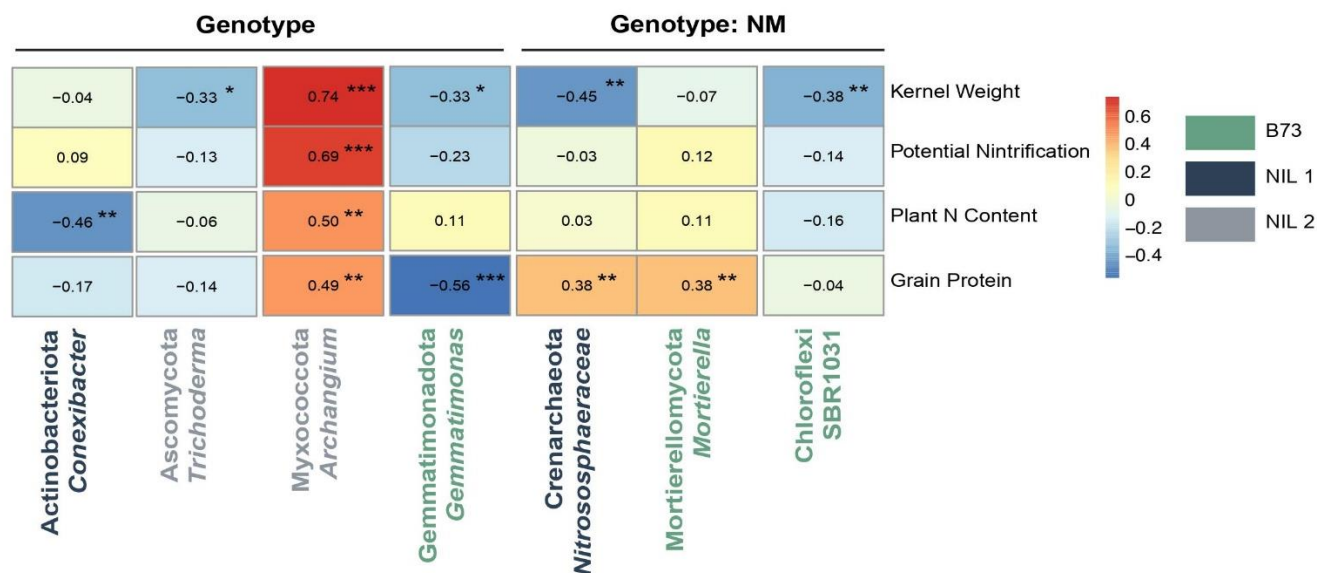


**Figure 7a-c** Genotype-specific plant nitrogen uptake and kernel weight and protein across levels of mineral N (0 and 67 kg ha<sup>-1</sup>), with (Proven) and without (None) application of an N-fixing inoculant. Plant N content at VT stage of maize growth (kg ha<sup>-1</sup>) (a), kernel weight (mg kernel<sup>-1</sup>) (b), and grain protein % (c) are shown. Detailed information on the significance of factors on plant N content is shown in Table S10.





**Figure 8** Genotype-specific N use efficiency regardless of management is shown. R<sup>2</sup> and P values are indicative of the general trend in grain N accumulation by increasing plant N content for each genotype, irrespective of management. The color-coded equations illustrate the trend of grain N accumulation for each genotype. Data was transformed using natural logarithm (ln) to meet the linearity assumption.



**Figure 9** Correlation between network hub taxa (phylum and genera) and nitrification rate, plant N accumulation, grain N concentration as well as protein%, applying Spearman correlation. Values of Spearman correlation coefficients are indicated from red (positive) to blue (negative). Network hub correlated genera extracted from network properties. P values were adjusted for multiple comparisons by the Benjamini-Hochberg method. Genotype  $\times$  management (with inoculant (Proven), mineral N fertilizer (N:67 kg ha<sup>-1</sup>)). Significance codes:  $p < 0.05$  ‘\*’,  $p < 0.01$  ‘\*\*’,  $p < 0.001$  ‘\*\*\*’

## Graphical abstract

