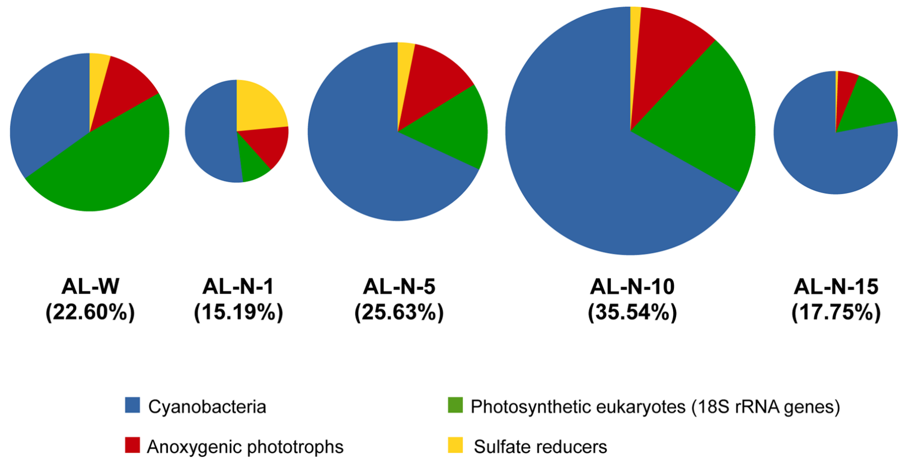

FIGURE 4 | Relative abundance of 16S/18S rRNA gene sequences affiliated to lineages displaying metabolisms favoring carbonate precipitation in Alchichica microbialites. Sizes of pie charts (and the values within brackets) indicate the total proportion represented by these sequences compared to the total number of rRNA gene sequences in each sample. Chloroplasts are not included (to see the proportion of photosynthetic eukaryotes based on chloroplast sequences see Supplementary Figure S4).

members of the Oscillatoriales are the dominant cyanobacteria in the AL-N-1 microbialite fragment. Finally, it might also be that the collected fragment (or part of it) was placed in a relatively shadowed area, and this particular situation might have selected for anoxygenic phototrophs, which are adapted to lower light intensities. At any rate, this observation indicates that the microbial communities vary within small spatial scales in response to the heterogeneous local physico-chemical conditions. It also suggests that anoxygenic photosynthesis and sulfate-reduction can be responsible for an important fraction of carbonate precipitation in relatively oxygen-poor microbialite zones, making them potentially interesting areas to study as analogs of stromatolites formed in the Precambrian before oxygen levels significantly raised (Bosak et al., 2007; Farquhar et al., 2011).

Nonetheless, oxygenic photosynthesis seems prevalent in modern Alchichica microbialites. Overall two different kinds of patterns were observed, with eukaryotic photosynthesis dominating AL-W and cyanobacterial photosynthesis dominating AL-N samples. Around 50% of the 18S rRNA genes belonging to taxa with carbonate-induction potential corresponded to photosynthetic eukaryotes, essentially diatoms, in AL-W. In this sample, the number of chloroplast 16S rRNAs as compared with the nuclear 18S rRNA genes of photosynthetic eukaryotes was higher, suggesting more chloroplasts per cell than in the AL-N samples (Supplementary Figure S3). Therefore, if the number of chloroplast genes is considered the eukaryotic contribution in AL-W samples appears even higher (Supplementary Figure S4). However, in this particular sample, given the local hydrochemistry influenced by the input of less saline and neutral pH waters (Kazmierczak et al., 2011) and the less mineralized nature of the biofilm growing on the microbialite surface, the overall biomineralization potential of this specific community is difficult to assess and might be questioned. It might be envisaged that the diatom fraction grows to the expense of Si-rich fresh seepage waters and that carbonate precipitation occurs at very local scale, deeper in the biofilm, promoted by a subset of the microorganisms more intimately associated with the microbialite and/or at some periods of the year when seeping activity is less important. The fact that Si concentration in the AL-W microbialite is comparable, and even smaller, than in the AL-N microbialites favors this hypothesis (**Table 1**). This suggests that the potential diatom input to the microbialite silicon content (**Table 1**; Zeyen et al., under reveiw) is not different from that of the rest of microbialites in the lake or, alternatively, that Si in the microbialites has not a diatom origin. On the contrary, the AL-N samples were strongly mineralized with many cyanobacteria and green algae intimately linked with the mineral substrate. This suggests that at least part of this diversity may be directly involved in biomineralization.

Effect of Depth and Chemical Parameters on Microbial Community Structure and Macroscale Evidence for Aragonite Biomineralization by Pleurocapsales

We looked for potential correlations between the community composition and the local physico-chemical parameters measured, essentially depth and the chemical composition of the microbialite fragments that we analyzed in parallel (**Table 1**). First, ordination analyses of bacterial plus eukaryotic community composition at the level of major taxa (**Figures 3B,C**) using NMDS clearly separated the different samples according to their location and depth (**Figure 5**). As expected, the three AL-W replicate samples clustered together, and were segregated from the AL-N samples along the NMDS1 axis. AL-N samples were discriminated along the second axis (NMDS2) according to depth. Similar results were observed when eukaryotes and prokaryotes were analyzed separately (data not shown).

We then used Mantel tests to investigate the significance of the correlations linking environmental parameters to the