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Objectives

The Landscape Evolution Observatory (LEO) project at Biosphere 2 consists of three replicated artificial landscapes which are sealed within a climate-controlled glass house. LEO is composed of basaltic soil material with low organic matter, nutrients, and microbes. The landscapes are built to resemble zero-order basins and enables researchers to observe hydrological, biological, and geochemical evolution of landscapes in a controlled environment. This study is focused on capturing microbial community dynamics in LEO soil, pre- and post-controlled rainfall episodes.

Testing Approach:

Two Soil Sampling Time Points over 40-day experiment:

Pre-rainfall, November 8th

Post-rainfall, December 21st

3 slopes, 6 sampling locations per slope, 5 depth* per location, 2 time points --- 180 samples

*Cores were subsampled every 15cm, and are labelled as 1-6 depending on length of the core recovered

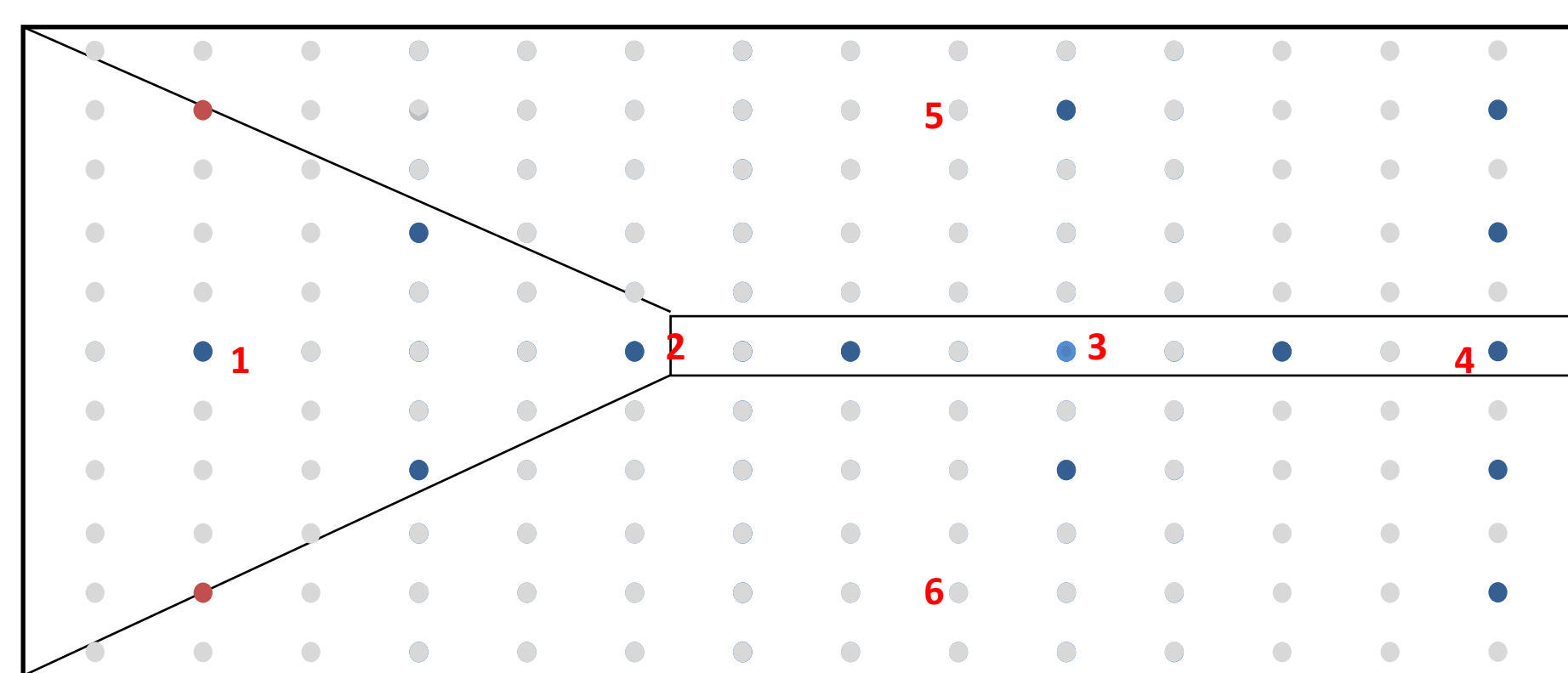


Figure 1: Soil water sampler locations included in the sampling are shown. Those sampled at four depths are shown in blue, those at three depths in red. Locations not included in the sampling scheme are shown in grey (2013 sampling scheme).

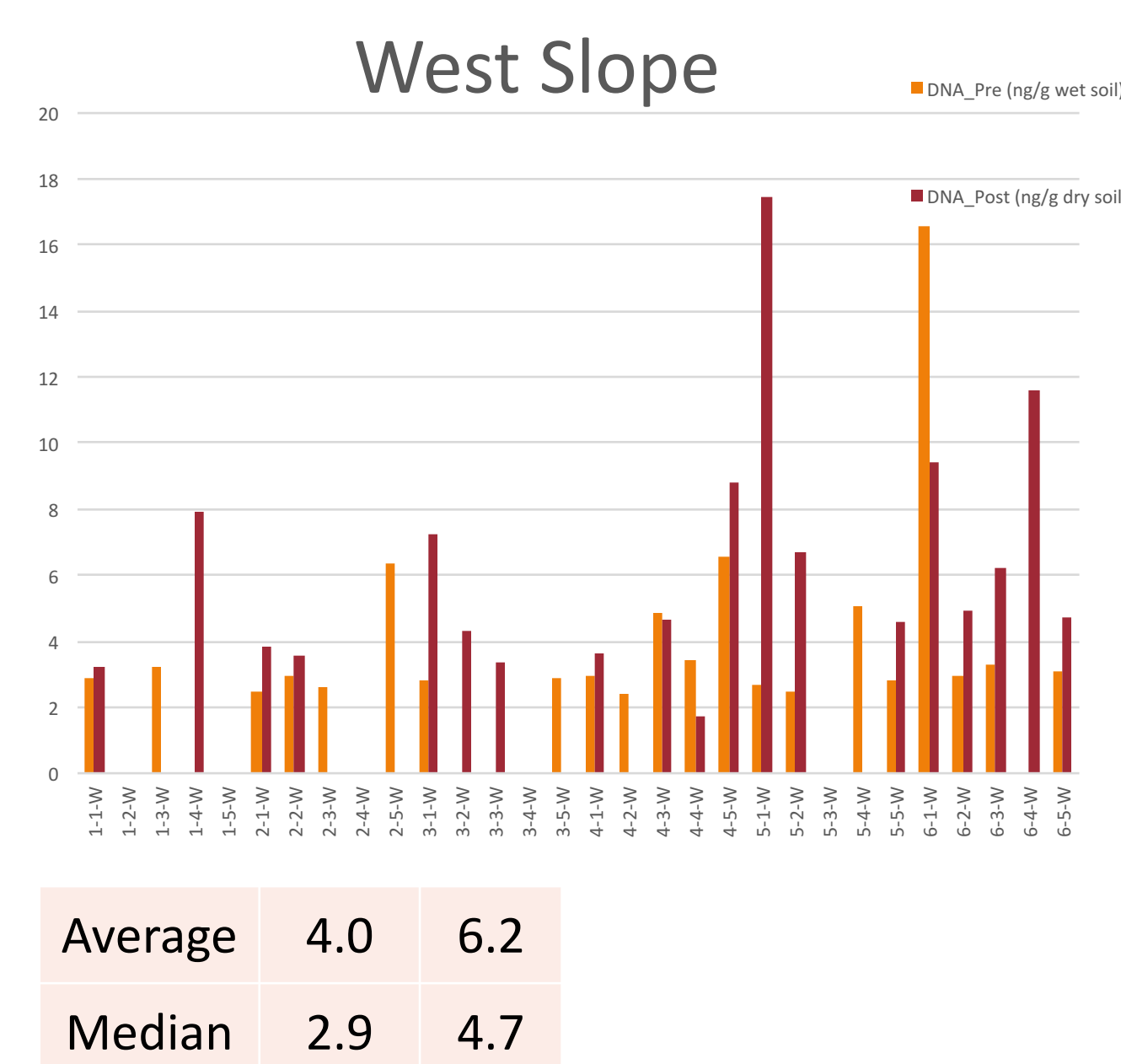
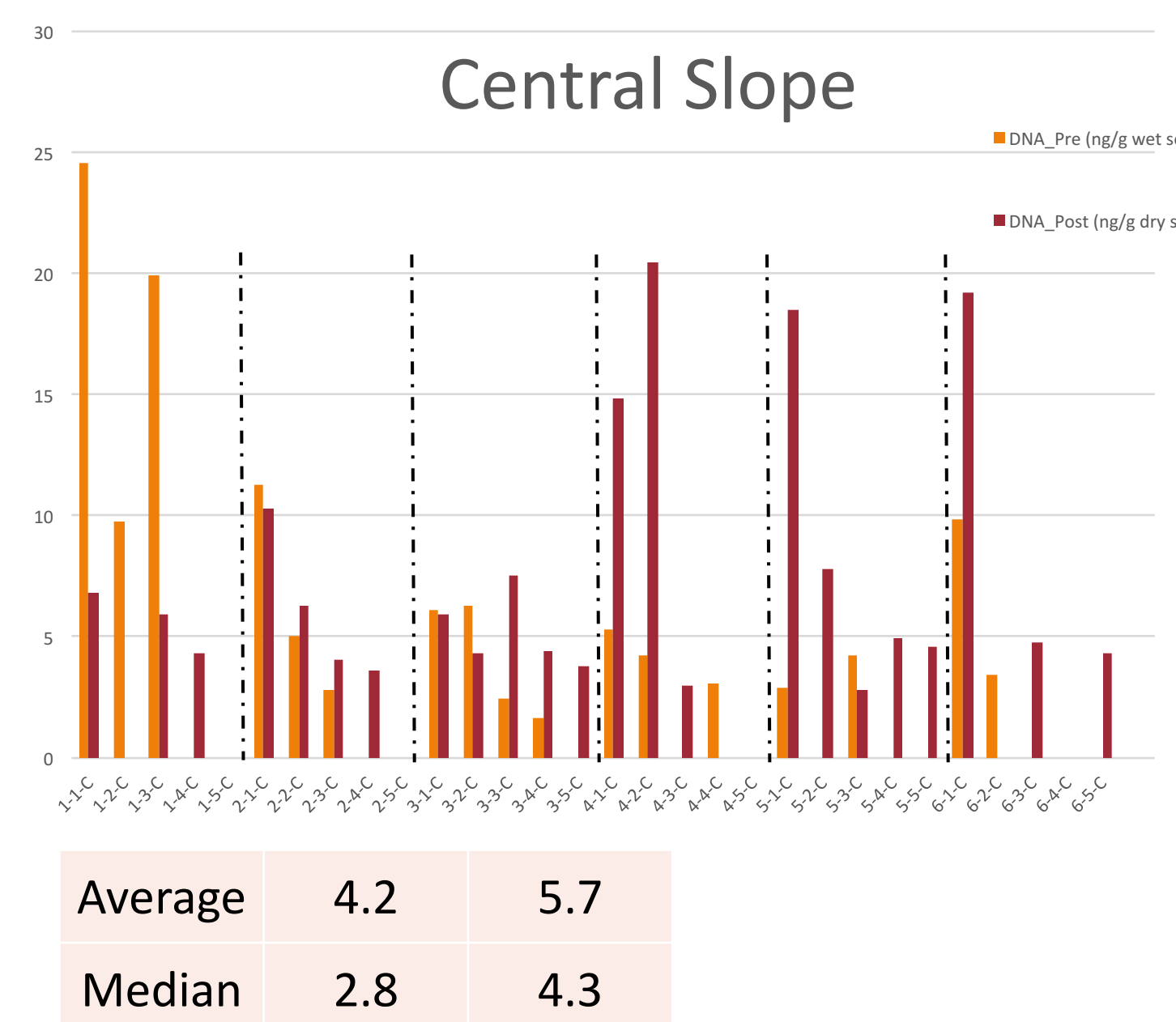
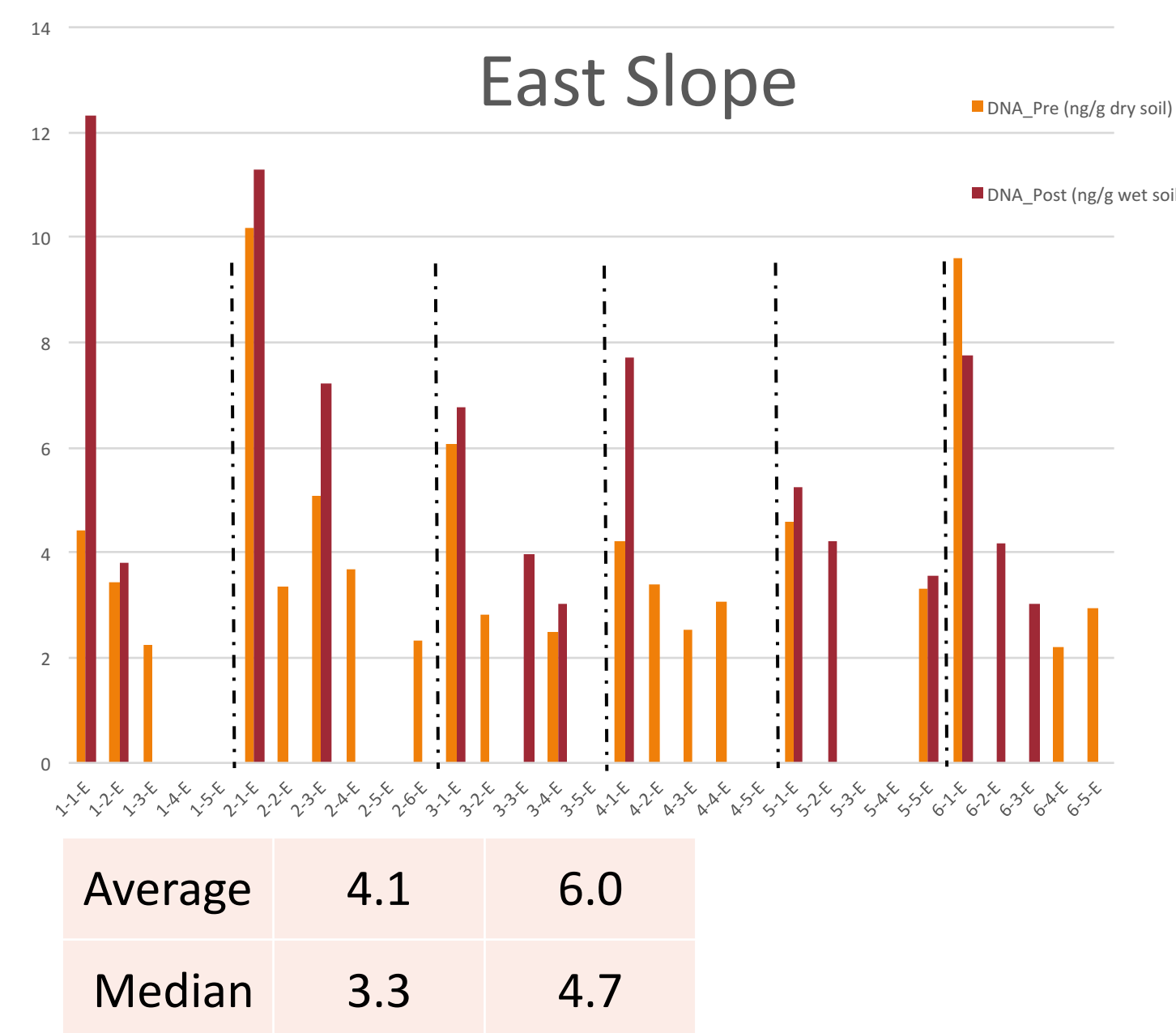
Numbers in red indicate soil core sampling locations

Methods

DNA extractions were performed in Dr. Raina Maier's Lab at University of Arizona using FastDNA Spin Kit (MP Biomedicals), as per manufacturer's instructions.

Numerical Analysis: Extracted DNA was quantified using Picogreen on a Qubit instrument and then sent in for sequencing.

Results



Discussion

The average concentration of DNA recovered from each sample was higher in the post-rainfall samples than the pre-rainfall samples. This trend was seen throughout all three slopes. However, the variance in results among the individual samples between the three slopes indicates a variability between the slopes. Amplicon sequencing of the 16S rRNA gene will inform advanced -omics analyses of the samples.

Applications

The sequence data will be evaluated to reveal spatial and temporal heterogeneity of the soil microbes, providing a more exact narrative of the microbes present in each slope and spatiotemporal trends of microbial life in the landscapes. This will inform advanced -omics analyses of the samples including metagenomics and metatranscriptomics. Response of microbial communities to wetting and drying will also be examined. This is particularly relevant to understanding response of microbial communities to precipitation perturbations as a consequence of global climate change.

References

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