Monitoring the impacts of saltwater intrusion on sediment communities

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Figure 1: Location of Kakadu National Park

Questions

- What is the prokaryotic and eukaryotic diversity of soils in Kakadu National Park?
- How does this community respond to changes in salinity?

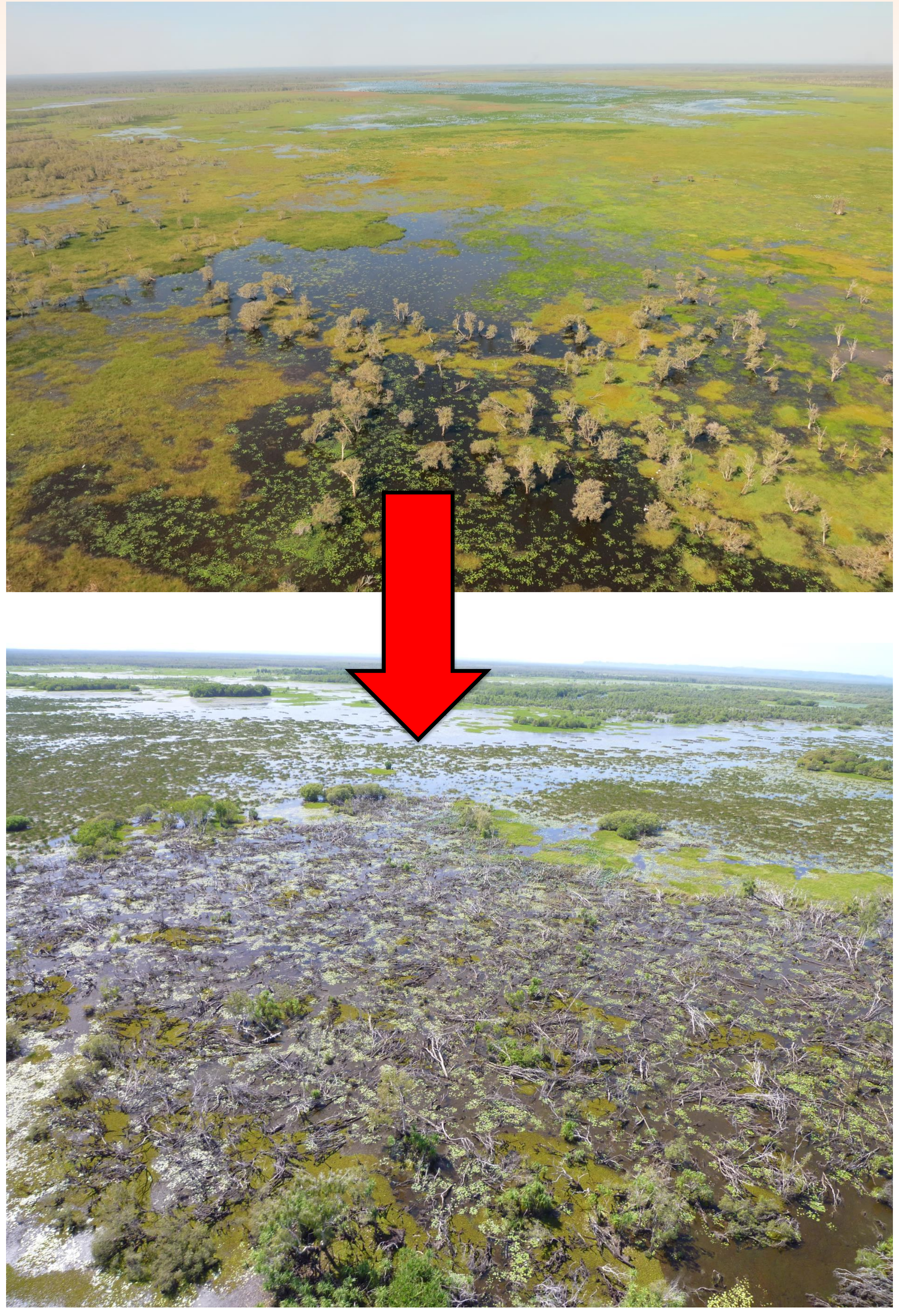

Figure 2: Impacts of saltwater intrusion on freshwater wetlands in Kakadu National Park. Freshwater wetlands in Kakadu National Park, Australia (top) are some of the most bio diverse areas. Intruding saltwater from sea level rise can cause large scale dieback (bottom). Photo credits: Tiffanie Nelson 2012.

Background

- Northern Australia's World Heritage Listed Kakadu National Park (Figure 1) is vulnerable to the impacts of climate change induced sea level rise which is predicted to rise 30 cm by 2050 resulting in a potential loss of 80% of wetlands [1,2].
- Large scale vegetation changes are obvious with saltwater intrusion due to a number of other impacts [3,4] (see Figure 2).
- Less obvious is how the community in the floodplain soil, responsible for nutrient and biogeochemical cycling, responds to the change in salinity.
- To address the questions posed above, we measured the diversity of soil organisms in the South Alligator River which is located in Kakadu National Park (Figure 1).
- This tidal river has a salinity similar to seawater (approx. 33 ppt) during the dry season (March-November) and during the monsoon (December-February) floodplains are inundated with rainfall to promote freshwater wetlands and swamps.

References

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[2] BMT WBM (2010), *A report to the Aus. Govt. Dept. of Climate Change*
[3] Mulrennan & Woodroffe (1998), *Journal of Environmental Management*
[4] Petty & Douglas (2010), *Journal of Tropical Ecology*
[5] Cole et al. (2009), *Nucleic Acids Research*
[6] Woodroffe et al. (1989), *Sedimentology*
[7] Schloss et al., *Applied & Environmental Microbiology*
[8] Clarke & Gorley (2006), *User Manual Primer-E*

Results

- We identified 1,415,876 sequences and of these, 29,019 were unique bacterial OTUs (operational taxonomic units).
- The 27 phyla represented are shown in Figure 3 and the majority (32%) were unclassified.
- **These data suggest there are 2,160 'species' per 1 g soil.**
- Bacterial community diversity was lower in areas close to the river channel (lower floodplain) and higher in areas furthest away from the river channel (swamp) (Figure 4).

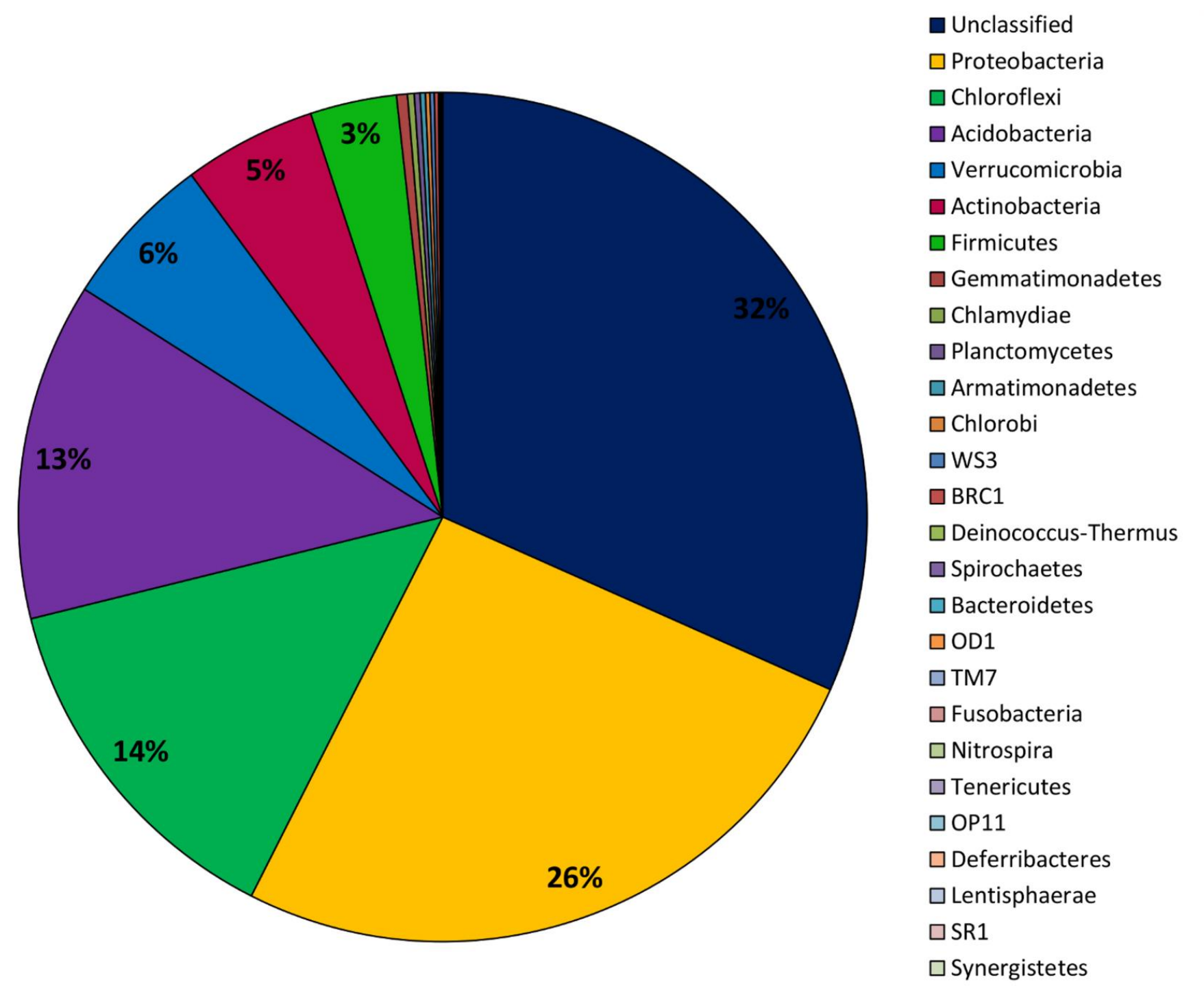

Figure 3: Bacterial phyla present in floodplain soils. OTUs were classified based on sequence similarity of more than 80% in the Ribosomal Database Project [5]. Phyla contributions not shown represent < 1%.

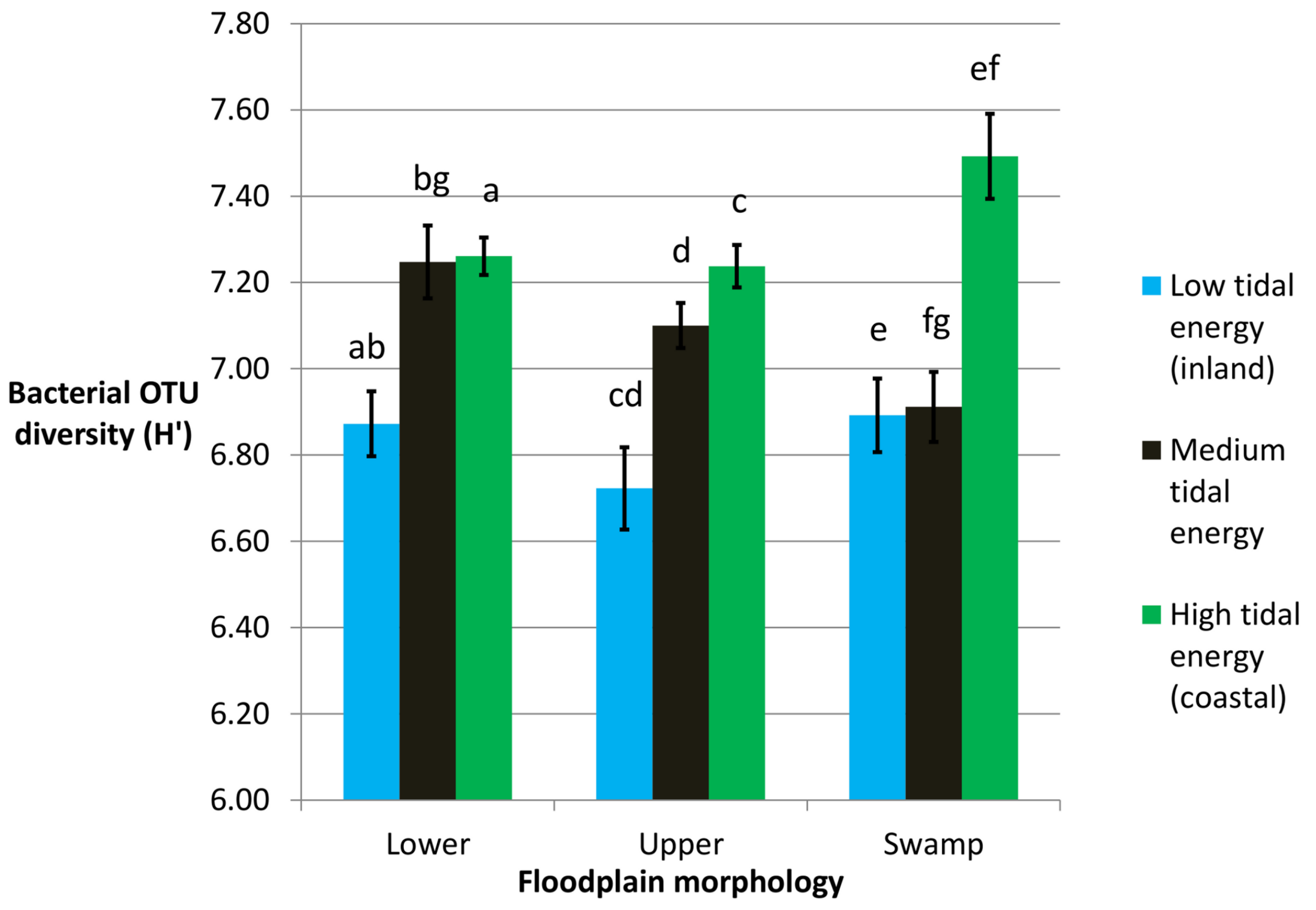

Figure 4: Bacterial diversity of floodplain soil communities grouped by morphological and tidal zones. Diversity of bacterial OTUs in floodplain soil was measured using the Shannon-Weiner Diversity Index (H'). Floodplain morphology of the South Alligator River is defined in Woodroffe et al. (1989) [6]. Lower floodplain is located closest to the river channel. Lowercase letters denote significant differences in diversity analysed by PERMANOVA where $p = < 0.05$.

Results…

- The bacterial community separated along the axis grouped by the floodplain morphology.
- Together all of the 21 variables measured explained 80% of the variation in bacterial community structure by DISTLM (Figure 5).
- The strongest associations were with: Na (12%), V (9%), pH (8%), S (5%), K (4%) & Ca (3%).

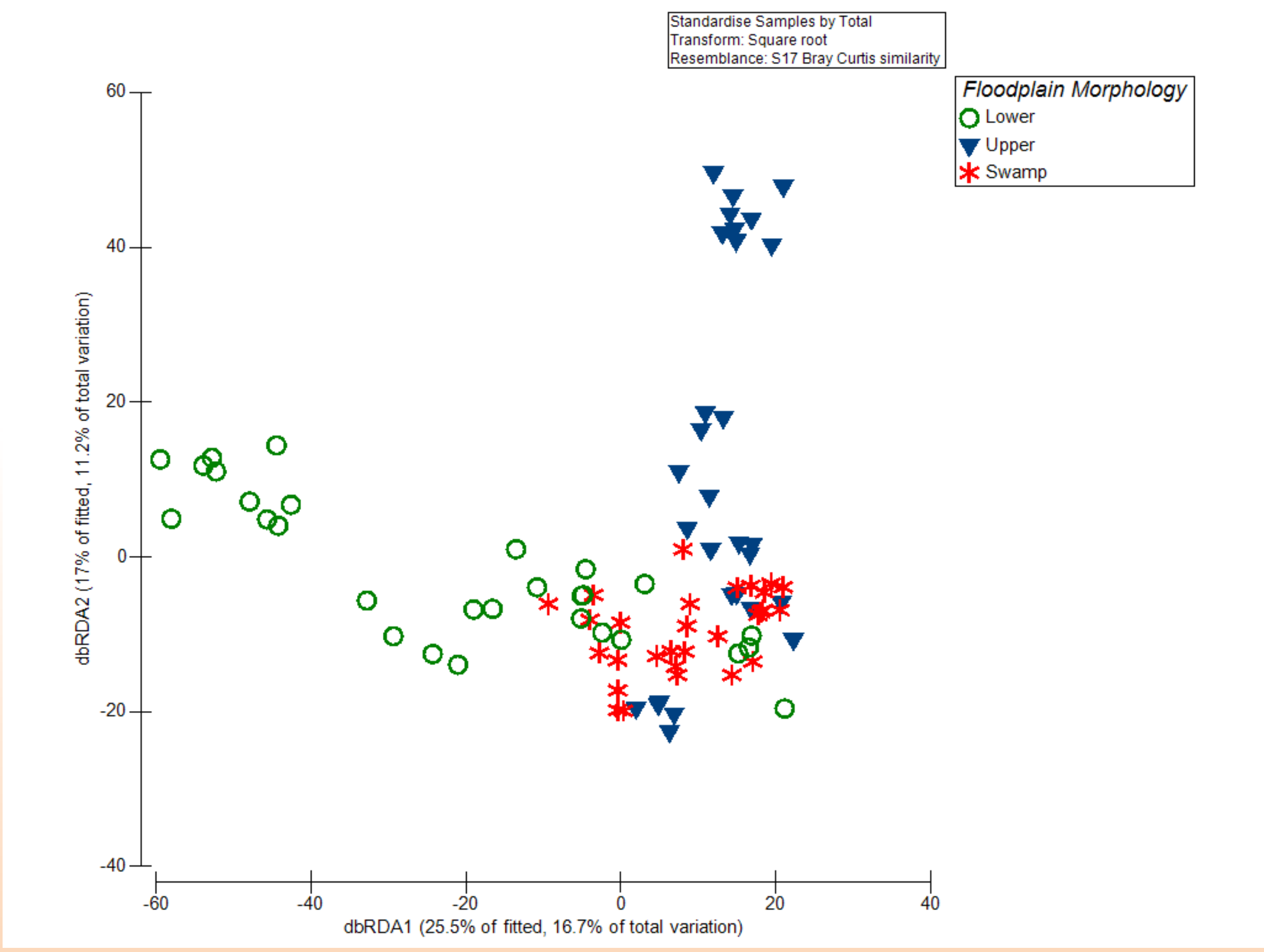

Figure 5: Bacterial community composition of floodplain soil. Up to 66% of bacterial community composition is explained by all 21 variables measured as analysed by DISTLM.

Results…

- A manipulative pilot study identified a significant difference in response of the bacterial community after 7 d exposure to both freshwater (PERMANOVA: $t=2.575$, $P_{MC}=0.011$) and saltwater ($t=2.709$, $P_{MC}=0.008$) treatments (Figure 6).

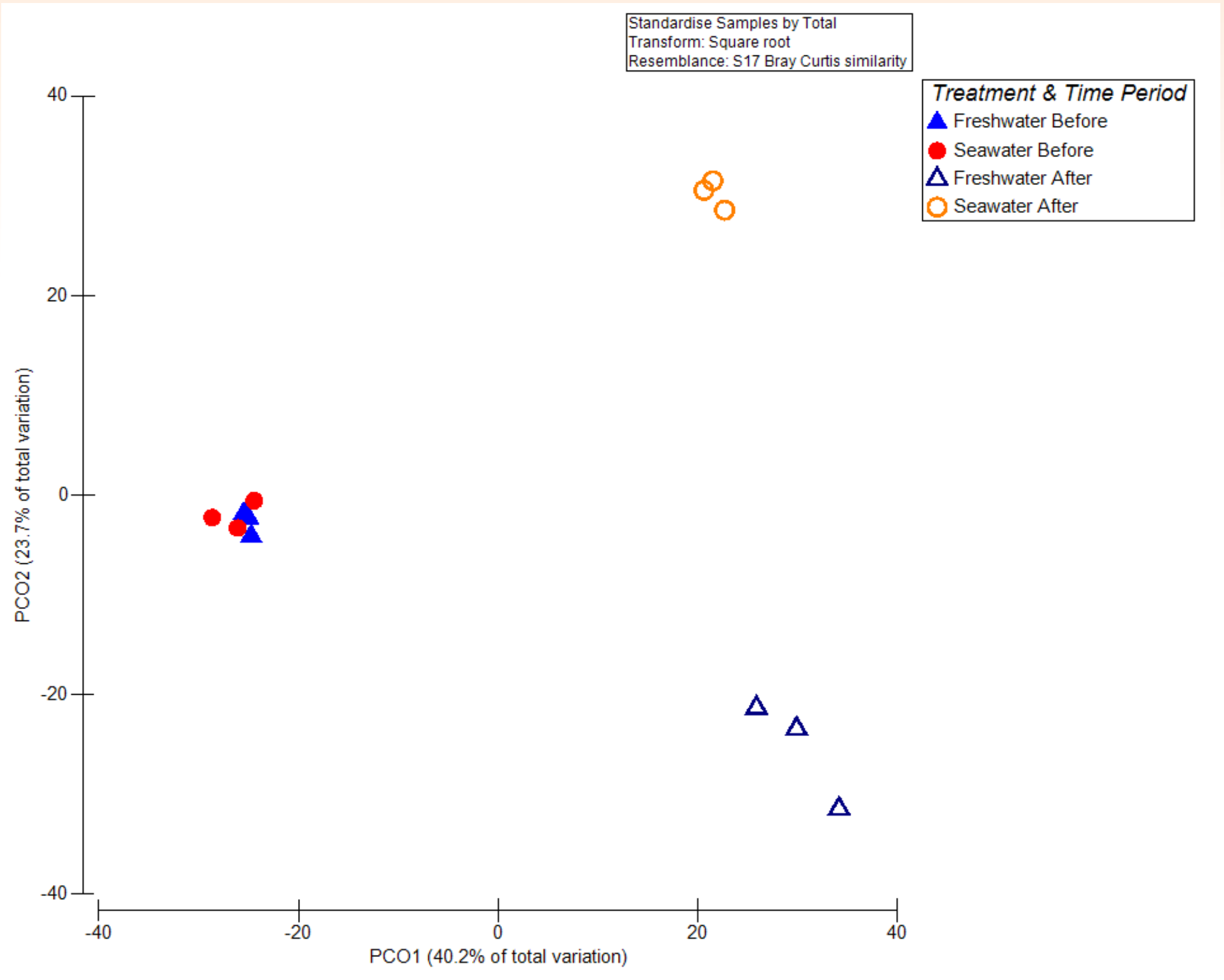

Figure 6: Bacterial community response after saltwater and freshwater treatments. Samples were collected before treatment and 7 d after exposure to saltwater and freshwater.

Discussion

- Floodplain soils are highly diverse ecosystems.
- Elements associated with saltwater (Na, K & Ca) have a strong influence on bacterial community composition on the floodplains.
- Preliminary pilot study results suggest saltwater exposure may considerably alter the bacterial community.
- Future experiments are in progress to understand how these changes relate to the functional capacity of the community.

Methods

- Ninety floodplain soil samples were collected from the South Alligator River, Kakadu National Park, Australia (Figure 1 & 7).
- Genomic DNA was extracted from soil samples using PowerMax DNA Kit (MoBio) and a region of the V4 & V6 16s rRNA gene was PCR-amplified and barcoded before pyrosequencing was carried out on the GS FLX+ System (454 Life Sciences) at the Australian Genome Research Facility.
- The following abiotic variables were measured by the Australia Institute of Marine Science Analytical Services: TOC, TN, Mg, Al, Ca, Cd, Co, Cr, Cu, K, Mn, Mo, Mg, Na, Ni, Pb, P, S, V, and Zn.
- Salinity and pH were measured on soils sampled in the field using handheld instruments.
- Data were analysed using the Mothur suite of software v 1.30 [7]. Statistical analyses were carried out using Primer-E [8].
- For the manipulative pilot experiment three replicates from two sites with differing histories of saltwater intrusion were each exposed to treatments of artificially made seawater and freshwater over a period of seven days.
- Genomic DNA was extracted from each treatment replicate before and after 7 d exposure. DNA was PCR amplified and sequenced using the methods described above.

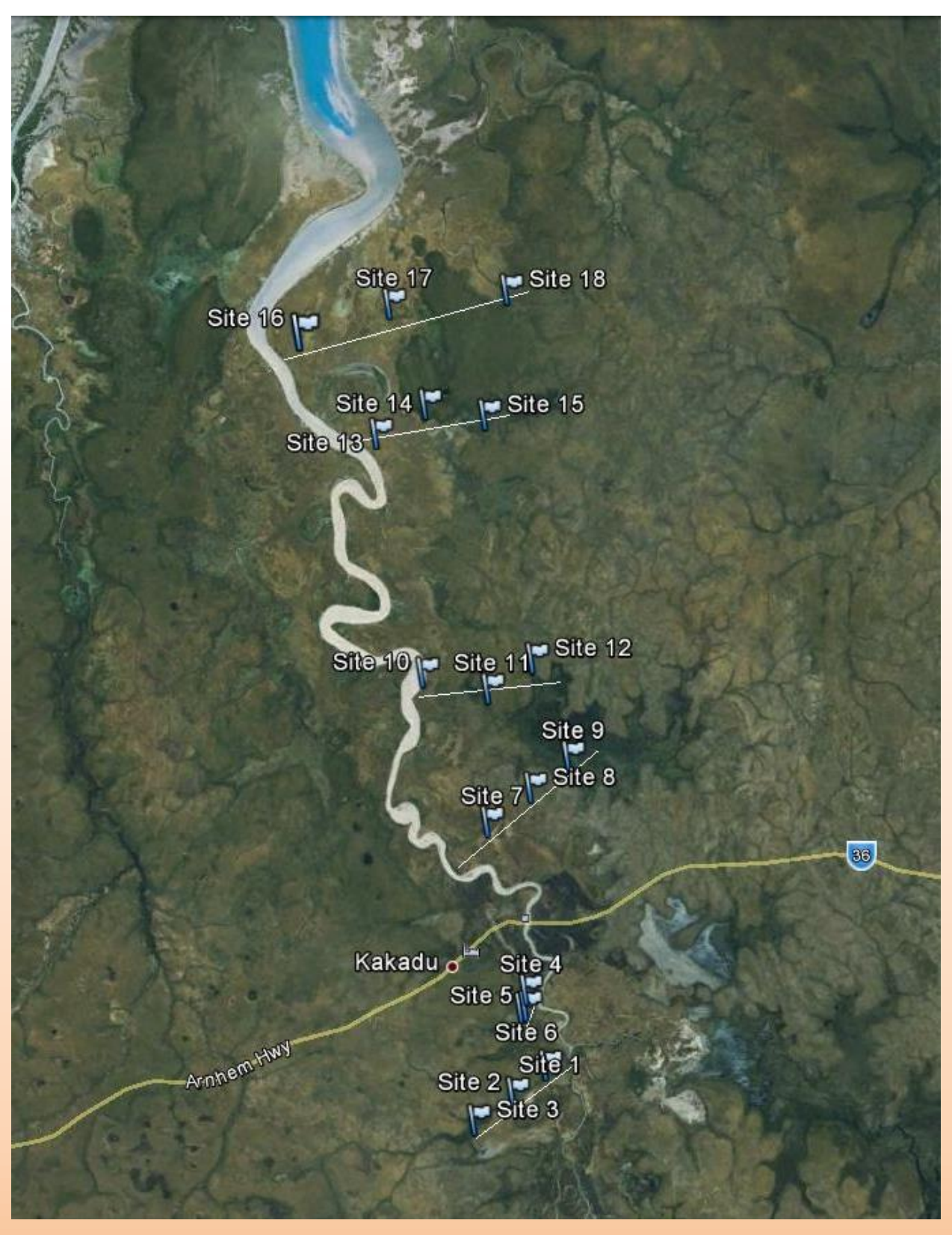

Figure 7: Floodplain soil sites along the South Alligator River, Kakadu.

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