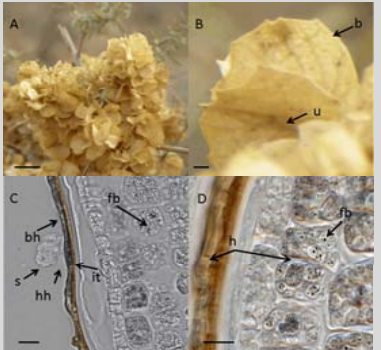
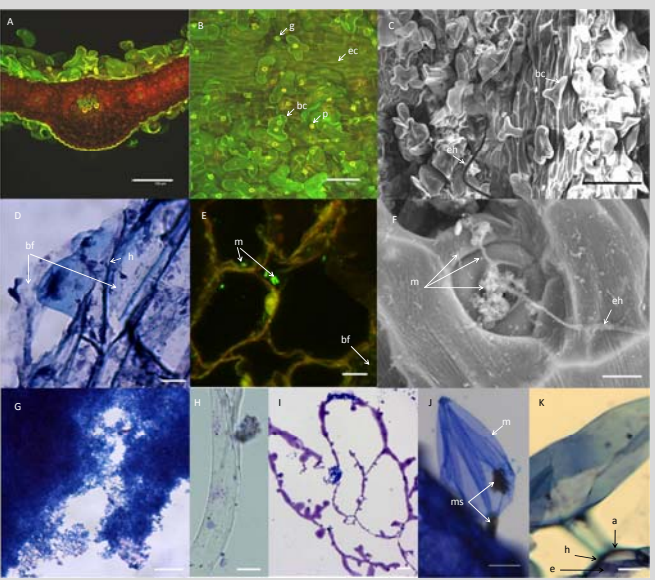


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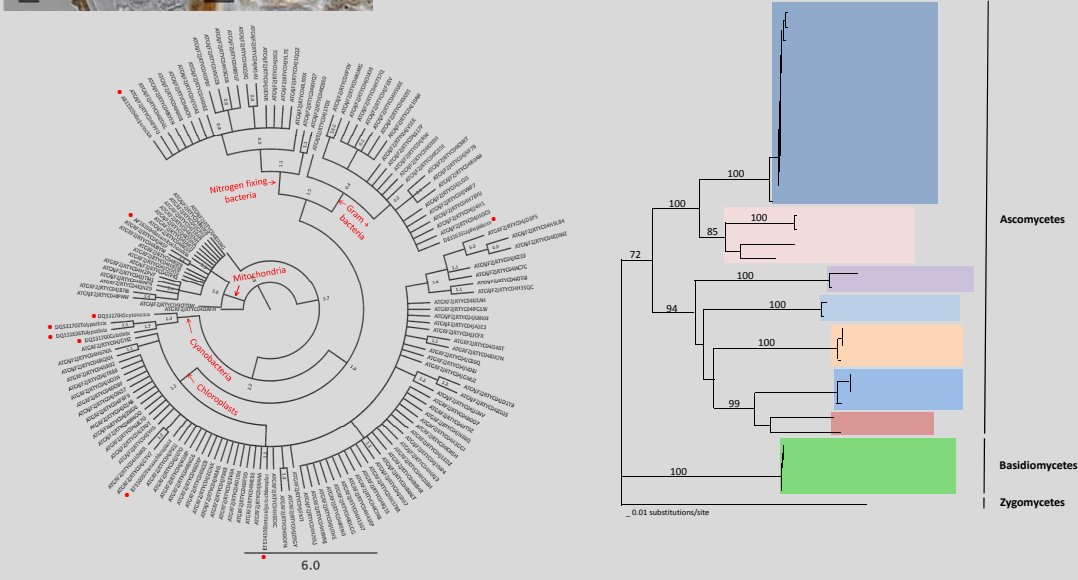
**Abstract:**  
 Cryptic symbiotic microbes influence host adaptation by improving nutrient uptake or stress tolerance. Current technologies for increasing plant productivity, whether for food and fuel production or for restoration and remediation, often utilize approaches that *bypass*, rather than *leverage*, microbial influences. Such technologies are insufficient for reversing desertification and increasing vegetative production to meet the increased demands of expanding populations and changing climates. Improved understanding of host-microbe interactions across ecological gradients may facilitate technology development that harnesses microbial power to augment vegetative production. We have identified numerous seed borne bacterial and fungal taxa believed to be vertically transmitted in *Atriplex* species, and have demonstrated potential for these microbes to increase plant production. Plans are underway to explore these and other taxa across temporal (evolutionary) and spatial gradients to learn how these microbes influence host plant adaptation to extreme or changing habitats. Findings are expected to magnify existing understanding of microbial interactions in plant ecosystems, providing insights relevant to restoration, carbon sequestration, biofuel, and agricultural technology development.



**Figure 1:** *A. canescens* produces abundant seeds (A), encased in hard utricles (B, u) surrounded by fibrous bracts (B, b). Seeds excised from the utricles (2C) reveal clear hyaline hyphae (hh) resting above aniline blue-staining hyphae (bh) surrounding the inner testa (it), or seed coat. Fungal bodies (fb) divide atop embryonic cells. Hyphae (h) are visible in the intercellular spaces of the developing embryo (2D).



**Figure 2.** Micrographs of leaf (A-C and E-K) and root (D) sections of micropropagated *Atriplex*. A. Regenerated shoots stained with SYTO 9 and propidium iodide. Bladder and epidermal cells, and cells within vascular bundles fluoresce green. B. Leaf surfaces reveal zones of green fluorescing elongated cells (ec) interspersed between dense regions of bladder cells (bc) which penetrate the epidermis, creating yellow-collared penetration points (p). Guard cells (g) surrounding the stomatal pores fluoresce green. C. Leaf surface SEM shows bladder cells (bc) interspersed with regions of elongated cells. A single elongated hyphae (eh) is visible above the bladder cell region. D. An 8 μM trypan blue stained root section reveals a putative biofilm (bf) containing both hyphae (h) and yeast-sized microbial cells. The biofilm, which covers all cells, is most visible where it has been slightly raised by the growing tip of a lateral root initial (bf). Scale bar = 10 μm. E. Syto 9 and propidium iodide-stained leaf mesophyll cells reveal green-fluorescing microbial cells (m) concentrated near plant cell walls, and a lightly fluorescing biofilm (bf). Scale bar = 10 μm. F. SEM of a stomatal complex. An elongated hyphae (eh) extends across the pore. Microbial cells (m) are clustered within the pore and on the surfaces of surrounding guard cells (g). G. A 2 μM section excised from above the surface of an *A. torreyi* leaf reveals clusters of trypan blue stained, yeast like cells. Scale bar = 10 μm. H. A 2 μM section excised just above the leaf surface reveals a single fungal hyphae similar to the superficial hyphae in 2C. Scale bar = 5 μm. I. A 2 μM section excised from above a leaf surface reveals a biofilm-like layer corresponding to the intracellular regions of the underlying leaf. Scale bar = 10 μm. J. Toluidine blue-stained, developing bladder cell contains microsclerotia (ms) in the stem and lateral region, and is covered with superficial microbial cells (m). Scale bar = 10 μm. K. Close up views of individual bladder cells could not clearly distinguish whether stem attachment points (a) were adjoined to the epidermal cells (e) or to associated hyphae (h).

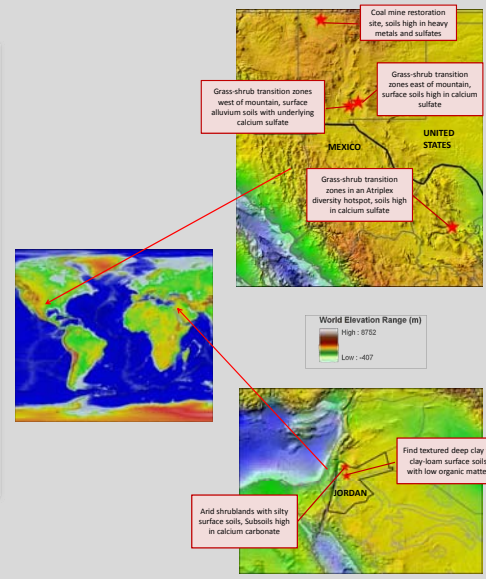


**Figure 3.** Numerous bacteria and organelles are passed to progeny via host plant seeds. Tag-encoded pyrosequencing of ribosomal 16S sequences reveals diverse bacterial endophyte and organellar sequences originating from *Atriplex* seeds *in vitro*. Red dots highlight reference sequences added for similarity comparisons

**Future directions:**  
 Microbial profiles obtained from metagenomic analyses of seeds, leaves, roots, and rhizosphere samples obtained from shrubs collected along well defined ecological gradients will be compared to host plant genetics and environmental data to identify microbes that best correlate with either host plant genetics or with environmental factors such as drought tolerance.

Microbes that best correlate with the host plant, regardless of habitat will be subjected to phylogenetic comparisons with the host to explore potential co-evolutionary roles.

Taxa that correlate best with dry or saline habitats will be subjected to laboratory bioassays testing the osmotic stress tolerance conferred to host plants.



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