

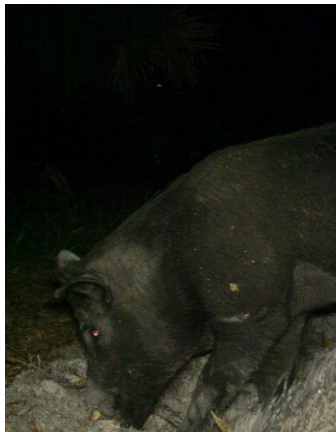


Have you ever wondered what those wild hogs root for?

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The wild hog (*Sus scrofa*) is one of the most widely distributed mammals in the world and is classified as an invasive species outside its native range. One factor that has allowed this species to establish itself in many regions is its broad and adaptable omnivorous diet. Wild pigs also exhibit a wide range of feeding behaviors including browsing, grazing, foraging, rooting, and direct predation on animals. In both their native and introduced ranges, plants dominate their diet. Both above-ground and below-ground food items are consumed – the latter made available through rooting.



The wild hog is therefore well known for its generalist diet, a contributing factor to its successful invasion around the globe. Although, when asked the question “What are wild hogs eating when they root around?” we have found it difficult to answer with confidence or detail. We therefore designed a study to figure out what those wild hogs consumed during a year living on a Florida ranch. To do this we used DNA metabarcoding analyses of scat to examine wild hog diet. Regions of DNA known as barcoding genes in both animal DNA and plant DNA were extracted and amplified for high throughput sequencing. These sequences (you can think of them as unique barcodes) were then identified using the online reference database “GenBank” housed at the US National Center for Biotechnology Information (NCBI). This database is the main reference used to identify species and has over 260,000 banked sequences.

The study site was divided into five sampling areas to ensure dispersed sampling across the ranch. At least five freshly deposited scats were collected every two months from each sampling area for a year to allow a full picture of the annual diet. Two hundred nineteen scat samples were collected. Of those, we discarded 23 samples because six samples contained highly-degraded DNA and could not be used for analyses, and 17 were non-wild hog in origin. These included samples from five cattle, four raccoons, three deer, two opossums, one coyote, one alligator, and one human! From our specific barcoding genes we found the following.

From the plant specific gene we identified eighty plant genera from 66 families. Within the unique plant sequences, 45 taxa were identifiable to species. The ten most commonly detected families in descending order were Fagaceae, Poaceae, Amaranthaceae, Commelinaceae, Fabaceae, Pinaceae, Polygonaceae, Cyperaceae, Rubiaceae, and Arecaceae (Figure 1). Oak

(*Quercus* sp. [Fagaceae]), torpedograss (*Panicum repens* [Poaceae]), joyweed (*Alternanthera* sp. [Amaranthaceae]), Bahiagrass (*Paspalum notatum* [Poaceae]), dayflower (*Commelina erecta* [Commelinaceae]), southern watergrass (*Luziola fluitans* [Poaceae]), and other grasses (Poaceae) occurred in over 60% of the scat samples analyzed. An additional 11 taxa belonging to the families Pinaceae, Arecaceae, Polygonaceae, Fabaceae, Araliaceae, Asteraceae, Rubiaceae, Ceratophyllaceae, and Onagraceae were detected in over 25% of the fecal samples (see Table 1 for explanation of scientific family names).

From the animal specific gene seventy-eight animal genera from 63 families were identified. Within the animal genera, 56 taxa were identified to species. The ten most commonly detected families in descending order were Glossoscolecidae, Calliphoridae, Muridae, Cricetidae, Psychopodidae, Sarcophagidae, Bovidae, Procyonidae, Bibionidae, and Staphylinidae (Figure 1, Table 1). Animals were present across a wide taxonomic breadth, but generally encountered less frequently than plants (Figure 1) with the exception of an exotic earthworm (*Pontoscolex corethurus* [Glossoscolecidae]), which was detected in 84% of samples. Cattle (*Bos taurus* [Bovidae]), house mouse (*Mus musculus* [Muridae]), cotton mouse (*Peromyscus gossypinus* [Cricetidae]), raccoon (*Procyon lotor* [Procyonidae]), mole cricket (Gryllotalpidae), white-tailed deer (*Odocoileus virginianus* [Cervidae]), and six fly taxa belonging to the families Calliphoridae, Bibionidae, Psychopodidae, and Sarcophagidae were recorded from over 10% of samples. This gene also identified fungi genera from 12 families. Within the fungi genera, two taxa were identified to species, *Amanita rubescens* and *Pleuotus ostreatus*. A *Psathyrella* sp. was detected in 28.8% of samples.

Figure 1. The top 10 most frequently occurring families in hog scat.

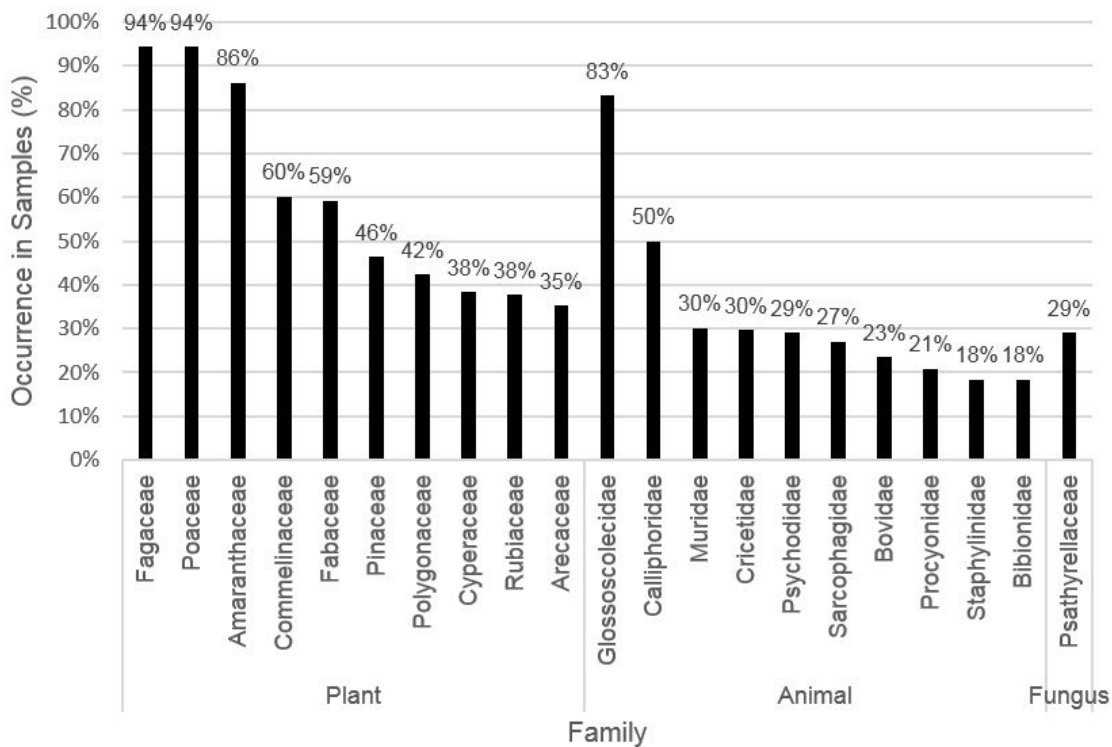


Table 1. Biological description of scientific family names.

	Family	Description	Example(s)
Plant	Fagaceae	Oaks and Beeches	Live oak tree
	Poaceae	Grasses	Torpedograss, bahiagrass, Bluestem
	Amaranthaceae	Annual or perennial herbs or shrubs	Joyweed, Alligator weed
	Commelinaceae	Dayflower or spiderworts	Dayflower
	Fabaceae	Legumes	Peas and beans
	Pinaceae	Pines, cedars, firs, spruces	Slash pine tree
	Polygonaceae	Knotweeds or smartweed-buckwheats	Sea grape, Buckwheat
	Cyperaceae	Sedges	Nutsedge, Sawgrass
	Rubiaceae	Coffee, madder or bedstraws	Buttonbush, Milkberry
	Arecaceae	Climber trees or shrubs	Palm tree
Animal	Glossoscolecidae	Earthworms	Nightcrawler
	Calliphoridae	Blow Flies	Blow and Carrion Flies
	Muridae	Old world rodents and mice	House mouse
	Cricetidae	Bew world rodents and mice	Cotton mouse
	Psychodidae	Flies and gnats	Drain flies, sewer gnats
	Sarcophagidae	Flesh flies. Laying live young on flesh and dung	"Red-eyed" flies
	Bovidae	Cloven-hoofed, ruminant mammals	Cattle, sheep, goats
	Cervidae	hoofed, ruminant animals	Deer, Elk
	Procyonidae	Small omnivororus mammals, related to carnivore	Racoons
	Staphylinidae	Rove beetles	Hairy rove beetle
	Bibionidae	Flies - the march flies	Lovebugs
Fungi	Psathyrellaceae	Dark-spored fungi	Inky cap mushrooms

In summary, we identified 66 plant, 68 animal, and 12 fungal families in wild hog scat. In the fungi the most common was *Psathyrella sp.* with many species in the genus (Figure 2, Brittlestem Mushroom as an example). Plant species dominated the diet with oaks (Figure 3), torpedograss, watergrass (Figure 4), joyweed, Bahiagrass, dayflower, and other grasses occurring in over half the samples analyzed. Other mast such as palm nuts was also found in the diet (Figure 5). Animals were present in wild hog scat across a wide taxonomic breadth, but encountered less frequently than plants with the exception of an exotic tropical earthworm (Figure 6). Cow, house mouse, cotton mouse (Figure 7), raccoon, mole cricket, Virginia opossum, and six species of fly were recorded from over 10% of fecal samples. In the case of some flies they were unlikely to have been consumed, but rather eggs were laid on a hog scat after deposition. Fly larvae on carrion consumed by hogs may be another way they become diet items in wild hog scat. In addition, wild hogs may also undertake coprophagy, eating the dung of other species such as cattle and deer, which could be why these species turn up as diet items. Unexpected species such as pig frogs (Figure 8) and several fish (Figure 9) were also in the diet, but we cannot tell if these are caught or scavenged. Through this genetic study we have shown, as expected, that wild hogs have very wide breadth of diet items. This re-enforces the theory that wild hogs do have the ability to impact a large variety of native flora and fauna species, and that further knowledge of their direct impacts on susceptible species is sorely needed. In addition, the ability of hogs to move invasive species, such as torpedo grass, across the landscape is highly likely.

For more information on wild hog studies and information please visit Dr Boughton at the Range Cattle Research and Education Center, and the Rangeland Wildlife and Ecosystems Services program (www.rangelandwildlife.com). If you have any questions please contact me at boughton@ufl.edu call 863-735-1314 ext. 216.

This collaborative project would not have been possible without the following people.

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Figure 2: Pale Brittlestem Mushroom



Figure 3: Southern Live Oak



Figure 4: Water grass



Figure 5: Palmetto Berries



Figure 6: Exotic earthworm



Figure 7: Cotton Mouse



Figure 8: Pig frog



Figure 9: Lake Chubsucker

