

Phylogenetic reconstruction of the callose synthase gene family using iTOL.

wall, inhibiting the spread of infections into healthy plant tissue. Callose synthase is the enzyme responsible for the synthesis of this critical polymer.

Neither the evolution of callose synthase in the plant response to pathogens nor its modification across green plants has yet been investigated. This study explores the callose synthase enzyme family across green plant species to understand how plant immune systems evolved throughout their 500-million-year evolutionary history.

To achieve this, 33 plant genomes representing different plant groups were analyzed. BLAST and HMMER searches, using callose synthase genes previously characterized in *Arabidopsis* as the query, identified 294 unique callose synthase proteins. Multiple sequence alignment using MAFFT revealed the relationship between these homologs. The resulting sequences were trimmed and used to build a phylogenetic tree using IQTree maximum-likelihood estimation.

This phylogeny showed that green algae form a clade by itself and that the remaining six callose synthase clades contain only land plant taxa, suggesting that the function of callose synthase diverged when plants evolved for land and became critical to their survival at that point. Additional changes among clades reflect significant modifications in plant pathogen defense strategies over time and identify likely targets of related proteins, which

can be further investigated to develop novel methods to enhance the innate pathogen response of plants.

Research advisor Chao Cai writes: “Gianna’s work explores the evolutionary history of callose synthase, which is an important player in the process of plant response to infection. Identifying callose synthases that are responsible for disease resistance in a variety of plant species will help with the design of disease control strategies, especially in crop plants.”

The Cross-Linguistic and Cross-Situational Association Between Accentedness and Its Impact as Rated by Speakers

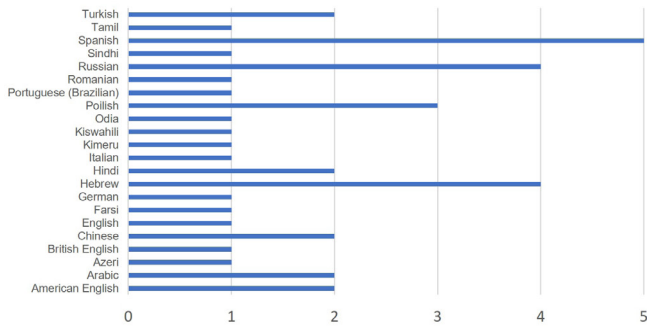
Student researcher: Makaila Groves, Senior

Accentedness is the extent of a foreign accent in one’s speech, which depends on how listeners perceive this speech to be different from their own variety. The scope of practice of speech-language pathologists (SLPs) includes providing services for accent modification to culturally diverse populations. Although SLPs are taught that accentedness is a language *difference*, not a *disorder*, training to provide accent-related services is not currently required, leaving clinicians to draw on their experience with disorders and assume that accent *modification* means accent *reduction*. Gaining understanding of the situation-specific ways in which accentedness can impact individuals would improve the SLPs’ ability to serve a variety of diverse clients.

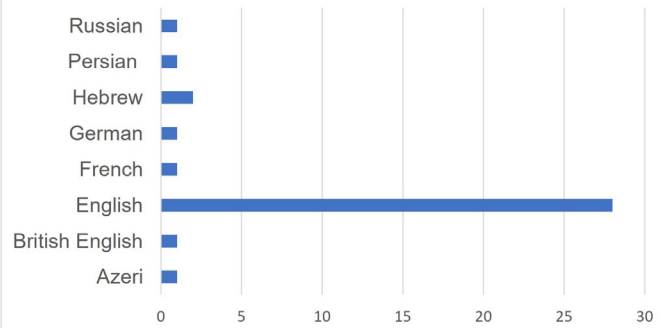
To determine the relationship between accentedness and its impact on speakers, 43 multilingual adults were asked to rate the consequences of their accentedness, from their own perspective, across a variety of situations (e.g., work, home, etc.). Responses were analyzed quantitatively by ranges of magnitude of accentedness and ranges of impact on the speakers’ lives (positive, negative, or neutral) and examined within the context of languages involved.

As hypothesized, this study confirms that the impact of accentedness is not limited to the magnitude of the accent. It also relates to the languages involved, and it is context/situation specific. A qualitative analysis of open-ended answers provided details of the sociolinguistic and sociocultural considerations that may have

Influencing Languages in our Data



Target Languages in our Data



All languages reported by participants as their influencing languages (the sources of the accent) and their target languages (the languages spoken with a foreign accent).

implications for the relationship found between accent- edness and its impact. These findings help inform the provision of accent-related services with wider implica- tions for advocating for culturally diverse populations.

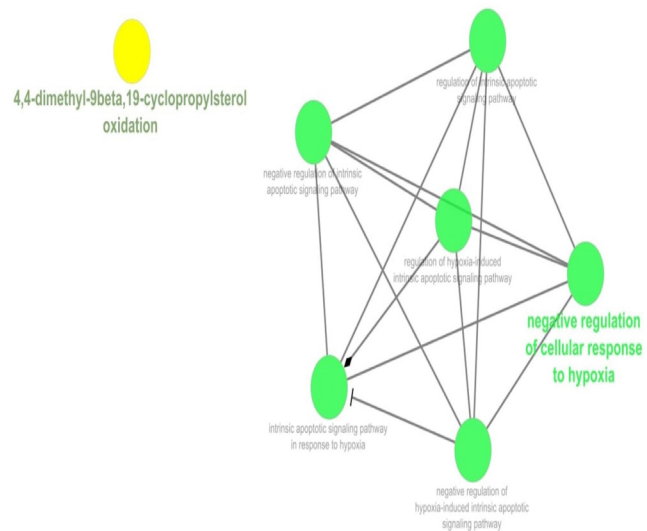
Research advisors Naomi Gurevich and Talia Bugel write: “Client-centered care requires us to consider the multi- faceted ways accents can affect speakers. Makaila’s research helps show that the relationship between the level of accentedness and its impact on speakers is situation-specific and not always direct, making a case for better understand- ing the sociolinguistic and sociocultural forces at play.”

Toward Improved Global Food Security: Uncovering How Tomatoes Fight Root-Knot Nematodes

Student researcher: Chingyan H. Huang, Sophomore

The nematode genus *Meloidogyne*, known as root-knot nematodes, are damaging parasitic worms that infect a plant’s roots and hinder its ability to take up nutrients. These nematodes may cost the world as much as \$100 billion in crop damages. Nematodes are typically controlled using pesticides, but the low efficiency and negative environmental impacts of chemical treatments call for the development of other *Meloidogyne* manage- ment techniques. In this study, we specifically examine the resistance response of tomatoes (*Solanum lycopersi- cum*) infected by *Meloidogyne*, because tomatoes are one of the world’s most economically significant crops with gross production earnings of \$88 billion, according to the FAO. Moreover, multiple studies have reported genes

that might confer resistance to *Meloidogyne* infection in different tomato plant cultivars. However, genetic pathways for nematode resistance in tomatoes merit further study due to the complex genetic backgrounds of different tomato cultivars. To examine nematode-resistance pathways, we curated transcrip- tomic profiling data collected using next-generation RNA sequencing from tomatoes infected with *Meloidogyne*. Curated reads from multiple studies will be pooled to estimate expression levels of different genes to identify common tomato genes that are significantly



Gene ontology diagram from a previous project, which found possible identities of differentially expressed genes by matching them to genes with known identities/functions from Arabidopsis thaliana. Groups of pathways that are expressed together are also highlighted. This diagram is a general representation of what a gene ontology analysis should look like.