GWAS From Spoken Phenotypic Descriptions: A Proof of Concept From Maize Field Studies

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ABSTRACT

Speech-derived phenotypic descriptions analyzed using existing Genome-Wide Association Study (GWAS) methods recover genomic regions involved in the maize plant height trait, demonstrating that non-structured, spoken descriptions of phenotypes can be used for association genetics. We collected phenotypes of *Zea mays* by recording spoken descriptions of plant traits such as height, color, leaf width, and feel of the texture of the leaves. To examine the relevance of spoken phenotypic descriptions for association genetics, we phenotyped the Wisconsin Diversity panel and developed two methods to process these spoken descriptions, in this case, for plant height. To measure semantic similarity, we generated a score that indicates how alike each observation is in meaning to the query "tall". For the second method, we binned manually scored phrases related to plant height, then assigned scores to each observation. These were compared to published genomic locations associated with plant height (and with data we manually collected). Both methods recover known plant height associations.

Keywords: spoken descriptions; association studies; phenotyping; maize; genes; plant height

1 INTRODUCTION

Collecting phenotype data can be slow, which limits the speed of association genetics and genomic studies for trait improvement. High-throughput phenotyping methods are an area of development that concentrates on engineering sensors and unmanned vehicles to collect (mainly visual) data about traits of various crop species (reviewed in Yang et al. (2020)). These methods are beneficial for collecting large amounts of data in an automated fashion, but there are difficulties in deploying these tools in a field environment, and some traits are not detectable by images alone. Additionally, manually collecting phenotypes with pen-and-paper or tablet-and-stylus is time-consuming and generally requires predefined traits of interest. Sensors, imaging, and barcodes make data organization easier for large quantities of data (Yao et al., 2021; Sarić et al., 2022; Kazic, 2020). An underdeveloped area of in-field phenotyping ripe for exploration is using natural language descriptions of plants. Platforms exist where audio descriptions are recorded (Kazic, 2020). However, the biologically relevant data in spoken phenotypes thus far has remained inaccessible for association studies and other applications.

As demonstrated by Oellerich, Walls, and colleagues, language-based descriptions of phenotypes can be analyzed computationally to recover known biological associations in plants (2015). Their work used structured language data, ontologies, structured as entity quality (EQ) statements (Mungall et al., 2010) (where an entity is a feature, e.g., whole plant, and quality is a describer, e.g., dwarf-like) results in less intensive computations. Semantic or word-meaning similarity methods have also

shown promise in ascertaining biologically meaningful genetic associations (Braun et al., 2020; Braun and Lawrence-Dill, 2020). Additionally, pre-trained models have enabled free-text descriptions of plant phenotypes for association studies based on semantics (Braun et al., 2021). The developments in the computational processing of natural language plant phenotypes through unstructured text formats contribute to conceptualizing methods for recording spoken descriptions of phenotypes.

To test whether associations between genomic variants and phenotypes could be derived from spoken language, we reasoned that a well-characterized diversity panel that had many associations already derived would be required as ground truth, which led us to select the Wisconsin Diversity (WiDiv) panel for this work. WiDiv (1) was developed to grow in the upper midwestern region of the United States; (2) includes only lines with similar flowering time and phenology, and (3) is made up of line that have both genetic and phenotypic diversity (Hansey et al., 2011). Researchers using the WiDiv panel have increased the included accessions, investigated flowering time and biomass yield traits, and generated genetic marker data for the panel (Hansey et al., 2011; Hirsch et al., 2014; Mazaheri et al., 2019; Mural et al., 2022b).

Because the WiDiv panel data has expansive genotypic and phenotypic trait data available, we collected spoken descriptions of phenotypes for numerous traits (height, leaf width, color, etc.) during the summer of 2021 (Yanarella et al., 2023a). The objectives of this research were to (1) detect phenotype descriptions from spoken descriptions, (2) demonstrate techniques for extracting phenotype data for a proof of concept analysis involving the plant height trait for GWAS, (3) perform GWAS with phenotypes derived from speech, and (4) use available gene function data to review and assess known and novel gene trait associations.

2 MATERIALS AND METHODS

We used a genotypic dataset that includes WiDiv panel taxa (lines). A dataset of 18 million SNP markers (Mural et al., 2022a) obtained from RNA-Seq and resequencing techniques for 1,051 taxa (described in (Mural et al., 2022b)). Phenotypic datasets, described in a manuscript that has been submitted, which contain 686 unique WiDiv panel taxa (Yanarella et al., 2023a), hereafter referred to as the Yanarella *et al.* dataset. This dataset contains an additional 25 taxa (Supplementary Table 1) that were positive controls for the analysis of spoken descriptions of phenotypes, as these plants were expected to have noticeable and describable phenotypes, though these taxa are not members of the WiDiv panel. Informed consent for the spoken data from participants was collected per Iowa State University's Institutional Review Board's (IRB) Exempt Project status, and volunteers provided informed consent for using their spoken observations. Phenotypic data obtained from these data include measurements for plant height and spoken descriptions of plants grown in a field environment. The Mural *et al.* and Yanarella *et al.* datasets have an intersection of 653 taxa (Figure 1), which were used for further analyses.

2.1 Spoken Phenotype Collection Summary

Phenotype descriptions recorded by de-identified student workers in the Yanarella *et al.* dataset were analyzed. The field in which the recordings were taken included two replicates planted in a randomized incomplete block design. The first block consisted of 31 WiDiv panel taxa for a seed increase, and the second block consisted of 8 B73 experimental control rows, 25 positive control taxa, and 655 unique WiDiv panel taxa. The second block contained two rows of the WiDiv panel line MEF156-55-2. Therefore, the recordings were taken over 720 rows in each replicate.

Each of the de-identified student workers selected NATO code names. The students who were undergraduate Agronomy, Biology, and Genetics Majors at Iowa State University are known as "Delta," "Golf," "Kilo," "Lima," "Mike," "Quebec," "Victor," "Yankee," and "Zulu." Each participant was instructed to state their NATO code name and the row tag number before observing the plants in each row (Figure 2 (a)). This procedure ensured the participant's de-identified connection to the row number and spoken observation while enabling the parsing of each observation so that multiple row observations could be recorded in the same file.

2.2 Phenotype Detection and Descriptions

A subset of spoken observation transcripts containing the positive control accessions were parsed. 4-6 terms from the description and phenotype records for each accession drawn from MaizeGDB (Woodhouse et al., 2021). One term from these lists was used to collect synonyms from Marriam-Webster (Merriam-Webster, 2023) and WordHippo (Kat IP Pty Ltd, 2008) thesaurus services (Table 1). The number of

rows containing at least one synonym related to each accession's descriptions and phenotype records was calculated as a proportion to the number of observations for that accession.

2.3 Preprocessing Genotypic Dataset

Trait Analysis by aSSociation, Evolution and Linkage (TASSEL) Version 5.0 Standalone (Bradbury et al., 2007) was used to convert the Mural *et al.* genotypic data from a variant call format (vcf) formatted file to a HapMap (hmp) formatted file. The data was then processed to contain marker information for the 653 taxa shared with the Yanarella *et al.* dataset, these data were grouped by chromosome, and HapMap files were generated for each chromosome. The chromosome files were sorted by maker position from lowest position to highest position.

The sorted chromosome files were reformatted to vcf files using TASSEL Version 5.0 Standalone, then vcftools v.0.1.14 (Danecek et al., 2011) concatenated these files, and the resulting file was zipped. PopLDdecay v3.42 (Zhang et al., 2018) was used to analyze and visualize Linkage Disequilibrium (LD) Decay of the Mural *et al.* genotypic data.

2.4 Preprocessing Phenotypic Datasets

2.4.1 Plant Height Measurement Data

R Scripts (v.4.2.2 and v.4.3.1) (R Core Team, 2023) were developed to process the measuring and scoring data from Yanarella *et al.* dataset such that only plant height observations were retained for each of the three observation groups. Replicate number was programmatically added to these data, and positive control were removed. The 653 taxa shared between the datasets were retained.

Best Linear Unbiased Estimators (BLUE) values were calculated for each taxa using R's built-in lm function to perform linear regressions and the emmeans v.1.8.7 package (Lenth, 2023), where taxa and replicate were fit as fixed effects. Best Linear Unbiased Prediction (BLUP) values were calculated for each taxa with the lmer function of the lme4 v.1.1-34 package (Bates et al., 2015) where taxa, replicate, and row number were fit as random effects. Visualization of diagnostics plots of the models (Supplementary Figure 1, Supplementary Figure 2) were generated using the ggResidpanel v.0.3.0 package (Goode and Rey, 2022).

2.4.2 Semantic Similarity for Plant Height Spoken Data

Text transcripts of spoken data from the Yanarella *et al.* dataset were processed using Python v.3.8.2 (Van Rossum and Drake, 2009). The spaCy v.3.5.1 package (Honnibal and Montani, 2023) and the TensorFlow v.2.12.0 (Abadi et al., 2016) spaCy Universal Sentence Encoder v.0.4.6 (Mensio, 2023) were used to process the transcripts to obtain semantic similarity scores. Three phrases, "tall," "tall plant," and "tall height," were compared to each row observation through spaCy's similarity function using the pre-trained large English universal sentence encoder (en_use_lg) from TensorFlow. A dataset of similarity scores in the form of values from 0 to 1 was generated (Figure 2 (b)).

Similarity scores for the 653 taxa shared by both datasets were retained, encompassing 35,709 rows or 91.92% of the original rows observed (Table 2). The similarity scores for the "tall" query were used as input to calculate BLUEs and BLUPs in the same manner as described in the *Plant Height Measurement Data* section, and visualizations of diagnostics plots of the models (Supplementary Figure 3, Supplementary Figure 4) were generated.

2.4.3 Binning for Plant Height Spoken Data

The transcripts of spoken plant descriptions were reviewed for phrases directly related to narrations about plant height. A set of 797 plant height phrases were manually curated and binned from 0 to 7, where 0: no growth, 1: very short plants, 2: short plants, 3: short-medium height plants, 4: medium height plants, 5: medium-tall height plants, 6: tall plants, 7: very tall plants. Bin values were assigned to observations for the 653 taxa shared by both datasets (Figure 2 (b)). Of the total text transcripts, there were 34,209 or 88.06% row observations that were retained and binned (Table 2).

BLUEs and BLUPs were calculated as described in the *Plant Height Measurement Data* Section, and visualizations of diagnostics plots of the models (Supplementary Figure 5, Supplementary Figure 6) were generated. Additionally, the R nnet v.7.3-19 package (Venables and Ripley, 2002) was used to perform multinomial logistic regression to predict height phrase bins, where taxa and replicate were fit as fixed effects.

2.5 Genome-Wide Association Studies

Genome Association and Prediction Integrated Tool (GAPIT) 3 v.3.1, 2022.4.16 (Lipka et al., 2012; Tang et al., 2016; Wang and Zhang, 2021) was used to perform Fixed and random model Circulating Probability Unification (FarmCPU) (Liu et al., 2016) and Mixed Linear Model (MLM) (Yu et al., 2005) on each of the phenotypic datasets using the Mural *et al.* marker dataset for genotypic input. Each chromosome was run individually, and PCA.total parameter was set to 3 for all analyses (Figure 2 (c)). This manuscript focuses on the FarmCPU analyses, the MLM processing and results are available as described in *Web resources* section.

2.6 Genome-Wide Association Study Analyses

Manhattan plots from the resulting GAPIT analyses were generated using the ggplot2 v.3.4.3 package (Wickham, 2016). We used the RAINBOWR v.0.1.29 package's (Hamazaki and Iwata, 2020) CalcThreshold to determine the Bonferroni threshold for each analysis with a sig.level of 0.05. SNPs that were identified as above the Bonferroni threshold for each analysis were viewed on MaizeGDB's implementation of GBrowse2 (Generic Genome Browser v.2.55) (Stein, 2013) using Maize B73 RefGen_v4; gene IDs were collected within +/- 300 kilobases (kb), based on the LD decay curve generated by PopLDdecay, of the identified SNPs (Supplementary Figure 7).

We collected a list of genes shown to influence plant height (Table 3, Supplementary Table 2) and compared the gene IDs from the GWAS analyses using a web-based intersection and Venn diagram tool (Sterck, 2021) to determine if these previously published plant height genes were identified within the +/- 300 kb region indicated by the LD decay curve for each of our analyses. Additionally, Gene Ontology (GO) terms for the gene IDs within +/- 300 kb of SNPs identified as significant were obtained using the B73 RefGen_V4 Zm00001d.2 annotations generated by Maize Go Annotation - Methods, Evaluation, and Review (maize-GAMER) tool (Wimalanathan and Lawrence-Dill, 2017; Wimalanathan et al., 2018) and the R package GO.db v.3.17.0 (Carlson, 2023) was used to collect terms associated to the GO IDs (Supplementary Table 3).

3 RESULTS AND DISCUSSION

3.1 Detecting Phenotypes from Spoken Descriptions

Student participants made three complete passes of the field ($\sim$4,320 observations per student participant (Table 2, *Total Rows Observed Count*) and used their individual wording and phraseology to describe the phenotypes in the field. Student participants recorded observations between 2 and 241 words in length (Figure 3). To explore the ability of the student participants to identify and describe phenotypes for traits of interest, 25 positive control accessions that, if grown in the appropriate environmental conditions, would show visually "dramatic" phenotypes.

The 25 positive control accessions were observed 53-55 times over all nine student participants (Table 1). We utilized Merriam-Webster (Merriam-Webster, 2023) and WordHippo (Kat IP Pty Ltd, 2008) thesaurus services to determine the participant's ability to identify words synonymous with descriptors that describe the positive control phenotypes as demonstated in Figure 4 (a-c). For example, accessions M241C *A1 A2 B1 C1 C2 Pl1 Pr1 R1-r* and 219L *B1-S; R1-r pl1-McClintock* (gene name *colored1* and *colored plant1*, Supplementary Table 1) had at least one synonym in each of the observations made by the student participants as indicated in Table 1 by the proportion of 1.000 for both Marriam-Webster and WordHippo synonyms. While accessions U740G *Fbr1-N1602* (gene name, *few branched1*), 703J *Rs1-O 1* and 703K *Rs1-Z* (gene name *rough sheath1*, Supplementary Table 1) had low proportions of observations having at least one synonym for each observation as indicated in Table 1.

Our findings indicate that participants, unaware of expected phenotypes, can identify and describe them in their own words. These results are limited in the number of synonyms identified for phenotype descriptions and the environment in which the plants were grown. The thesaurus services could deflate the proportion of observations with at least one synonym if the participants used informal descriptors. Additionally, the student participants would only have described our intended positive control phenotypes if the field environment and weather conditions were conducive to displaying the expected phenotypes.

3.2 Extracting Phenotype Data for Plant Height from Spoken Descriptions

Two methods were employed to preprocess text transcriptions of spoken descriptions of plants. The semantic similarity method of comparing the term "tall" to each row observation retained 91.92% of the

full set of row recordings captured (including the 25 positive controls and 33 accessions unique to the Yanarella *et al.* dataset) by the student participants, demonstrating that 35,709 row observations were made with taxa in both datasets (Table 2). The manual bin method of identifying phrases related to plant height and binning them based on apparent semantic similarity retained 86.06% of the full set of row recordings captured by the student participants and 95.80% of the observations with plant height phrases made with taxa in both datasets, which results in 34,209 row observations for manually binned data (Table 2).

Both methods parse information about the plant height traits and process the data into a format appropriate as input into available GWAS tools and models. Using a query term for plant height and semantic similarity requires less manual curation and was implemented on a larger subset of data. The benefit of the binning method is that it reduces the noise; only observations with plant height-related terms were considered.

A limitation of the query term and semantic similarity method is retaining noisy data because this method compares the ”tall” query to each observation and relies on pre-trained models. An example of noise comes from the participant whose NATO code name ”Victor's” recording for row 1,456 on 07/16/2021, *tall and height green all the way to the bottom ... super short hairs on top that are quite prickly ... in general there are the brace roots are short fat and light green in color*, in which the similarity function of spaCy University Sentence Encoder (Mensio, 2023) when compared to the ”tall” query string determine the semantic similarity score as 0.0848. The shortcomings of the binning method are the time-consuming nature of curating lists of phrases relevant to the trait of interest and the loss of data where phrases directly related to plant height were not specified.

3.3 Association Studies using Phenotypes Derived from Speech

We performed association studies using FarmCPU (Liu et al., 2016) on three categories of phenotype data. The first phenotype category was ground truth (measured) plant height data using BLUEs (Figure 5 (a)) and BLUPs (Figure 5 (b)). For the BLUE analysis, 21 significant SNPs above the Bonferroni threshold of 8.55 were identified, and of those SNPs, we discovered 10 (Supplementary Table 3) in which at least one plant height gene was detected in the literature within +/- 300 kb (Supplementary Table 2). The BLUP analysis identified 29 significant SNPs, 9 (Supplementary Table 3) where at least one plant height gene was discovered in the literature within +/- 300 kb (Table 3, Supplementary Table 2).

The second phenotype category used BLUEs (Figure 6 (a)) and BLUPs (Figure 6 (b)) for tall query and semantic similarity of spoken phenotype descriptions. These analyses identified 27 and 23, respectively, significant SNPs (Supplementary Table 3), respectively, above the Bonferroni threshold of 8.55. Of these, 9 and 8 genes, respectively, were formerly detected for plant height within +/- 300 kb of the SNP (Table 3, Supplementary Table 2).

The third phenotype category used BLUEs (Figure 7 (a)) and BLUPs (Figure 7 (b)) for manual binning of spoken phenotype descriptions with plant height terms. These analyses identified 32 and 33, respectively, significant SNPs (Supplementary Table 3), above the Bonferroni threshold of 8.55 respectively. Of these, 13 and 12 have genes formerly reported within +/- 300 kb of the SNP (Table 3, Supplementary Table 2). An additional analysis was completed using predicted values from a multinomial regression (Supplementary Figure 8, Supplementary Table 2) in which 21 SNPs were significant, and 3 had genes detected within +/- 300 kb of the SNP in the literature (Table 3, Supplementary Table 2).

Having demonstrated that transcripts of spoken descriptions of plants can be computationally processed and applied as phenotypic input for existing GWAS tools, we further sought to determine whether the data collected in this experiment are practical for association studies. To do this, we utilized ground truth measurements of plant height and identified SNPs associated with plant height that have been reported in other publications.

The semantic similarity method with the tall query to generate phenotype values for each spoken observation using spaCy's similarity function (Honnibal and Montani, 2023) and the Universal Sentence Encoder (Mensio, 2023) was successful. We were able to perform GWAS, and there were significant SNPs from regions associated with plant height. As this is a proof of concept study, we acknowledge that other pre-trained models exist capable of calculating semantic similarity or models that can be adapted to generate similarity scores related to plant height such as BioBERT (Lee et al., 2019), those implemented by the Python gensim package (Řehůřek and Sojka, 2010), or others reviewed in Koroleva et al. (2019). Further, additional queries could be employed for relating the text observations to a height value.

The binning method for plant height phrases appears to be a promising method for association studies with phenotype data extracted from spoken descriptions. This method reduces the noisiness of the transcription data and scores observations on only phrases detailing features of plant height. Additionally, the GWAS performed with BLUE and BLUP values generated from the binning method detected more known regions associated with plant height formerly reported than the manually measured and semantic similarity query methods (a comparison of the SNPs identified by each method for the plant height trait can be found in Supplementary Table 4).

We demonstrate our use of a multinomial regression to generate phenotypic input with binned data, although we recognize that FarmCPU is not optimized for multinomial input. GWAS tools that utilize an ordered multinomial regression model to predict multinomial values for association studies were developed in the medical research field (German et al., 2019). Regardless, FarmCPU with multinomial binned input for plant height detected regions of the genome associated with plant height.

While participant language was not constrained, input that is less noisy and with lower data loss could be attainable if an emphasis were placed on stating specific aspects of the plant accompanied by a descriptor and reducing literary descriptive comments. An example of describing a specific aspect of a plant is ”tall, green, and long” compared to ”this row has tall plants.” The former statement is unclear whether the whole plant is described or a specific aspect of the plant, while the latter makes it clearer that the total plant height is described. Literary language descriptions are more difficult to compute because context is necessary to determine the meaning behind a phrase, an example, candy cane stripe. While candy cane stripe may induce a mental image of a candy cane, unless a computation model is trained to identify the literary description, the model would not be able to discern the spoken description of phenotype as a particular striped pattern.

3.4 Investigating GO Terms from GWAS Results

After identifying the gene IDs associated with the regions +/- 300 kb of the significant SNPs, we investigated the GO terms annotated to these genes. The full list of GO terms for each model discussed above is available in Supplementary Table 3 and Supplementary Table 5. To examine how these terms align with plant height terms, we queried the dataset for the words auxin, brassinosteroid, and gibberellin because of their known functions in plant height regulation ((Li et al., 2020) reviews the importance of these hormones). The term ”auxin” was more frequently present in these datasets when compared to brassinosteroid or gibberellin (Table 4).

Additionally, other GO annotations identified in our analyses have functions that may affect plant height. Examples of these GO terms include developmental growth (GO:0048589), anatomical structure formation involved in morphogenesis (GO:0048646), and shoot system development (GO:0048367). Further, using GWAS, we found genomic regions with functional annotations related to plant hormone functions that were not identified by the literature in Table 3. These regions can be of potential interest for the plant height trait.

While examining GO terms, descriptions that do not relate to plant functions but were annotated to gene IDs occurred. Errant assignments of GO terms for plant-specific tasks has been described in Fattel et al. (2022). An example is the gene ID *Zm00001d008201* being assigned the term animal organ development (GO:0048513). Interestingly, this ID was also assigned the terms auxin-activated signaling pathway (GO:0009734) and post-embryonic development (GO:0009791). These results demonstrate a compelling argument for reviewing GO terms produced by plant-specific annotation tools to remove non-plant terms.

4 CONCLUSION

Spoken, unstructured phenotypic descriptions can be used to recover known associations and to identify potentially new regions of the genome contributing to well understood traits. This work required that we develop methods to process recordings of spoken observations of plants in a field environment as phenotypic input for commonly used GWAS tools. We found that both methods we employed for generating phenotypic data from transcripts of spoken observations recovered known genomic regions of interest for plant height. Additionally, novel regions were identified and could be investigated for their role in the plant height trait. These methods provide a framework for further exploratory research, including expanding the methods employed to obtain biologically relevant information from spoken data and expanding the number of traits in which spoken descriptions are the basis of phenotypic data for

GWAS. Additional traits were collected for this WiDiv dataset by speech and manual scoring to contribute to these prospective research undertakings and are publicly available (Yanarella et al., 2023a).

Beyond these demonstrations that spoken, unstructured phenotypic descriptions can be used to recover known associations, there are two other conceptual benefits that should be considered. Firstly, when people are describing what they see in the field rather than exclusively collecting predefined traits, the potential to uncover novel phenomena is perhaps increased. Secondly, it is the case that for many years we have used computers to analyzed structured data, so those collecting the data have limited themselves to documenting data in a structured, computer-friendly format. This is, in effect, asking people to structure their thinking and documentation like - and for - a computer. With the methods described here, the people collecting the data are enabled to think and behave in a more naturally human way for data collection. This has implications for the rate of data collection and for cognitive burden as follows. Over three weeks of data collection, each participant made three complete passes of the field, recording spoken observations. However, when the participants collected manual scoring and measurement data, none were able to make a complete pass of the field. Our experimental design enabled the student participants to speak and describe plant traits using their unique vocabulary and speech patterns. Participant ”Zulu” reported that recording spoken observations was simpler and easier than measuring and scoring because they could make more detailed observations about different parts of the plants because recording spoken observations was both less strenuous and less mentally taxing.

Some may wonder why having a person describe phenotypes matters at all given that image-based data collection is improving all the time, and seems to be a great way to collect data for image-based machine learning analytics of phentypes and traits (reviewed in Xiao et al. (2022)). Clearly image analysis can be useful for many traits, but for those traits that involve tactile, odor, or other sensory observations, image-based data collection cannot collect relevant data. Coupled with image-based data collection and analysis, it is becoming clear that language-based annotations, both spoken and written, are poised to both allow and enable human perception and interpretation to fill nuanced understanding of phenotypes and traits.

5 WEB RESOURCES

Code to recreate the analysis in this manuscript is available at CyVerse Data Commons from (Yanarella et al., 2023b) and can be accessed from: `https://datacommons.cyverse.org/browse/iplant/home/shared/commons_repo/curated/Carolyn_Lawrence_Dill_Maize_WiDiv_Association_Studies_Dataset_September_2023`.

6 DATA AVAILABILITY

The de-identified spoken data described in this manuscript is exempted by Iowa State University's Institutional Review Board (IRB ID: 21-179-00). Phenotypic data was obtained from (Yanarella et al., 2023a) and is available from: `https://datacommons.cyverse.org/browse/iplant/home/shared/commons_repo/curated/Carolyn_Lawrence_Dill_Maize_WiDiv_Summer_2021_Dataset_June_2023`. Genotypic data was obtained from (Mural et al., 2022b,a) and can be accessed from: `https://figshare.com/articles/dataset/Maize_WiDiv_SAM_1051Genotype_vcf_gz_genotype_file/19175888/1`. Gene Ontology data was obtained from (Wimalanathan and Lawrence-Dill, 2017) and is available from `https://datacommons.cyverse.org/browse/iplant/home/shared/commons_repo/curated/Carolyn_Lawrence-Dill_maize-GAMER_maize.B73_RefGen_v4_Zm00001d.2_Oct_2017.r1`.

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9 CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

10 AUTHOR CONTRIBUTIONS

CFY and CJLD conceived the idea for this project. CFY performed the analyses and drafted the initial version of the manuscript. CFY and LF evaluated the GO term analysis. All authors have read, edited, and approved the manuscript.

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12 FIGURES

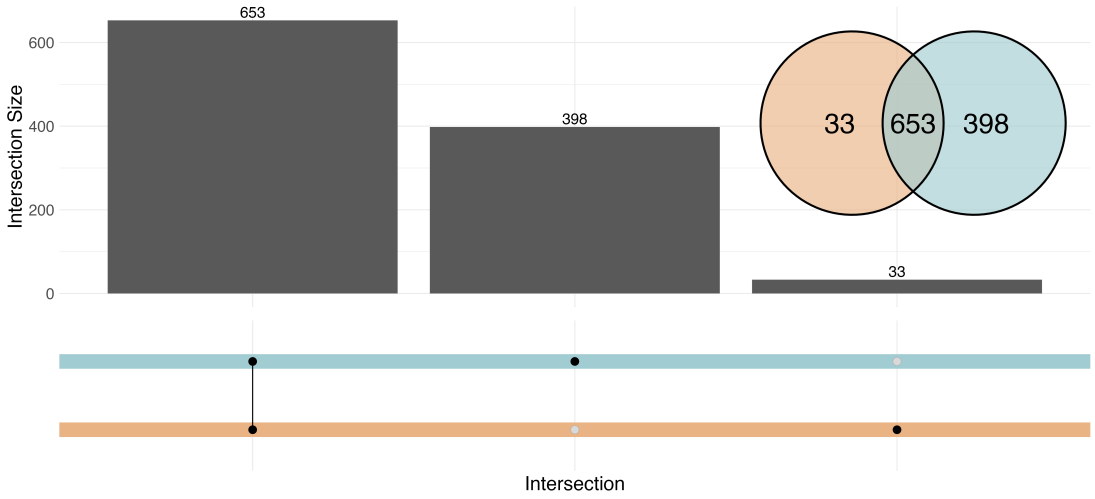

Figure 1. Comparison of intersections of Mural *et al.* and Yanarella *et al.* WiDiv dataset taxa (positive controls not included), where n is the number of unique taxa in each dataset. Mural *et al.* dataset (in blue, n = 1,051), and Yanarella *et al.* dataset (in orange, n = 686).

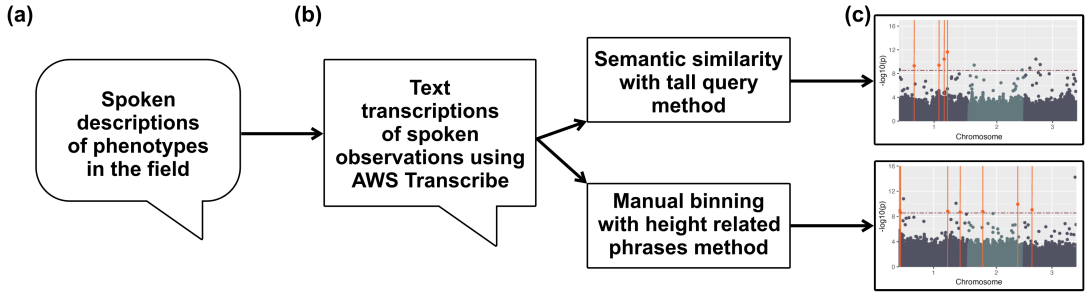

Figure 2. Spoken phenotype process overview. (a) In field spoken phenotype descriptions collection, (b) Spoken phenotype data processing, including transcript production and methods for generating numeric representations of phenotypes for traits, and (c) GWAS using data derived from spoken observations.

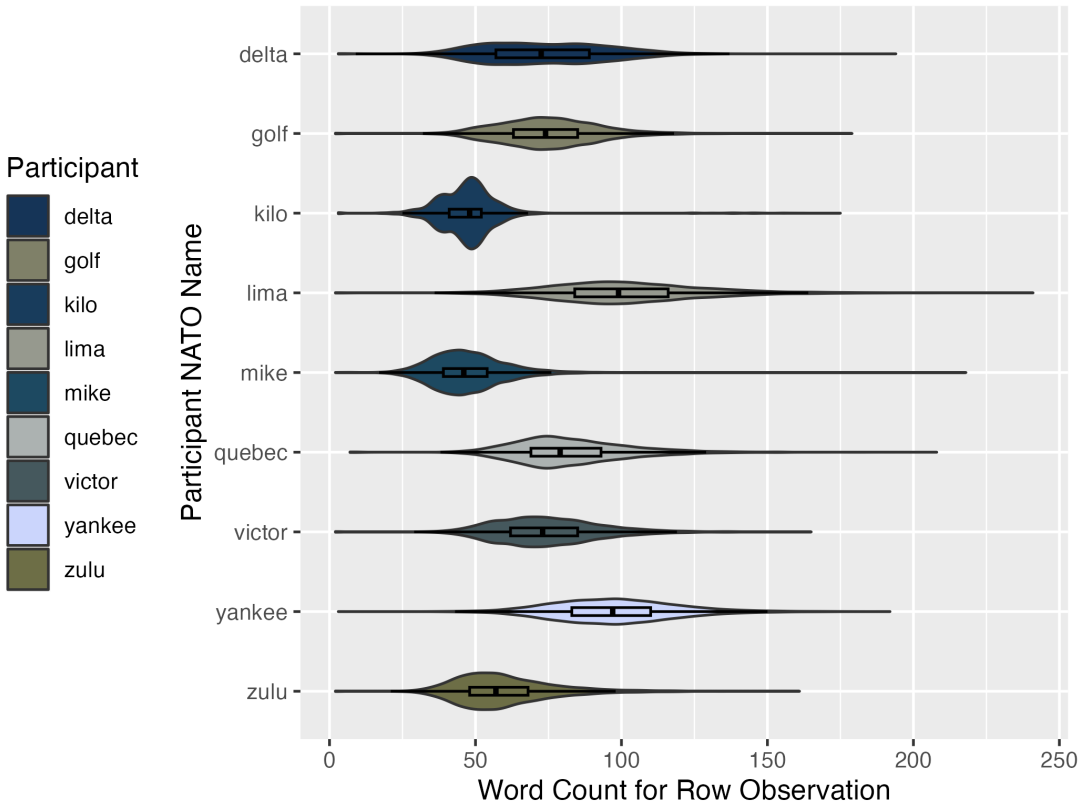

Figure 3. Distributions for each student participants word count per observation. A boxplot is included in each of the violin plots, individual outlier points not represented.

(a) 1248: "these plants are overall these plants are overall tall they are unique andy have purple stalks the stalks are skinny the midribs and the leaves are purple and the tassels they have are purple there's no ears on them the leaves are long and narrow there's some white spotting around the margins some of the leaves from the lower leaves are curling somewhat there's some wrinkles and bumps around the outer edges of some of the leaves the brace roots are purple with a little bit of white mixed in and these plants overall are are very unique due to their color patterns"

(b)

M241C

A1 A2 B1 C1 C2 Pl1 Pr1 R1-r

(c) **Phenotype Descriptions: purple, red, marbled, pigment, striped, and spotted**

Merriam-Webster	**WordHippo**
Synonyms Searched for: red	**Synonyms Searched for:** purple
Phenotype Descriptions and Synonyms: blooming, bloomy, blowsy, blowzy, blushing, bronzed, brown, cherubic, florid, flush, flushed, full-blooded, glowing, marbled, pigment, pink, pinkish, purple, red, rosy, rubicund, ruddy, sanguine, spotted, striped, suntanned, tanned, and warm	**Phenotype Descriptions and Synonmys:** amaranthine, amethyst, blue, bluish, dark, heliotrope, lavender, lilac, magenta, mauve, mulberry, orchid, periwinkle, perse, plum, pomegranate, purple, red, reddish, violaceous, violet, wine, purple, red, marbled, pigment, striped, and spotted
At least one term from "Phenotype Description and Synonyms" present:	
Yes	**Yes**

Figure 4. Example of detecting phenotypes from positive control accession descriptions. (a) Transcript of a spoken description for positive control accession M241C *A1 A2 B1 C1 C2 Pl1 Pr1 R1-r*, (b) Image of positive control accession M241C *A1 A2 B1 C1 C2 Pl1 Pr1 R1-r*, (c) Example of phenotype description terms, and synonyms from Marriam-Webster and WordHippo, to demonstrate a description having at least one instance of a synonymous word for the phenotype of interest.

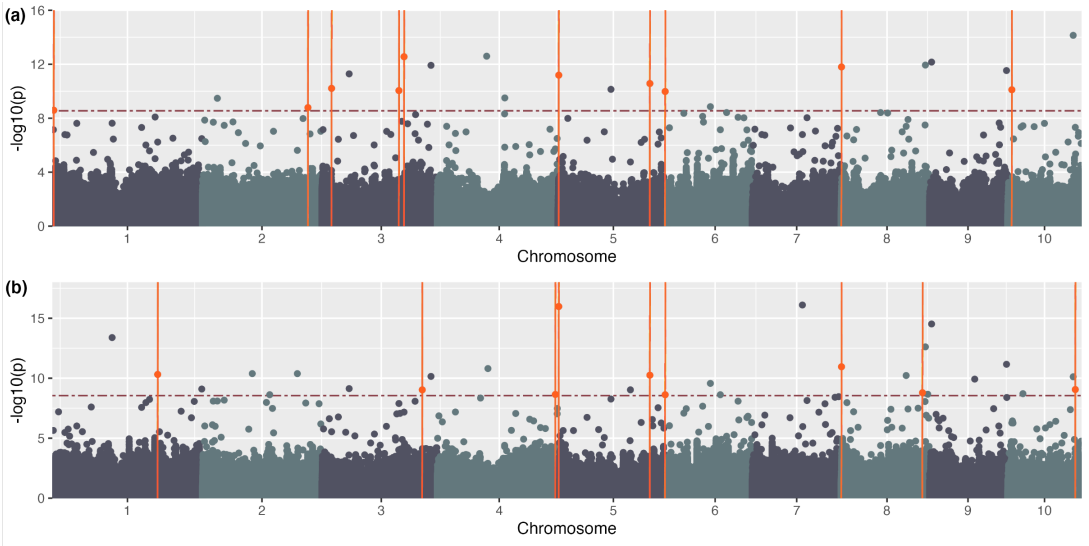

Figure 5. Manhattan plot of measured height phenotypic data. Plot generated using GAPIT and FarmCPU using measured height data (a) BLUEs and (b) BLUPs using Mural *et al.* genotypic data. The red dashed line indicates the Bonferroni threshold ((a) -log_10(p) = 8.55; (b) -log_10(p) = 8.55), orange points indicate identified SNPs with known plant height genes within +/- 300 kb, and orange vertical lines indicate positions +/- 300 kb identified SNPs with known plant height genes.

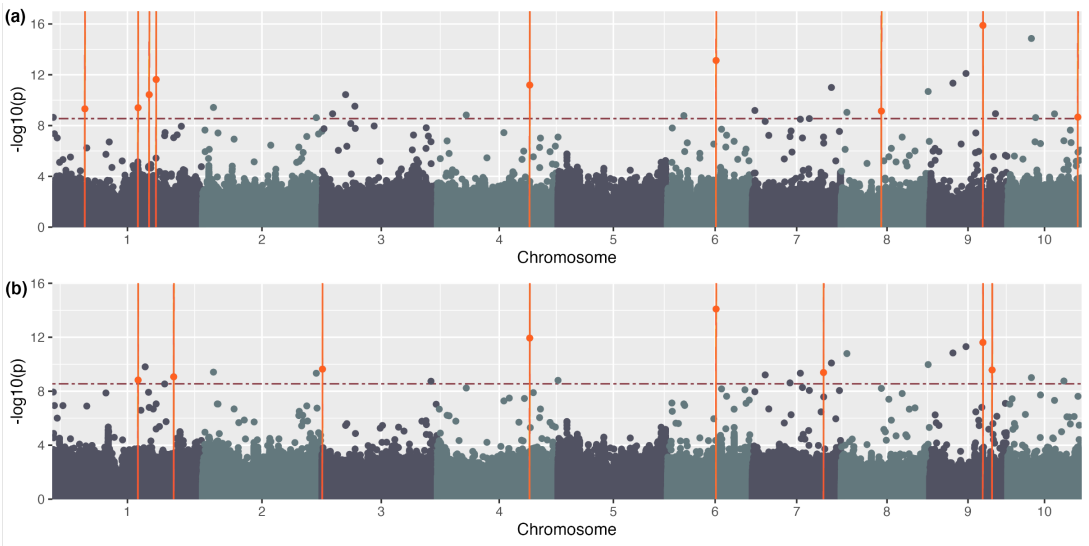

Figure 6. Manhattan plot of tall query semantic similarity phenotypic data. Plot generated using GAPIT and FarmCPU using semantic similarity score data (a) BLUEs and (b) BLUPs using Mural *et al.* genotypic data. The red dashed line indicates the Bonferroni threshold ((a) -log_10(p) = 8.55; (b) -log_10(p) = 8.55), orange points indicate identified SNPs with known plant height genes within +/- 300 kb, and orange vertical lines indicate positions +/- 300 kb identified SNPs with known plant height genes.

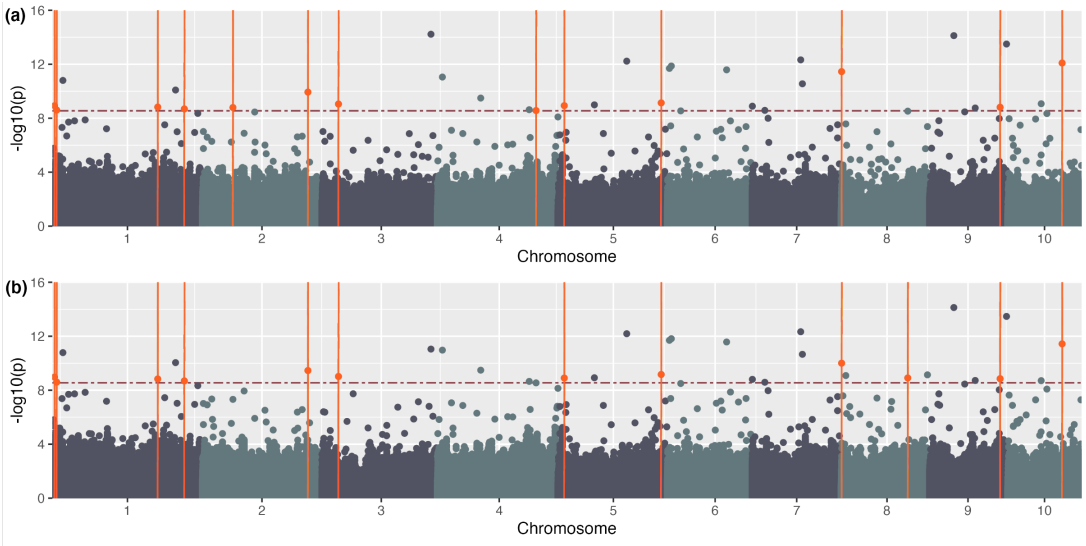

Figure 7. Manhattan plot of binned plant height phrases phenotypic data. Plot generated using GAPIT and FarmCPU using binned plant height data (a) BLUEs and (b) BLUPs using Mural *et al.* genotypic data. The red dashed line indicates the Bonferroni threshold ((a) -log_10(p) = 8.55; (b) -log_10(p) = 8.55), orange points indicate identified SNPs with known plant height genes within +/- 300 kb, and orange vertical lines indicate positions +/- 300 kb identified SNPs with known plant height genes.

Table 1. Proportion of word usage for describing positive control accessions.

Accession	Rows Observed Count	Merriam-Webster		WordHippo	
		Number of Synonyms	Proportion	Number of Synonyms	Proportion
528A *Hsf1-N1595*	53	32	0.2264	85	0.7358
528AA *Hsf1-N2559*	55	32	0.2000	85	0.6727
528J *Hsf1-N1603*	54	32	0.2778	85	0.8148
X28F *cr4-6143*	54	34	0.4815	83	0.5000
X29C *cr4-N590C*	54	34	0.5370	83	0.4630
X29D *cr4-N647*	54	34	0.6296	83	0.5741
702B *o2 v5 ra1-Ref gl1*	53	34	0.3208	73	0.4528
703D *o2 ra1-Ref gl1*	54	34	0.4074	73	0.5185
711H *ra1-N408E*	54	34	0.5000	73	0.5370
117D *tb1*	53	32	0.2075	71	0.3208
117DA *tb1-8963*	54	32	0.3889	71	0.4630
X03A *sr3*	55	32	0.5455	22	0.4364
X03J *sr3-N504A*	54	32	0.5926	22	0.6296
104B *rli1-N2302A*	54	49	0.1667	77	0.1667
104C *rli1-N2276*	55	49	0.2182	77	0.2000
703J *Rs1-O*	54	49	0.1667	77	0.2037
703K *Rs1-Z*	54	49	0.1667	77	0.2593
219L *B1-S; R1-r pl1-McClintock*	54	28	1.0000	28	1.0000
617A *pl1-0 c1-EMS Sh1 B1-S R1-r*	55	28	0.2182	28	0.2727
M241C *A1 A2 B1 C1 C2 Pl1 Pr1 R1-r* [a]	54	28	1.0000	28	1.0000
M341B *A1 A2 B1 C1 C2 pl1 Pr1 R1-r*	55	28	0.8364	28	0.8364
U740G *Fbr1-N1602*	54	31	0.0000	6	0.0370
916G *Trn1-N1597*	54	28	0.9815	57	0.9815
708C *o15-N1117*	54	71	0.3333	120	0.7037
119E *Ts6*	54	43	0.2778	47	0.8889

[a]Accession used for example illustrated in Figure 4.

Table 2. Observation retention by spoken phenotype method.

Participant	Total Rows Observed Count [a]	Spoken Phenotype Processing Method	
		Tall Query [b]	Manual Bins [c]
Delta	4,326	3,974 (0.9186)	3,911 (0.9041; 0.9841)
Golf	4,317	3,969 (0.9194)	3,711 (0.8596; 0.9350)
Kilo	4,321	3,973 (0.9195)	3,960 (0.9165; 0.9967)
Lima	4,322	3,975 (0.9197)	3,747 (0.8670; 0.9426)
Mike	4,302	3,953 (0.9189)	3,937 (0.9152; 0.9960)
Quebec	4,308	3,959 (0.9190)	3,241 (0.7523; 0.8186)
Victor	4,329	3,980 (0.9194)	3,946 (0.9115; 0.9915)
Yankee	4,308	3,960 (0.9192)	3,943 (0.9153; 0.9957)
Zulu	4,314	3,966 (0.9193)	3,813 (0.8839; 0.9614)
Sum	38,847	35,709 (0.9192)	34,209 (0.8806; 0.9580)

[a]Rows observed count includes data collected for all taxa within the Yanarella *et al.* dataset, including 25 positive control taxa and 33 taxa not found in the Mural *et al.* dataset.

[b]The count of row observations utilized for semantic similarity for spoken data methods represents the data 653 intersecting taxa between Yanarella *et al.* and Mural *et al.*, and the data in parentheses is the proportion of data retained from total rows observed.

[c]The count of row observations utilized for binning for spoken data methods represents the data 653 intersecting taxa between Yanarella *et al.* and Mural *et al.*, and the data in parentheses is the proportion of data retained from total rows observed (left) and the proportion of data retained from the 653 intersecting taxa which have plant height terms (right).

Table 3. Plant height gene models count identified from publications.

Publication	Plant Height Related Gene Model Count[a]
Jansson (1994)	1
Winkler and Helentjaris (1995)	1
Austin and Lee (1996)	3
Multani et al. (2003)	2
Blakeslee et al. (2005)	1
Geisler and Murphy (2005)	1
Brooks et al. (2009)	1
Wu et al. (2009)	7
Bai et al. (2009)	6
Lawit et al. (2010)	2
Hartwig et al. (2011)	1
Salvi et al. (2011)	4
Weng et al. (2011)	1
Teng et al. (2012)	1
Gallavotti (2013)	1
Peiffer et al. (2014)	7
Wallace et al. (2016)	312
Mazaheri et al. (2019)	10
Azodi et al. (2019)	876
Mural et al. (2022b)	347

[a]Count of gene model IDs identified for gene model set Zm00001d.2 gene model set and Zm-B73-REFERENCE-GRAMENE-4.0 assembly version.

Table 4. Appearance of GO terms by plant hormone for each method.

Analysis	auxin		brassinosteroid		gibberellin	
	Literature [a]	This Study [b]	Literature	This Study	Literature	This Study
Measured BLUEs GO Terms	2	15	0	3	0	4
Measured BLUPs GO Terms	3	22	0	8	0	6
Semantic Similarity Tall Query BLUEs GO Terms	12	5	0	5	0	7
Semantic Similarity Tall Query BLUPs GO Terms	2	15	0	3	0	6
Manual Term Bin BLUEs GO Terms	1	16	0	8	1	10
Manual Term Bin BLUPs GO Terms	1	15	0	6	1	9
Manual Term Bin Multinomial GO Terms	0	10	0	3	0	1

[a] Appearance count for GO terms of prior literature in Table 3.
[b] Appearance count for GO terms unique to this study.