Quantitative Methods for Studying Fruit Morphology in Strawberry

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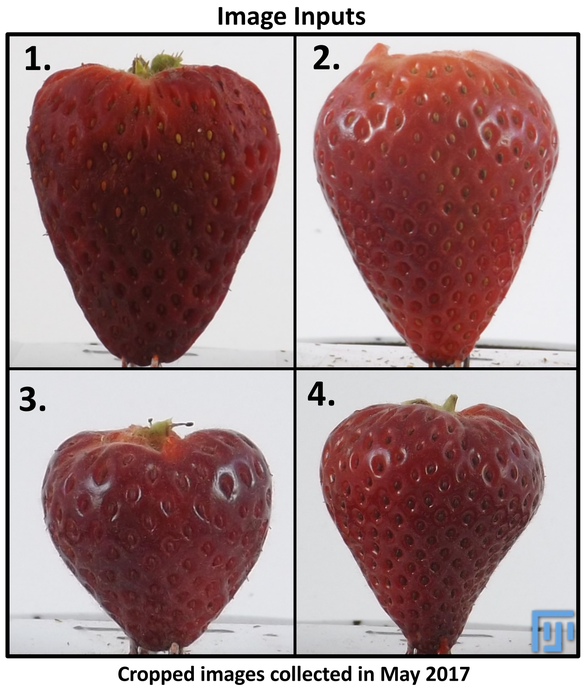
Introduction

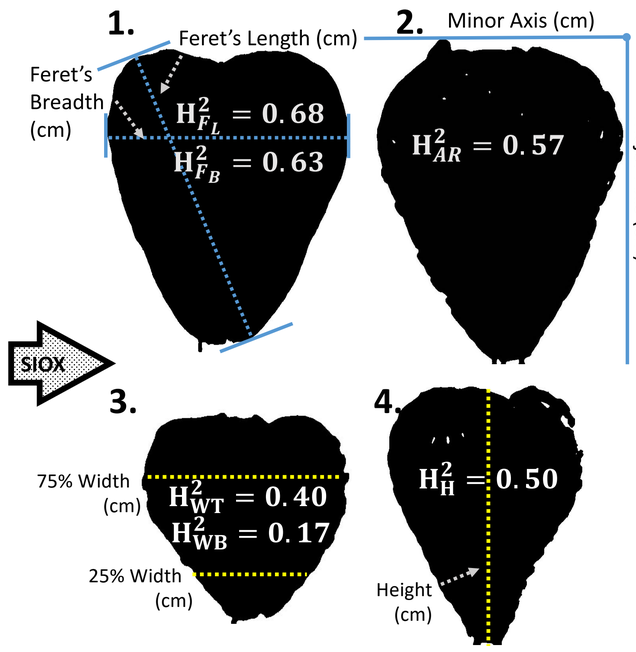
Several phenotypic characteristics, including, shape, and external color, are determinants of both grower- and consumer-centric fruit quality in strawberry (*Fragaria* × *ananassa*). Strong artificial selection for superior shelf-life, increased yield of marketable fruit, and other commercial production traits has significantly changed fruit morphology and quality attributes to produce high yielding cultivars with large, ultra-firm fruit. The genotype-to-phenotype networks underlying these changes have not been investigated in depth, and genes targeted by selection have not yet been identified in strawberry. Moreover, it remains unclear what level of phenotypic complexity is necessary and sufficient to support genomic-based inquiries and discoveries, expand what is known about modern germplasm, and enhance breeding practices in strawberry. Here, we demonstrate the quantitative methods being deployed to study fruit morphology in strawberry.

Methods

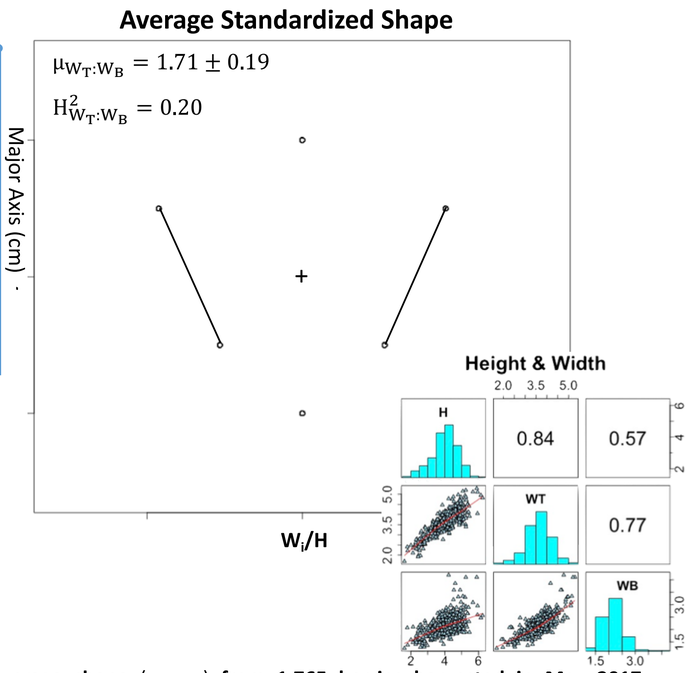
In One Dimension



Cropped images collected in May 2017

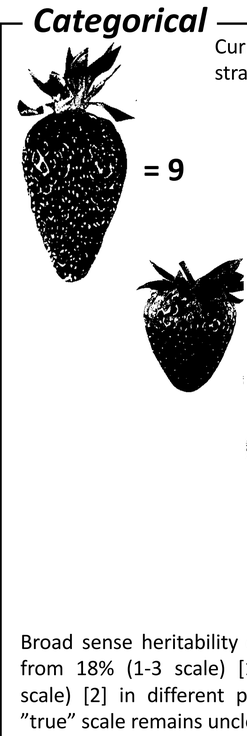


Masks generated using the SIOX algorithm in FIJI [1]. Broad sense heritability of each trait estimated as $H^2 = \sigma_G^2 / \sigma_P^2$



Average shape ($\mu_{WT:WB}$) from 1,765 berries harvested in May 2017. Height and width measurements are standardized by height, such that the height of every berry is 1 cm.

Categorical

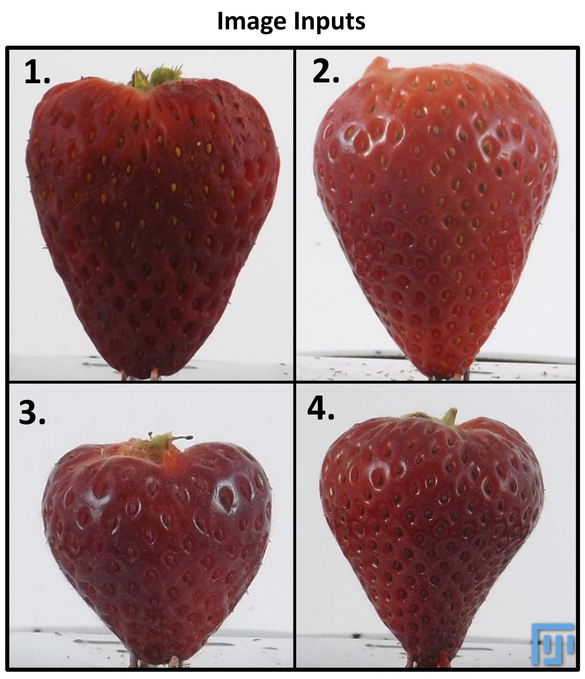


Current shape phenotyping protocols for strawberry rank fruit into categories (1-*n*).

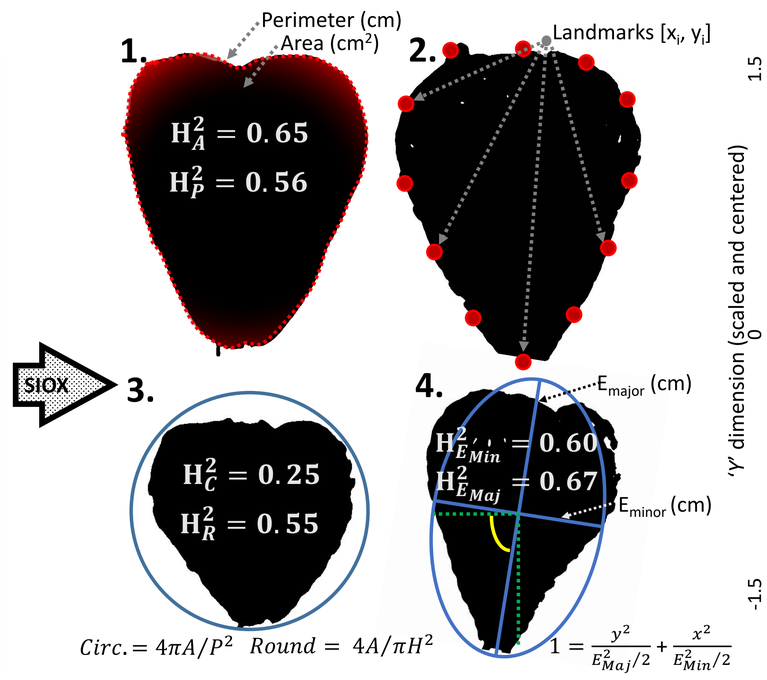
#	ID1	ID2	ID3	ID4	μ
1	1	2	1	1	1.25
2	2	2	2	1	1.75
3	3	3	3	3	3

Broad sense heritability estimates range from 18% (1-3 scale) [1] to 88% (1-5 scale) [2] in different populations. The "true" scale remains unclear.

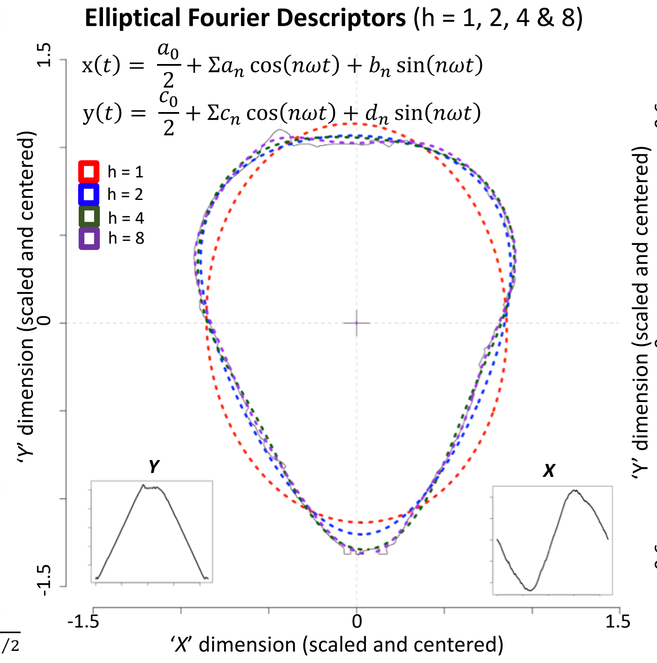
In Two Dimensions



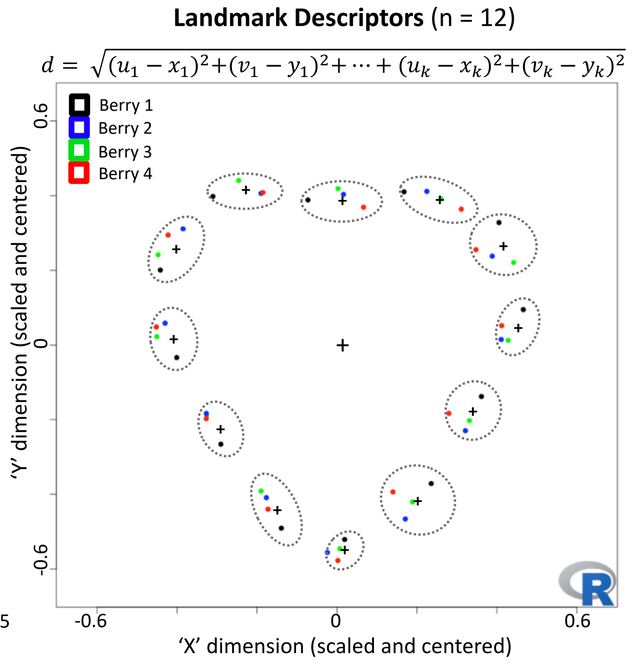
Cropped images collected in May 2017



Masks generated using the SIOX algorithm in FIJI [1]. Broad sense heritability of each trait estimated as $H^2 = \sigma_G^2 / \sigma_P^2$

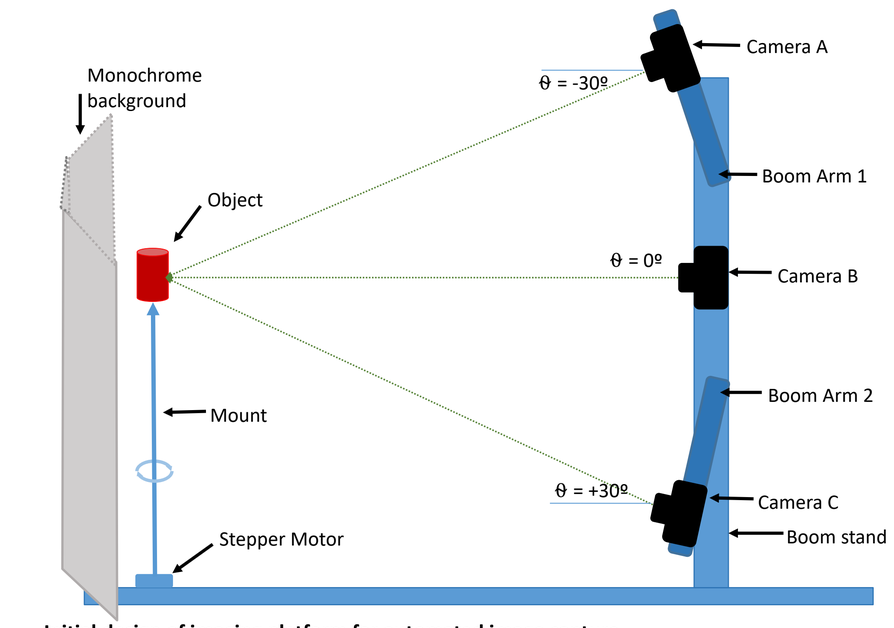


Elliptical Fourier Descriptors generated using "*Momocs*" in R [4]. The "Momocs" package in R provides a simple for calculating functional shape descriptors of closed form outlines.

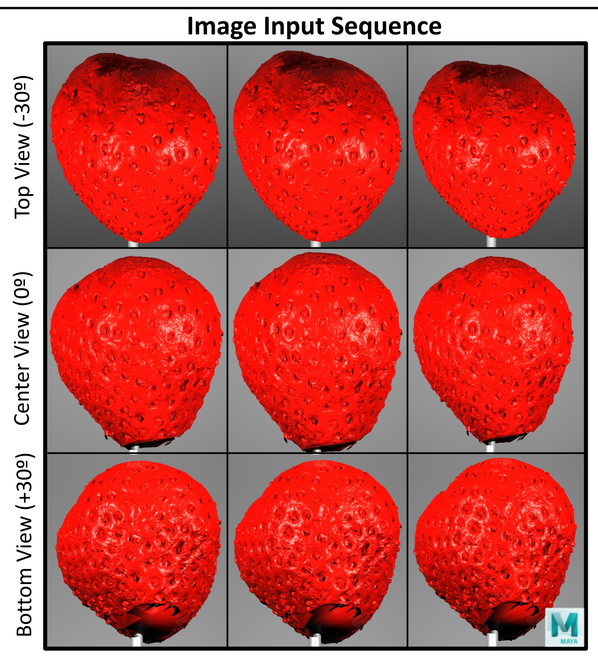


Unaligned pseudo-landmarks extracted in R. 12 evenly spaced points along the closed outline for the four strawberries are depicted along with centroid of each cluster.

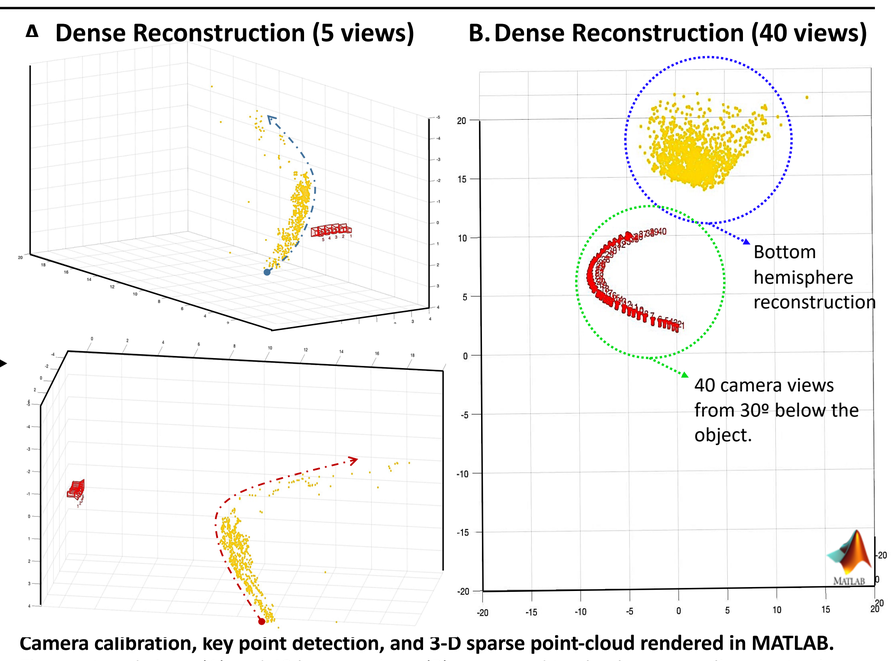
In Three Dimensions



Initial design of imaging platform for automated image capture. Digitally implemented in the AutoDesk® Maya® software to capture images from 3-D models.



Images digitally rendered in Maya® by AutoDesk®. 60 views (6º between views) per rotation, per camera were captured for each digital object.



Camera calibration, key point detection, and 3-D sparse point-cloud rendered in MATLAB. Five centered views (A) and 40 bottom views (B) were used to check camera alignment using in MATLAB. Observed a collapse in the angular spacing of our known camera positions

Conclusions

1. Both one and two dimensional traits, which are cheap and easy to acquire and assess, have broad sense heritability on the range of [0.17, 0.68] demonstrating the genetic control of these phenotypes.
2. Multiple proprietary software have failed to detect and register key points during camera calibration for the 3-D reconstruction of strawberries giving credence to our work.
   - Images generated from 5 cameras seem to align well and generate dense clouds that resemble strawberries.
   - We are yet to obtain a full 3-D reconstruction of a strawberry as the angle between individual cameras seems to collapse from 6º to 4º.
3. Three dimensional traits avoid the symmetry assumptions of both one and two dimensions and provide detailed topological information for performing functional data analytics and generating genomic insights.

Future Directions (and Dimensions)

1. Fix issues with camera calibration and validate accuracy of 3-D fruit models.
2. Determine which morphological features are most relevant for classifying strawberries into distinct categories.
3. Implement genome wide-association and genomic selection to determine signal in 1-D, 2-D, and 3-D parameterizations.
4. Explore the biological development of morphological features through time and differential gene expression.

References: [1] Schindelin et al. Nat. Meth. (2012); [2] Whitaker et al. J. Amer. Soc. Hort. Sci. (2012); [3] Antanaviciute, L. Thesis. (2016); [4] Bonhomme et al. J. Stat. Soft (2014);

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