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Traity: An Open-Source Platform for Automated Phenotyping of Fruit Internal Structure



Cranberry
Genetics and
Genomics Lab

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BACKGROUND

- Understanding internal fruit structure is essential for studying fruit development, physiology, and key traits such as texture, size, and shape.
- Existing methods (e.g., X-ray CT, image analysis) are limited by cost, manual intervention, and lack of batch-processing capabilities.
- We developed **Traity**, an open-source tool for automated, high-throughput analysis of 2D fruit slice images.
- We validate Traity's accuracy against ImageJ using cranberry samples and demonstrate its application in QTL mapping for breeding programs.
- Traity is adaptable across multiple fruit species, demonstrating its versatility as a universal phenotyping platform.

METHODS

Validation study: Fruit slices (25 slices per cultivar) from 25 cranberry cultivars were scanned. Using Traity, we extracted measurements for traits comparable to ImageJ (Abràmoff et al., 2004). The same slices were analyzed with ImageJ macros to assess agreement between platforms.

QTL mapping application: Internal fruit morphology of 168 individuals from a cranberry biparental population (harvested in 2019–2020) was phenotyped using Traity from fruit stamps (25 stamps per genotype). Texture was measured independently using a 10% compression test (López-Moreno et al., 2024). From the 34 Traity-derived traits, the 17 most variable traits were selected for genetic analysis. GBLUPs were used to detect trait–marker associations to support QTL discovery.

RESULTS

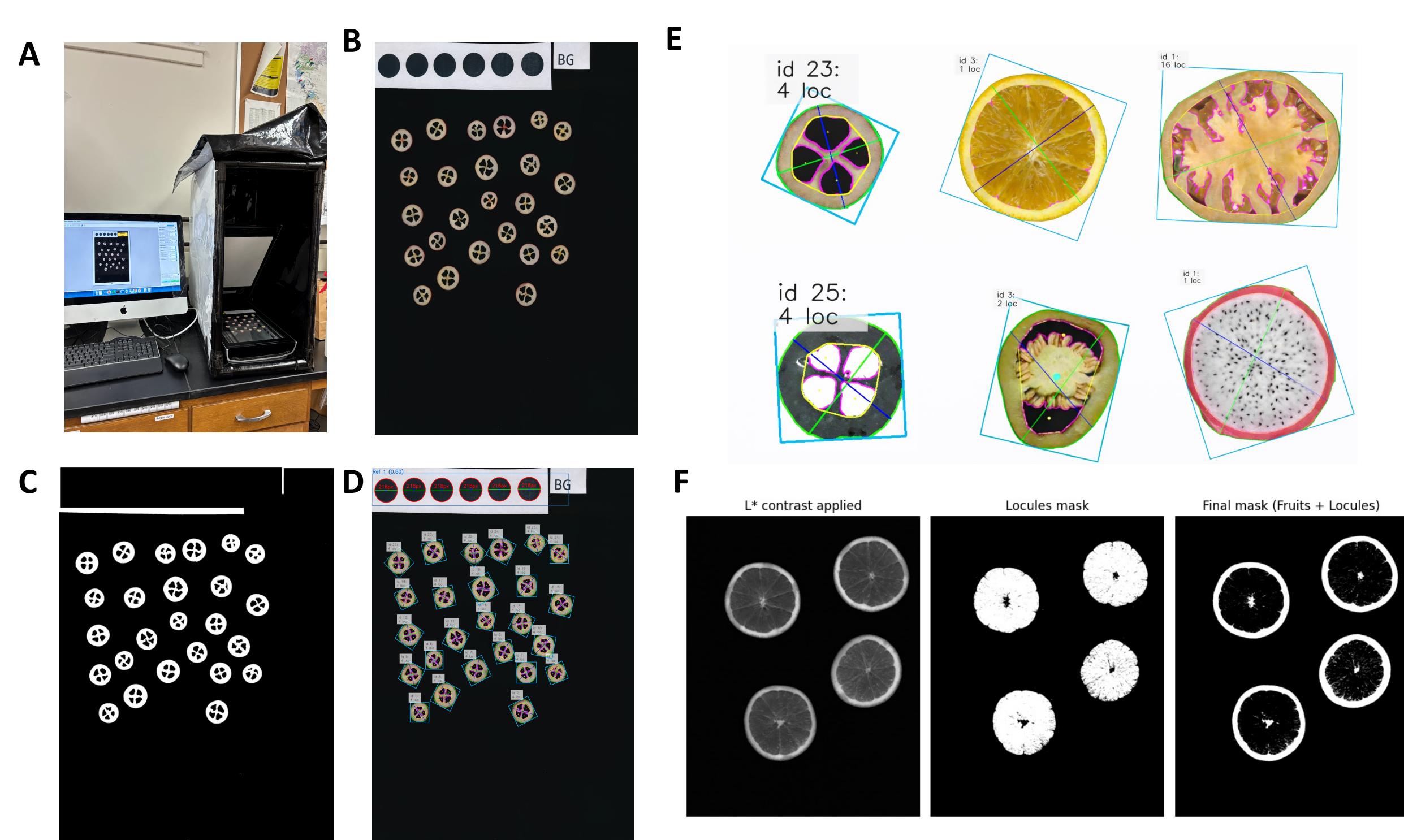


Figure 1. Fruit processing and image segmentation. A) Scanned fruit slices used for image acquisition. B) Input image. C) Traity masks for fruit and locule segmentation. D) Traity annotations showing the bounding box (blue), fruit contour (green), locule contours (pink), inner pericarp boundary (yellow), locule centroids (yellow dots), and major/minor axes (blue/green); fruit ID and locule number are displayed. The diameter of the size reference is shown in red. E) Representative fruits analyzed with Traity (cranberry, orange, tomato, cranberry stamps, pepper, dragon fruit). F) Image-processing workflow for fruits with complex locule structure.

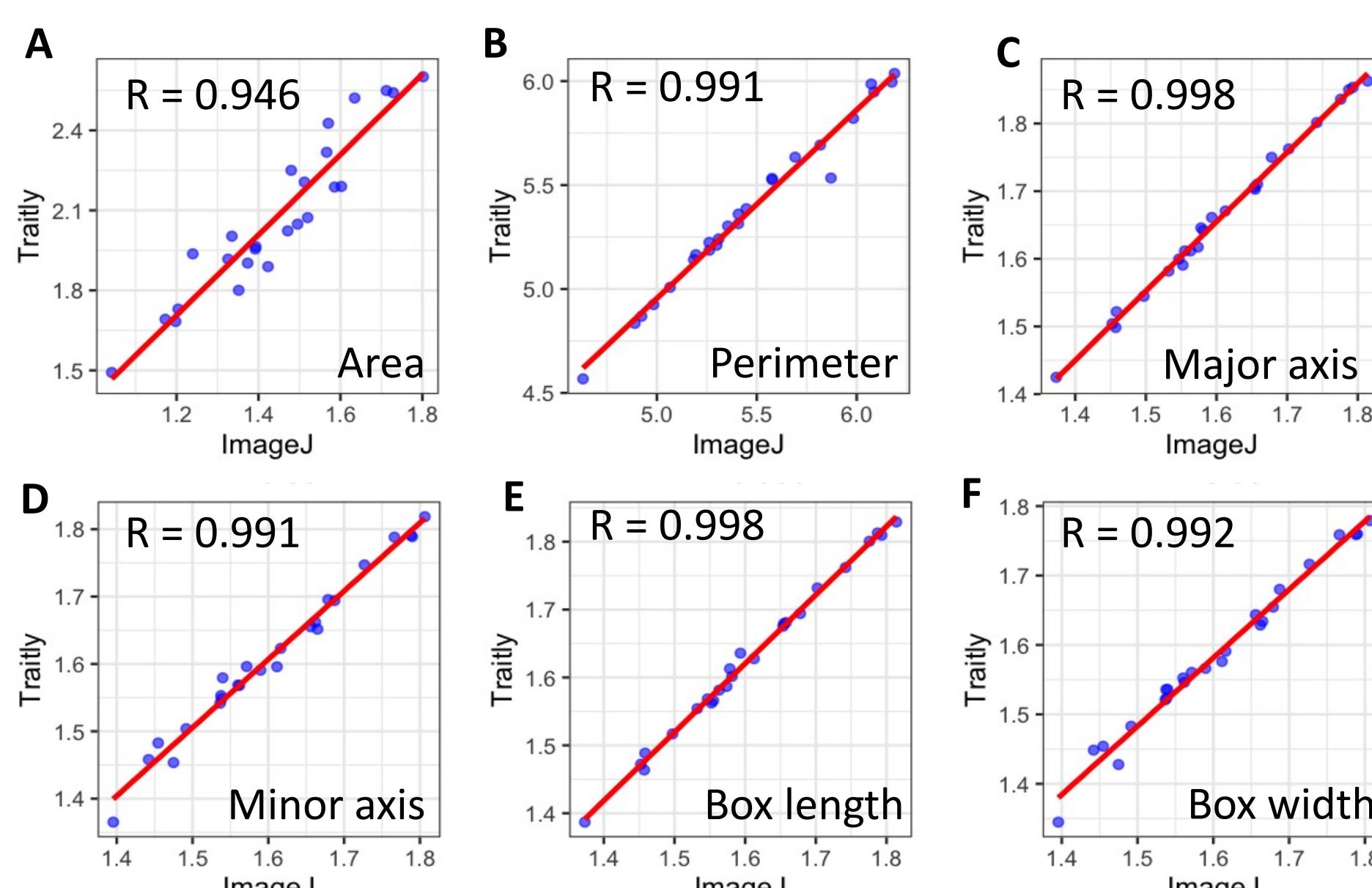


Figure 2. High Pearson correlations between Traity and ImageJ measurements. A) total fruit area, B) fruit perimeter, C) major axis (fruit length), D) minor axis (fruit width), E) bounding-box height, and F) bounding-box width. Trait names follow Traity nomenclature. Traits C–F were compared against ImageJ width and height measurements, which refer to bounding-box dimensions. Blue dots = genotype means; red line = linear regression. R = Pearson correlation coefficient.

CONCLUSIONS

- Traity outputs showed high agreement with ImageJ ($R > 0.94$) while enabling automated extraction of additional internal traits, reducing total processing time to ~1–3 seconds per image and improving reproducibility and efficiency.
- Traity successfully analyzed multiple fruit types, demonstrating versatility and applicability across diverse species beyond cranberry.
- PCA revealed coordinated patterns between internal morphology and texture, with parental lines and checks separating along major axes of variation.
- QTL for internal fruit structure accounted for 3–27% of phenotypic variance, with several co-localizing with texture QTL. These associations identify promising targets for marker-assisted improvement of fruit texture.
- Taken together, these findings establish **Traity** as a reliable and scalable framework for high-throughput phenotyping of internal fruit traits in breeding programs.



Figure 3. Phenotypic variation in cranberry internal traits revealed by PCA. Red vectors represent texture traits, whereas gray vectors correspond to internal morphology traits. Colored points indicate the parental genotypes (CQ and MQ) and check cultivars (ST). Blue points correspond to individuals from the CNJ02 biparental population. Axes indicate the proportion of phenotypic variance explained by each principal component.

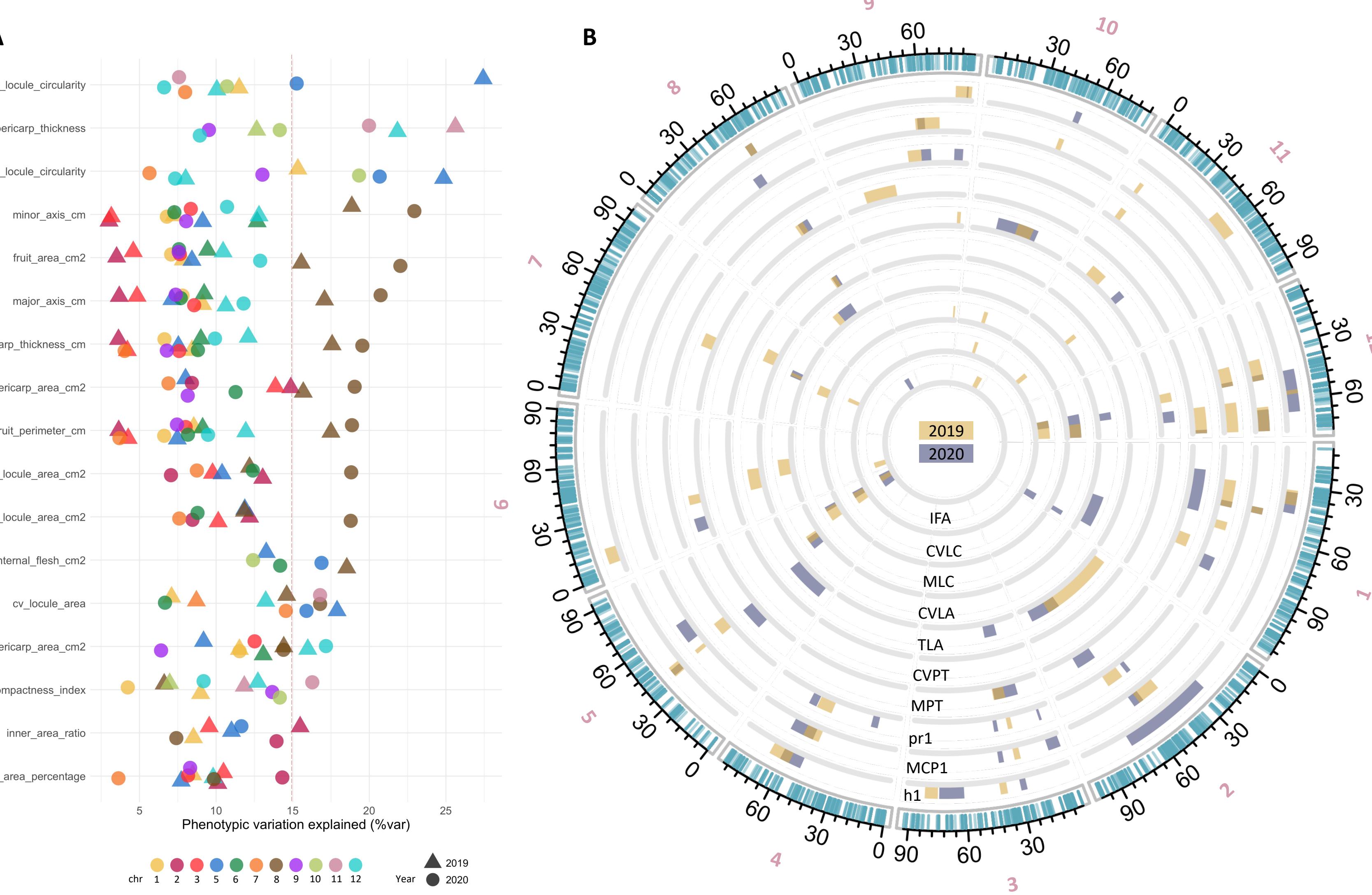


Figure 4. Summary of QTL results for the cranberry biparental population CNJ02. A) Distribution of QTLs identified for internal structure and texture traits. The outer ring represents marker distribution on the genetic map, while inner rings display QTL results for each trait: h1 = maximum force, MCP = maximum contact pressure, pr1 = maximum stress, MPT = mean pericarp thickness, CVPT = coefficient of variation of pericarp thickness, TLA = total locules area, CVLA = coefficient of variation of locules area, MLC = mean locules circularity, CVLC = coefficient of variation of locules circularity, IFA = inner flesh area. QTL intervals (rectangles) are colored purple or brown if detected in 2019 or 2020, respectively. Pink numbers indicate chromosomes. B) Percentage of phenotypic variance explained by each QTL identified in both years. Circle color indicates chromosome; shape indicates year. For both panels, only QTL surpassing the LOD significance threshold are shown.

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References:

1. Abràmoff, M. D., Magalhães, P. J., & Ram, S. J. (2004). Image processing with ImageJ. *Biophotonics International*, 11(7), 36–42.
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