

Optimizing Pea Biomass Estimation: Unveiling Insights from Multimodal Image-Based Phenotyping under Drought Conditions

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Introduction

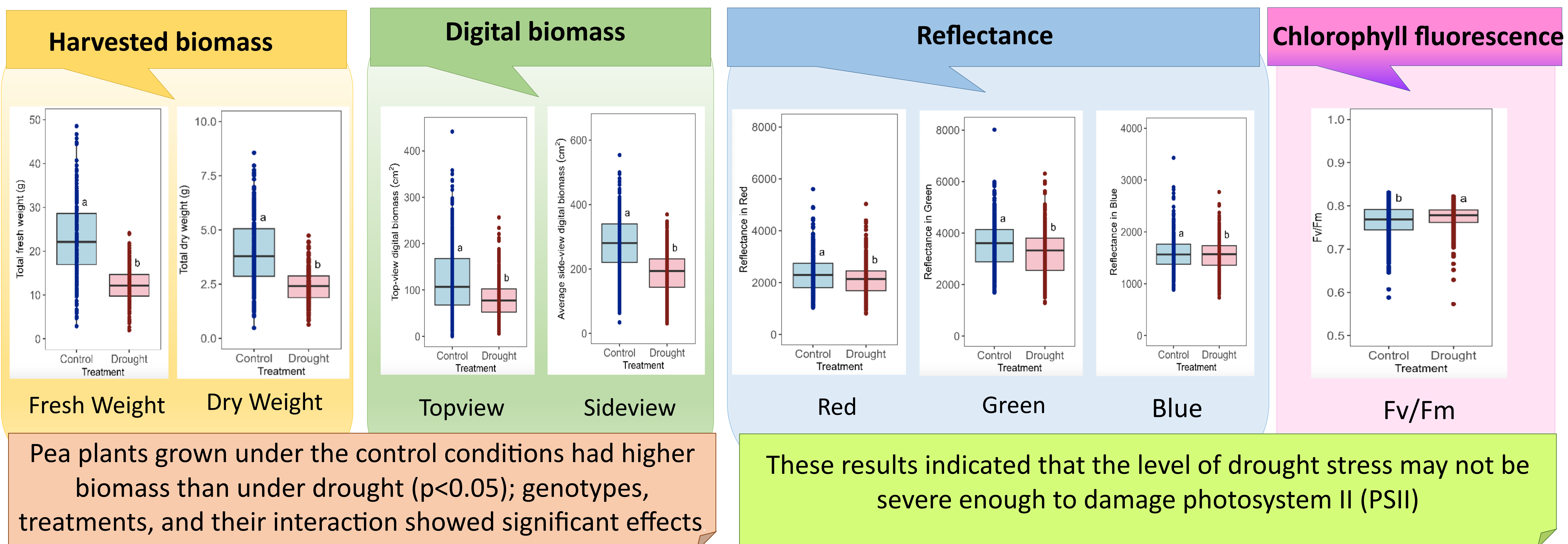
Peas (*Pisum sativum* L.) are excellent nutrient sources for both humans and livestock, and their sustainable production contributes to soil fertility. However, the increasing global frequency of **droughts** has adversely affected pea yield and protein content. Breeding programs must prioritize enhancing pea adaptation to **drought stress**, while safeguarding and promoting the most nutritious types.

This study aimed to use **Image-based high-throughput phenotyping platforms** for the non-destructive acquisition of various phenotypic traits as well as biomass estimation.

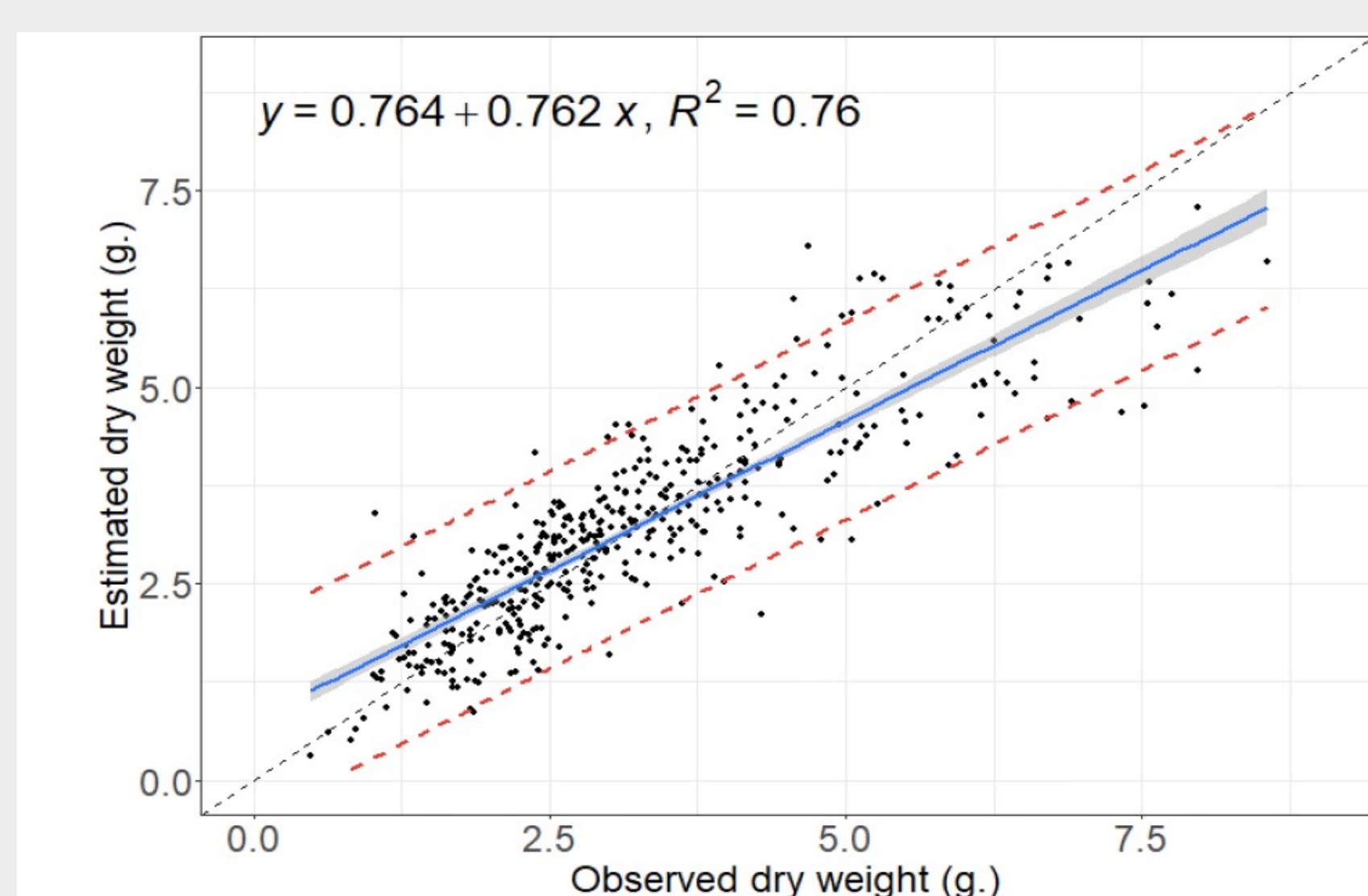
Methods

The **180 pea accessions** were grown at a conveyor system in **NPEC** (Netherlands Plant Eco-phenotyping Centre) greenhouse, and different morphophysiological traits were evaluated under both **well-watered** (70% of field capacity) and **drought** (30% of field capacity) conditions. Imaging occurred every 48 hours using different camera systems to monitor diverse phenotypic parameters. At the end of the experiment, plants were destructively harvested for **biomass assessment**. Furthermore, correlations between image-based traits and biomass were examined, leading to the formulation and evaluation of **biomass estimation models**.

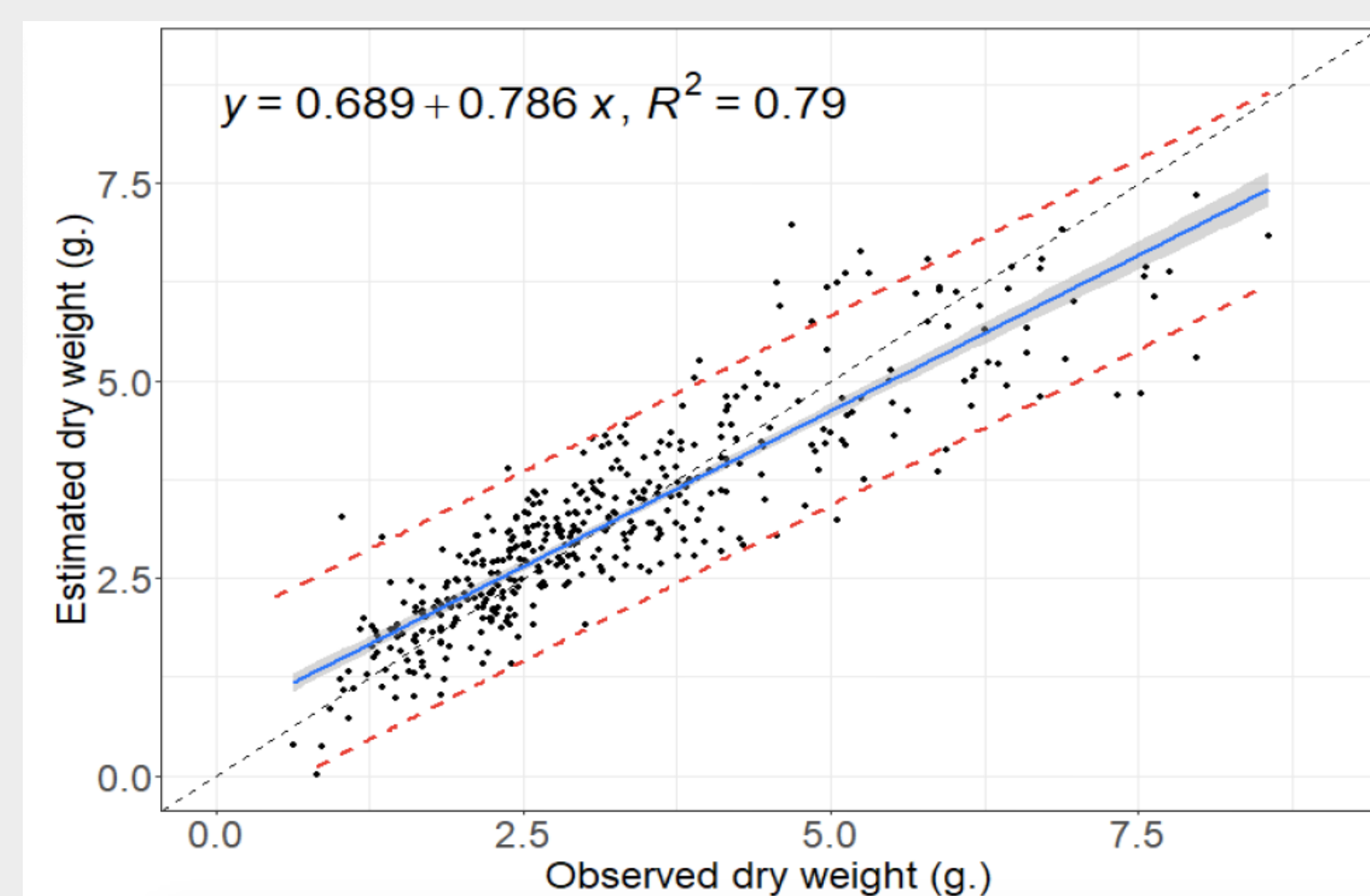
Results



Model comparison



Single trait: RGB Sideview traits
 $R^2 = 0.76$, RMSE = 0.72



Multiple traits: RGB + spectral imaging traits
 $R^2 = 0.79$, RMSE = 0.68

Combining different image-based traits in multiple-trait models allowed for small increases in biomass estimation accuracy compared to single-trait models.

Conclusions

- ❖ Water stress negatively impacted the morpho-physiological traits evaluated in the 180 pea accessions, but the severity of the impact differed **depending on genotype**.
- ❖ This study underscores the potential of integrating diverse traits to enhance biomass estimation accuracy, providing insights for advancing high throughput, non-destructive, plant phenotyping.

Acknowledgments

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