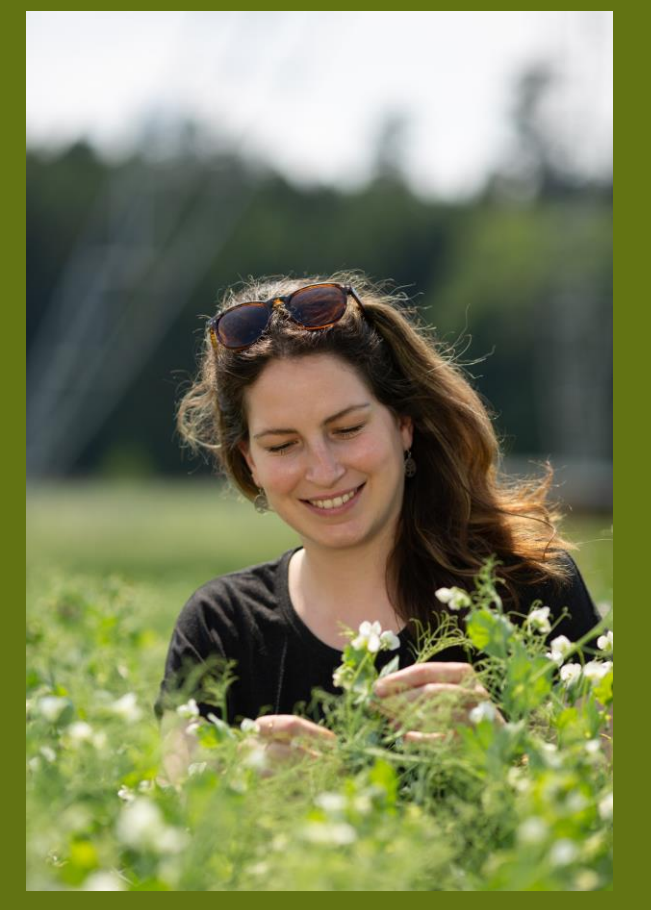


Assessment of Pea Flowering by using High Throughput Field Phenotyping

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1 Introduction

High Throughput Field Phenotyping (HTFP) is a promising approach to support breeding by gathering a vast amount of standardized data on relevant traits in an objective manner. Flowering is one of the most important processes in a plant's life. The start and duration of flowering are traits that indicate how well adapted a variety is to a certain location². However, flowering is today visually rated by human evaluators, which is highly time-consuming and leads to subjective results. Our HTFP-research seeks to provide a more reliable assessment of flowering time by using deep learning models.

2 Material & Method



Figure 1: Overview Methods. A: Region of interest in the field (manually counted in the field). B: Region of interest in a FIP-Image, C: Example of the manually counted flowers on an image.

- We worked with the stationary Field Phenotyping Platform (FIP)¹ of the Crop Science Group, ETH Zurich, Switzerland.
- RGB images of 12 pea varieties in 36 plots were acquired with the FIP twice per week during flowering in 2022 and 2023.
- The images were used to train a deep learning object detection model (YOLOv8)³, to detect flowers on the images.
- As ground truth, we compared the results from the model with manually counted flowers in a region of interest (50 x 50 cm) in the field and on the images (Figure 1). In addition, we rated the BBCH stages of flowering timepoints.

3 Accuracy of the Model

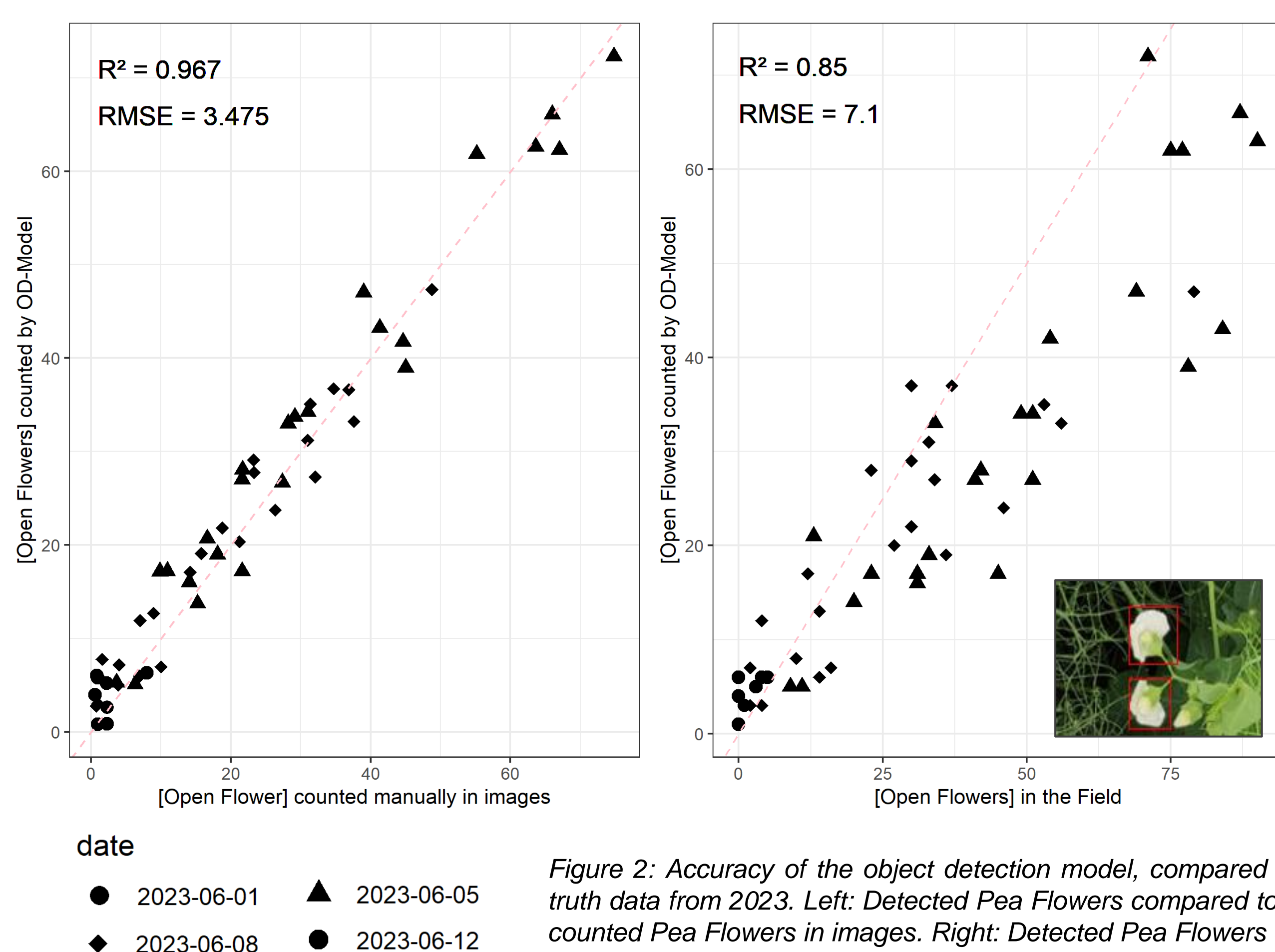


Figure 2: Accuracy of the object detection model, compared to ground truth data from 2023. Left: Detected Pea Flowers compared to manually counted Pea Flowers in images. Right: Detected Pea Flowers compared to manually counted Pea Flowers in the Field.

4 Flowering Dynamics of three Genotypes

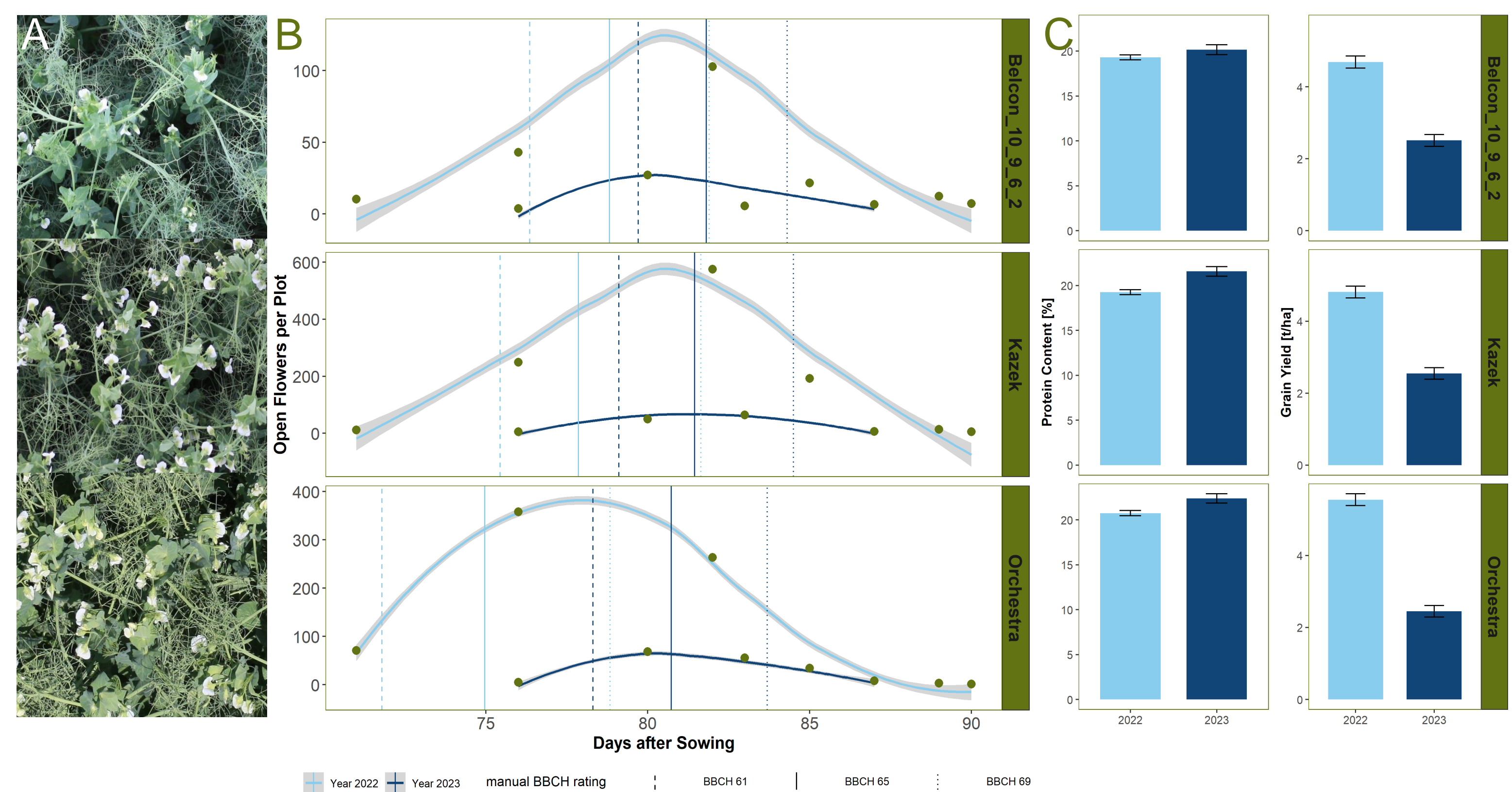


Figure 3: Overview of three contrasting genotypes. A: Section of an image of each genotype on the day when the maximum number of flowers was open (2022). B: The evolution of open flowers of the different genotypes over time in days after sowing, data from 2022 and 2023. The green points indicate measured values (spatially corrected for each genotype), while the line indicates fitted values (fitted with Loess regression). Vertical lines show manually rated BBCH stages (spatially corrected) for comparison. C: Yield data from the different genotypes, spatially corrected.

- The model achieves a high accuracy, when compared to manually counted flowers on the images. However, there are some pea flowers that do not appear on images taken from above (Figure 2; $R=0.967$).
- The comparison of three contrasting genotypes (Figure 3B) highlights the differences in flowering pattern between the genotypes.
- The progression of BBCH-ratings coincided nicely with the AI-based flower counts: AI-detected flowering maxima (fitted values) were later, the later a certain BBCH-stage was reached.
- In 2022 the genotypes had significantly more open flowers per day, which also resulted in a higher grain yield, but slightly lower protein content in the seed (Figure 3C).

5 Conclusion

- The use of HTFP offers a promising alternative to manual rating of flowering, which could also be interesting for other legumes.
- The object detection model showed high accuracy for pea flowers visible on images. However, for more insight in flowering structures, multi-view images would be an approach.
- Flowering dynamics varies between genotypes making it an interesting topic for further breeding research.

References

1. Kirchgessner, N. et al. The ETH field phenotyping platform FIP: a cable-suspended multi-sensor system. *Funct. Plant Biol.* 44, 154 (2017).
2. Weller, J. L. & Ortega, R. Genetic control of flowering time in legumes. *Front. Plant Sci.* 6, (2015).
3. Jocher, G., Chaurasia, A., & Qiu, J. (2023). YOLO by Ultralytics (Version 8.0.0) [Computer software].