

UAV-Hyp: UAV Dataset for Remote Sensing-Based Phenotyping of *Hypericum perforatum*

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Abstract

Quantitative flowering phenotypes are needed to support breeding and harvest management in *Hypericum perforatum* L. (St. John's wort), but manual flower assessment is slow and difficult to standardize under field conditions. UAV-Hyp is a multi-temporal UAV RGB dataset containing 12,653 high-resolution images acquired at 26 measurement dates across the complete flowering period of 15 *H. perforatum* accessions. The images represent variable illumination, soil moisture, weed pressure, and developmental stages. The dataset provides 59,163 plant bounding boxes and 107,054 flower bounding boxes. As an application example, cascaded YOLOv8 plant and flower detectors achieved mAP@0.50:0.95 values of 0.977 and 0.950, respectively. UAV-Hyp supports scalable flower quantification and the development of time-series phenotyping methods for genotype comparison and quality-oriented medicinal-plant breeding.

Dataset: <https://doi.org/10.5447/ipk/2026/6>

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Keywords: *Hypericum perforatum*; UAV remote sensing; phenotyping; YOLOv8

1. Introduction

High-throughput phenotyping remains a major bottleneck in plant breeding because phenotype acquisition is labor-intensive, time-consuming, and often subjective, even as genotyping has become more accessible [1,2]. This limitation is especially important for flowering traits, which change rapidly and therefore require repeated measurements. Computer vision and unmanned aerial vehicle (UAV) imaging can provide objective, spatially explicit, and scalable observations across field trials [3,4].

For *Hypericum perforatum* L. (St. John's wort), repeated flowering phenotypes are directly relevant to medicinal-plant breeding and quality assessment. Breeding has traditionally emphasized hypericin and hyperforin as major bioactive marker compounds, while additional studies have reported neuroprotective activities of *H. perforatum* extracts [5–8]. Several bioactive constituents are concentrated in floral tissues, and hyperforin and pseudohypericin have been reported to reach their highest levels in fully opened flowers [9]. Flower abundance and flowering progression may therefore provide useful phenotypic indicators for selection and harvest timing.

Manual flower counting is poorly suited to large breeding trials because it is slow, difficult to repeat at short intervals, and sensitive to observer bias, occlusion, plant-to-plant



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heterogeneity, and variable illumination [4]. A reusable multi-temporal image dataset is therefore needed both to train automated detectors and to evaluate their robustness across developmental stages and field conditions. Such a dataset should also support benchmarking of object-detection methods, including YOLOv8 [10–12] and the derivation of multi-temporal flowering summaries.

Existing public UAV datasets address tasks such as aquatic-plant classification and forest-scene segmentation, whereas publicly accessible images of *H. perforatum* are generally embedded in herbarium or broader multi-species collections [13–16]. These resources do not provide a species-specific, field-scale benchmark that combines dense plant and flower annotations with repeated acquisitions spanning the complete flowering season. This gap limits reproducible algorithm comparison and the development of flowering time-series analyses for medicinal plants.

UAV-Hyp addresses these limitations by providing (i) 12,653 high-resolution RGB images from 26 temporal measurement points; (ii) 15 *H. perforatum* accessions and an adjacent non-target control plot; (iii) images representing variable illumination, soil moisture, weed pressure, and developmental stages; (iv) 59,163 plant bounding boxes and 107,054 flower bounding boxes; and (v) an application example based on cascaded plant and flower detection. Twelve orthomosaics passed quality control for full-scene analysis, while quality-controlled image chips from the remaining 14 acquisitions were retained, thereby distinguishing the 26 acquisition dates from the 12 dates used for the field-scale time-series example [17–19].

Together, these components provide a standardized resource for developing and benchmarking automated flowering phenotypes and for future studies linking visual traits with biochemical profiles, genetic architecture, metabolite yield, and medicinal quality [20–24].

2. Data Description

2.1. Field Trial

The plant material used in this study comprised 15 *H. perforatum* accessions derived from legacy stocks maintained at the Julius Kühn Institute (Table 1). The accessions were established in a randomized block field trial to capture genotypic and phenotypic variation under field conditions. The experimental design consisted of seven randomized blocks, with all 15 accessions represented in each block. Each accession was represented by 11 plants per block, resulting in 77 plants per accession across the entire experiment and a total of 1155 plants at establishment. Plants were established at a spacing of 80 cm. During the experimental period, 42 plants died, resulting in 1113 surviving plants at the end of the experiment.

Table 1. The germplasm list used in this study.

ID	Species	Received	Origin (Country)
HYPID0266	<i>H. perforatum</i>	2000	Germany
HYPID0267	<i>H. perforatum</i>	2000	Germany
HYPID0268	<i>H. perforatum</i>	2000	Germany
HYPID0269	<i>H. perforatum</i>	2000	Germany
HYPID0270	<i>H. perforatum</i>	2000	Germany
HYPID0271	<i>H. perforatum</i>	2000	Germany
HYPID0272	<i>H. perforatum</i>	2000	Germany
HYPID0273	<i>H. perforatum</i>	2000	Germany
HYPID0274	<i>H. perforatum</i>	2000	Germany
HYPID0275	<i>H. perforatum</i>	2000	Germany

Table 1. Cont.

ID	Species	Received	Origin (Country)
HYPID0276	<i>H. perforatum</i>	2000	Germany
HYPID0277	<i>H. perforatum</i>	2000	Germany
HYPID0278	<i>H. perforatum</i>	2000	Germany
HYPID0279	<i>H. perforatum</i>	2000	Germany
HYPID0280	<i>H. perforatum</i>	2000	Germany
MoID0002	<i>Melissa officinalis</i>	2000	Germany

A separate plot of *Melissa officinalis* located directly adjacent to the experimental field served as a non-target control for assessing detection specificity under field conditions. The control plot comprised 64 plants arranged in an 8×8 layout, with a plant spacing of 50 cm. Two plants died during the course of the experiment, resulting in 62 surviving control plants at the end of the experiment. The field layout and representative plants are shown in Figure 1.

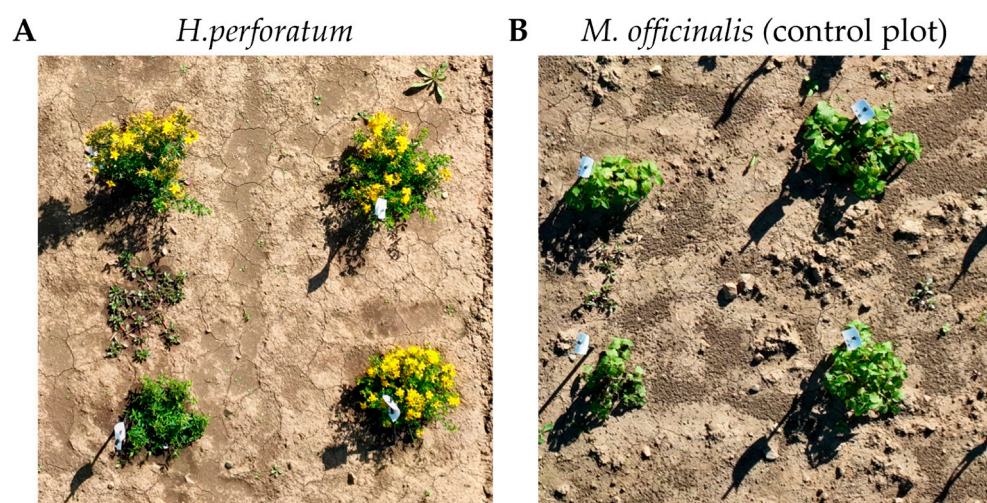


Figure 1. Close-up view of (A) *H. perforatum* plants and (B) *M. officinalis* plants serving as the control group.

2.2. UAV Imaging

High-resolution aerial RGB imagery of flowering plants was acquired using an unmanned aerial vehicle (UAV). A DJI Mavic 3 Enterprise (Mavic 3E; DJI, Shenzhen, China) was flown at a constant flight altitude of 3 m to acquire nadir images of the floral canopy. The UAV was operated at flight speeds ranging from 0.75 to 0.90 m s^{−1}. In total, 35 flights, including test flights, were conducted during the flowering season, resulting in 26 temporal measurement points.

The Mavic 3E wide-angle camera featured a 4/3-inch CMOS sensor with an effective resolution of 20 MP, an image size of 5280 × 3956 pixels, a 24 mm equivalent focal length, and an aperture range of f/2.8–f/11. Images were acquired using the automatic camera mode, with exposure parameters controlled automatically. Flight missions were configured with 80% forward overlap and 70% side overlap between adjacent images.

Whole-field orthomosaics were generated from the overlapping RGB images using the visible-light 2D reconstruction workflow in DJI Terra v4.0.0 (DJI, Shenzhen, China). The *Field* mapping scenario was used for reconstruction, while the remaining aerotriangulation and 2D reconstruction parameters were retained at the standard DJI Terra settings. A representative whole-field orthomosaic is shown in Figure 2.

Orthomosaic *Hypericum* plot



Figure 2. Orthomosaic of the field trial generated from nadir UAV imagery acquired at an altitude of 3 m above ground level. The orthomosaic is produced using DJI Terra. The *H. perforatum* plot is outlined in purple, whereas the *M. officinalis* control plot is outlined in pink.

The resulting dataset captured the complete blooming period of *H. perforatum*, which in Germany typically extends from late June to early September [25]. During this interval, flowering intensity increased, reached a peak, and then gradually declined as plants transitioned to capsule formation. This temporal progression is illustrated in Figure 3, where the flowering cycle of a representative individual is shown. By early September, flowering had largely ceased, and seed development was visible.

The images represented substantial heterogeneity in plant appearance and background conditions. They covered multiple developmental stages, wet and dry soil, variable weather, different solar positions and shadow patterns, and varying levels of weed infestation and mixed vegetation. This diversity increased the practical relevance of the dataset and provided a realistic basis for model training and evaluation under field conditions.

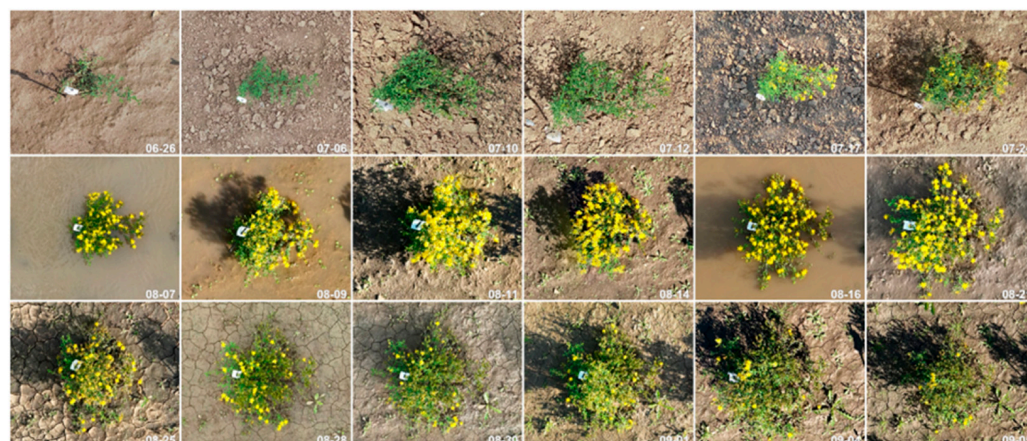


Figure 3. Representative examples showing the development of one plant from 26 June to 5 September and the environmental variability represented in the image dataset, including differences in illumination, soil moisture, weed infestation, and mixed vegetation cover.

2.3. Image Labeling and Quality Control

Plant images were annotated with Labellmg [26] using bounding boxes and were exported in YOLO format [10–12]. In total, 2216 images were annotated, resulting in 59,163 annotations for plants. LearningSpiral (Kolkata, India) annotated 1994 images, yielding 107,054 flower bounding boxes across diverse field conditions. These annotations were used to train the YOLO models [10–12]. Table 2 summarizes the principal dataset, annotation, quality-control, and repository quantities reported throughout the manuscript.

Table 2. Summary of the UAV-Hyp dataset, annotations, and quality-control subsets.

Component	Count	Description or Quality Status
<i>H. perforatum</i> accessions	15	HYPID0266-HYPID0280 (Table 1).
Randomized blocks	7 blocks with 11 plants/accession	Resulting in 77 plants
Plant establishment and survival	1155 at establishment; 1113 surviving	42 plants died
Non-target control	64 at establishment; 62 surviving	<i>M. officinalis</i> in an adjacent 8 × 8 control plot; two plants died during the experiment
UAV flights	35	Total includes test flights.
Temporal measurement points	26	Acquisitions spanning the complete flowering period.
Orthomosaics retained for full-scene analysis	12	Passed stitching-accuracy and coverage-completeness quality control.
Orthomosaics represented by QC-passed image chips	14	Not retained for full-scene analysis; accepted chips were retained.
UAV RGB image chips	12,653	High-resolution images in the released dataset.
Plant annotation set	2216 images	59,163 plant bounding boxes.
Flower annotation set	1994 images	107,054 flower bounding boxes.
Flower-annotation QC subset	15 images	1023 outsourced labels, 813 in-house labels, and 718 matched labels.
Flower-count sampling dates	12	7 August–5 September; per-date summaries without cross-date individual tracking.

Table 2. Cont.

Component	Count	Description or Quality Status
Plant train/validation/test split	Train: 1772; validation: 222; test: 222 images	Available records document subset image counts.
Flower train/validation/test split	Train: 1562; validation: 195; test: 196 images	1953 images are covered by the documented split; 41 additional images contained no detectable flowers, for 1994 images overall. Handling of these 41 images in the original split is not retained.
Repository package	38 GB	8356 files organized in 21 folders.

Of the 26 acquired orthomosaics, 12 met the stitching-accuracy and coverage-completeness criteria for full-scene analysis. The remaining 14 orthomosaics were not retained for full-scene analysis; however, individual UAV image chips that passed quality control were retained for plant and flower detection. Annotation quality was assessed using 15 representative images. LearningSpiral annotated 1023 flowers, and in-house experts independently annotated 813 flowers in the same image set (Figure 4).

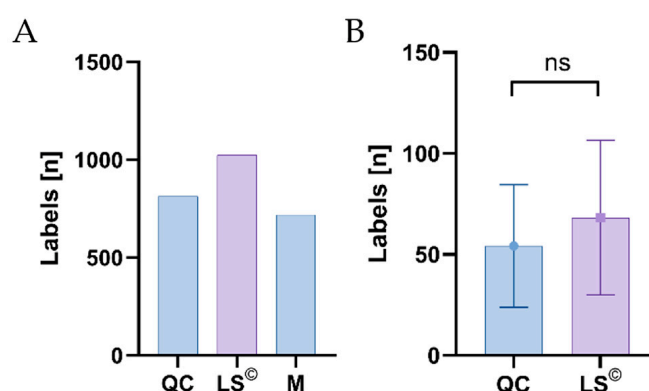


Figure 4. Comparison of in-house quality control/annotation (QC) and Learning Spiral (LS) annotation across 15 representative images. (A) Cumulative total number of labels assigned, including matching labels (M) between QC and LS. (B) Comparison of the number of labels per image for QC and LS. ns indicates no statistically significant difference ($p > 0.05$).

Comparison of the two annotation sets identified 718 matching labels. The numbers of annotated objects per image did not differ significantly ($p > 0.05$), indicating that the outsourced annotations met the predefined quality criteria and were suitable for model training. Plant bounding boxes were annotated in-house at the Julius Kühn Institute.

2.4. Three-Layer Cascading Structure

We used the cascade workflow described in Zhang et al. [4]. At the data-cascade layer, the dataset was partitioned according to the experimental design. At the model-cascade layer, multiple models were linked sequentially, with detection targets becoming progressively more specific. At the phenotypic analysis layer, the outputs of these stages were integrated to derive fine-grained phenotypic traits, thereby supporting downstream genotype–phenotype analyses and sequence-level studies (Figure 5).

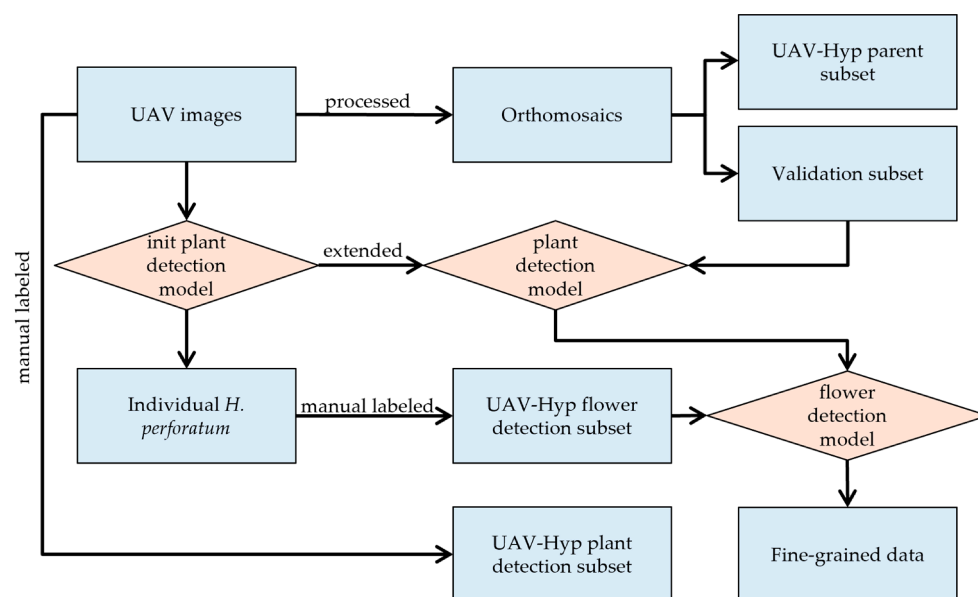


Figure 5. Overview of the cascaded dataset and sequential modeling framework. The dataset is divided into UAV-Hyp Plant and UAV-Hyp Flower, with blue blocks representing the respective data subsets and red blocks indicating the cascading models. Arrows indicate the workflow between the individual components. The outputs of both components are integrated to generate fine-grained phenotypic analysis data for *H. perforatum*.

2.5. Slicing Aided Hyper Inference

Large-scale scenes were processed using a sliding-window strategy implemented in Slicing Aided Hyper Inference (SAHI) [27]. Orthomosaics were divided into 2048×2048 pixel tiles with 10% overlap to reduce memory requirements while retaining objects located near tile boundaries (Figure 6). This procedure enabled efficient inference on scenes that would otherwise have been computationally demanding to process as a whole.



Figure 6. Sliding-window strategy used to process large-scale orthomosaics. Each image chip measured 2048×2048 pixels, with a 10% overlap between adjacent chips. Dashed boxes of different colors represent distinct image chips that scan the entire orthomosaic using a sliding-window approach.

3. Methods: Implementation and Evaluation

3.1. Plant Detection

For plant detection, 2216 annotated images were divided into training, validation, and test subsets comprising 1772, 222, and 222 images, respectively. The corresponding subsets contained 47,418, 6160, and 5585 plant bounding boxes. Dataset partitioning took into account the quality status of the orthomosaics generated for the 26 acquisition dates. For 12 acquisition dates, the reconstructed orthomosaics passed the quality-control criteria for stitching accuracy and spatial coverage. Images originating from these dates were used for model development, with the test subset generated using a date-wise random sampling strategy in which 5–25% of the available images from each acquisition date were held out for testing. The validation subset was constructed to represent both orthomosaic quality groups: approximately 50% of the validation images originated from the 12 acquisition dates with QC-passed orthomosaics, whereas the remaining 50% originated from the 14 acquisition dates whose orthomosaics did not meet the criteria for full-scene analysis.

YOLOv8 Large (YOLOv8-l_plant), Small (YOLOv8-s_plant), and Nano (YOLOv8-n_plant) models were trained for a maximum of 800 epochs with an early-stopping patience of 100 epochs, a batch size of 16, an input image size of 640×640 pixels, and RandAugment [28]. Each of the three YOLOv8 models was trained once using a single training run. Results are presented in Table 3. Models were evaluated using precision (P), recall (R), mean Average Precision mAP@0.50, and mAP@0.50:0.95. YOLOv8-l_plant achieved the highest mAP@0.50:0.95 value (0.977) (Table 3).

Table 3. Evaluation of YOLOv8 plant-detection models.

	P	R	Best Epoch	mAP@0.50	mAP@0.50:0.95	Inference (ms/Image)
YOLOv8-l_plant	0.998	0.995	733	0.995	0.977	4.4
YOLOv8-s_plant	0.993	0.991	764	0.995	0.956	1.6
YOLOv8-n_plant	0.987	0.983	524	0.994	0.923	1.5

The three YOLOv8 variants achieved high plant-detection performance under the reported evaluation conditions. Precision ranged from 0.987 to 0.998, recall from 0.983 to 0.995, and mAP@0.50 from 0.994 to 0.995. YOLOv8-l_plant achieved the best overall localization performance, with a precision of 0.998, a recall of 0.995, an mAP@0.50 of 0.995, and an mAP@0.50:0.95 of 0.977, but it had the slowest inference speed (4.4 ms/image). YOLOv8-s_plant retained similar precision and recall with an inference speed of 1.6 ms/image. YOLOv8-n_plant was fastest (1.5 ms/image) but had the lowest mAP@0.50:0.95 (0.923).

These quantitative results were consistent with the visual examples in Figure 7. The *M. officinalis* control plot with saturated soil, in nadir-view imagery, exhibited visual characteristics similar to *Hypericum*. In the illustrated scenes, the model differentiated the target plants from the control plot despite noise, partial occlusion, and spectral or textural similarity among vegetation classes.

3.2. Flower Detection

Of the 1994 images reviewed for flower annotation, 1953 contained flowers and were included in the documented training, validation, and test split; 41 images contained no flowers and were excluded from this split. The 1953 flower-containing images were divided into 1562 training, 195 validation, and 196 test images, containing 84,123, 11,052, and 11,879 flower bounding boxes, respectively. The training hyperparameters were identical to those used for plant detection. Each of the three flower-detection models was trained once. Results are presented in Table 4. YOLOv8-l_flower achieved the best overall results, with a precision of 0.997, a recall of 0.995, an mAP@0.50 of 0.995, and an mAP@0.50:0.95

of 0.950. YOLOv8-s_flower and YOLOv8-n_flower had lower mAP@0.50:0.95 values of 0.871 and 0.806, respectively, but faster inference speeds of 4.4 and 3.6 ms/image compared with 6.9 ms/image for the large model.

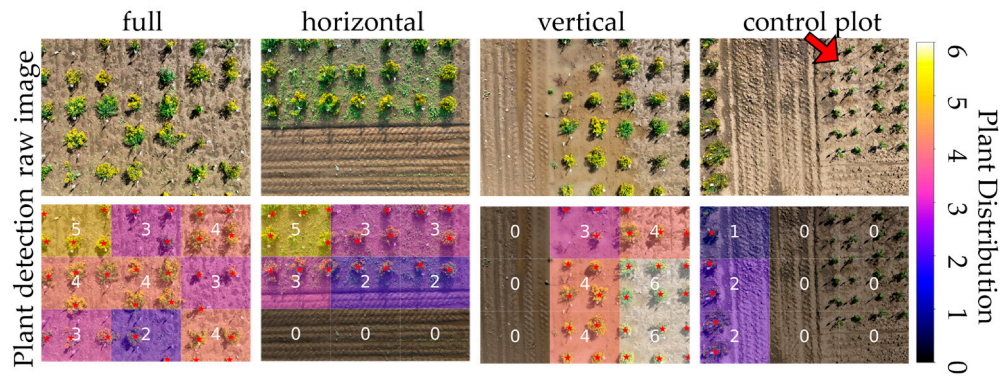


Figure 7. Representative detection results obtained with the trained YOLOv8-s model, demonstrating accurate detection and localization of *Hypericum* plants under varying environmental conditions. The heatmap on the bottom illustrates the spatial distribution and abundance of plants detected in the original images shown on the top. Detected plants are indicated by red stars, the red arrow marks the control plot, and the color gradient from dark blue to bright yellow represents plant density within standardized quadrants.

Table 4. Evaluation of YOLOv8 flower detection models.

Model	P	R	Best Epoch	mAP@0.50	mAP@0.50:0.95	Inference (ms/Image)
YOLOv8-l_flower	0.997	0.995	648	0.995	0.950	6.9
YOLOv8-s_flower	0.973	0.970	620	0.987	0.871	4.4
YOLOv8-n_flower	0.941	0.930	590	0.965	0.806	3.6

The quantitative results were consistent with the visual examples shown in Figure 8, which demonstrated that the flower detection model was able to identify individual blossoms across a broad range of environmental conditions and plant developmental stages. Accurate detection was maintained even in image regions with reduced flower contrast caused by strong illumination and local overexposure, allowing the spatial distribution of blossoms within individual plants to be resolved reliably.

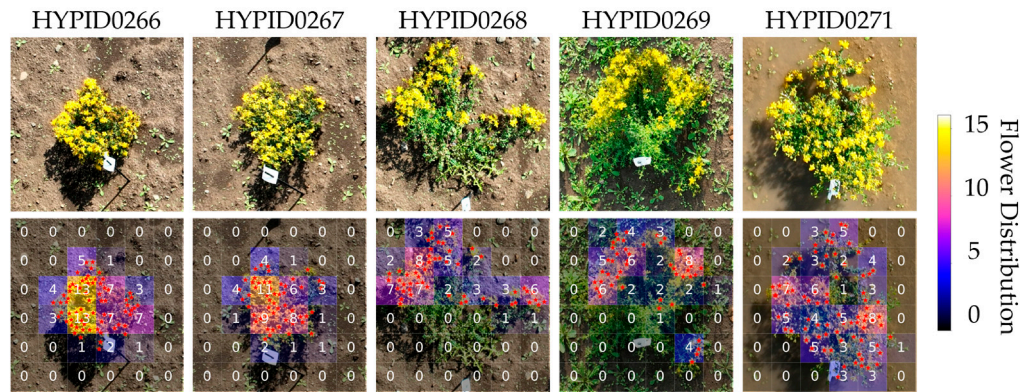


Figure 8. Representative flower detection results under real-world conditions obtained with the trained YOLOv8-l_flower model, shown together with the corresponding heatmaps. In each image pair, the original photograph is displayed on the bottom and the heatmap on the top. The heatmap is subdivided into 36 squares to enable detailed analysis of flower distribution within each plant. Flower density in each square is indicated by both a numerical value and a color scale ranging from deep blue (0 flowers) to bright yellow (>15 flowers). Detected flowers are marked with red stars.

By combining the outputs of the plant and flower detection models, a cascaded analysis workflow was established in which plant instances were first localized within each acquisition and subsequently analyzed for flower traits on a per-plant basis. The analysis presented in this manuscript does not link detection boxes for the same individual plant across different acquisition dates.

Figure 9 shows the temporal distribution of detected flower counts per plant at each sampling date. The mean increased from 25.6 flowers per plant on 7 August to a maximum of 50.0 on 28 August and then decreased to 38.3 by 5 September. The maximum observed count followed the same pattern and reached 305 flowers on 28 August. These per-date summaries demonstrate temporal changes in flower abundance across the field. Because detections were not linked across dates at the individual-plant level, the figure does not represent trajectories of the same plants. Differences among plants may reflect both genotypic and environmental variation and require formal genotype-level analysis.

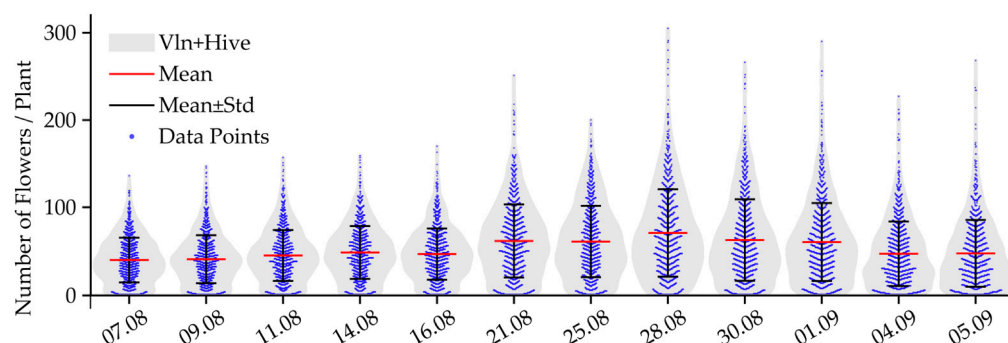


Figure 9. Distribution of detected flower counts per plant across 12 sampling dates from 7 August to 5 September. The violin shapes and blue points show the per-date distributions and individual observations; the red line indicates the mean, and the black lines indicate the mean $\pm$ standard deviation. Detections are summarized independently for each sampling date; no cross-date individual-plant tracking is implied.

4. User Notes

UAV-Hyp provides an automated phenotyping pipeline tailored to *H. perforatum* using a cascaded YOLOv8 detection framework [4,10–12]. The dataset represents variable illumination, soil moisture, weed interference, and plant developmental stages. Within each acquisition, the first detection stage extracts plant-specific image regions from field-scale imagery, and the second stage quantifies floral traits within those regions [29]. This design supports scalable per-date analyses of floral abundance across the monitoring period. The present study does not perform cross-date individual-plant tracking.

This cascading workflow enables a fine-scale quantification of floral abundance and scalable comparison of flowering patterns among sampling dates.

Detection of fully developed flowers may also provide an operational phenological marker for harvest management. Because flowering in *H. perforatum* is associated with elevated concentrations of the pharmacologically relevant naphthodianthrone hypericin and pseudohypericin, image-based flower measurements may help to estimate an appropriate harvest window [30]. Direct prediction of phytochemical content, however, will require paired image and chemical measurements.

In the qualitative examples acquired under suitable weather and lighting conditions, no false-negative flowering plants were observed [31]. Detections were less confident under low-angle light and deep shadow. These cases should be treated as current limitations because they were underrepresented in the training data. Future dataset extensions should include more edge cases and should report performance across repeated training runs and acquisition dates to quantify robustness and generalizability [32].

Once detection reliability has been further optimized, the system could be extended to investigate quantitative relationships between flower abundance and key phytochemical traits, particularly those associated with the medicinal value of *H. perforatum* [30]. Beyond flower detection, the framework could also be expanded to include additional morphological and physiological traits, such as biomass estimation through canopy segmentation or the quantification of biotic and abiotic stress symptoms, including pathogen infestation and drought effects [3]. This would enable the development of a more holistic phenotyping platform capable of delivering comprehensive trait profiles at scale. In the longer term, such a system could provide a basis for precision breeding in *H. perforatum* by supporting the identification of superior genotypes through the integration of visual, chemical, and genetic data streams.

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Informed Consent Statement: Not applicable.

Data Availability Statement: This dataset is deposited in e!DAL (electronic data archive library) of IPK (Leibniz Institute of Plant Genetics and Crop Plant Research): <https://doi.org/10.5447/ipk/2026/6>. It comprises initially a total volume of 38 GB, consisting of 8356 files organized across 21 folders.

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