The prospects of quantitative phenotyping of oilseed crops

Dnipro State Agrarian
and Economic University,
Serhiya Yefremova st.,
25, Dnipro, 49600, Ukraine.

Institute of Oilseed Crops of the
National Academy of Agrarian
Sciences of Ukraine, Instytutska st.,
1, village Soniacne, 69055,
Zaporizhia district,
Zaporizhia region, Ukraine.
Tel.: +38-068-861-44-37.
E-mail: aliev@meta.ua

E. B. Aliiev

Dnipro State Agrarian and Economic University, Dnipro, Ukraine
Institute of Oilseed Crops of the National Academy of Agrarian Sciences of Ukraine, Soniacne, Ukraine

Abstract. Plant phenotyping is a comprehensive evaluation of complex traits in plants, such as growth, development, resistance, architecture, physiology, ecology, yield, as well as the basic measurement of individual quantitative parameters that form the basis for more complex traits. This article provides an analysis of visualization methods applied in plant phenotyping and presents software for image processing. The analysis included the most significant global research in plant phenotyping. The directions of work on plant phenotyping were carried out by well-known geneticists, breeders, and engineers at the Institute of Oil Crops of the National Academy of Agrarian Sciences. Based on the global experience and the results of research at the Institute of Oilseed Crops of the National Academy of Agrarian Sciences, we propose the following development of plant phenotyping in domestic agricultural science. Integrated approaches of well-known selection-process methodologies, from molecular to field, are necessary for the development of sustainable agriculture, ensuring high yields, and the use of limited resources. Despite significant progress in the molecular and genetic approaches in recent years, quantitative analysis and systematization of plant phenotypes (plant structures and functions) have become major challenges. Plant phenotyping is a science that combines genomics, ecophysiology, and plant agronomy using modern automated selection and systematization methods. The functional plant body (phenotype) is formed during plant growth and development through dynamic interactions between genotype and the surrounding environment in which plants grow. These interactions determine the practical result of crop cultivation in terms of quantity and quality of production. This includes crop yield and its quality: oil content, seed size, shape, and seed density, among other factors. Systematizing oilseed crops based on a complex of phenotypic characteristics, taking into account gene penetrance and trait inheritance, will reduce the time and effort required for decision-making. Mechanotronic systems for material separation, selection, and classification using neural networks will significantly reduce costs. Therefore, one of the solutions to this problem is the development of a methodology for systematic genotyping of sunflower based on phenotypic expression using neural networks.

Keywords: assessment; genetics; selection; screening; methodology; systematization.

Introduction

Ensuring an adequate supply of agricultural products to meet the needs of the human population, which is expected to exceed 9 billion by 2050, is a monumental challenge for agriculture in terms of increasing crop yields (Cleland, 2013; Bera, 2019; Gaigbe-Togbe et al., 2022). This goal is particularly complex because the average annual growth rate of agricultural production is only 1.3%, and it lags behind population growth. By bridging genotype with phenotype, it becomes possible to select high-yielding, stress-resistant plants much more rapidly and effectively than is currently feasible (Phillips, 2010). The lack of access to phenotyping capabilities limits our ability to analyze the genetics of quantitative traits related to growth, yield, and stress adaptation (McMullen et al., 2009). Improving phenotyping is of paramount importance for harnessing developments in the breeding and seed production process for creating new plant varieties and hybrids.

Plant phenotyping is a comprehensive assessment of complex plant traits such as growth, development, resilience, architecture, physiology, ecology, yield, along with basic measurements of individual quantitative parameters that serve as the foundation for more intricate characteristics (Jannink et al., 2010; Newell & Jannink, 2014; Pieruschka & Schurr, 2019). The plant phenotype encompasses these complex traits, and examples of their direct measurable parameters include root morphology (Walter et al., 2009; Clark et al., 2011; Flavel et al., 2012; Kumar et al., 2014), biomass (Menzel et al., 2009; Golzarian et al., 2011), leaf characteristics (Jansen et al., 2009; Arvidsson et al., 2011), fruit attributes (Brewer et al., 2006; Monforte et al., 2014), traits related

to yield (Duan et al., 2011), photosynthetic efficiency (Bauriegel et al., 2011; Aliieva et al., 2022), as well as responses to biotic and abiotic stressors (Balachandran et al., 1997; Rao & Laxman, 2013). Given the rapid development of high-throughput genotype screening in plant breeding and genomics to enhance growth, yield, and resistance to various biotic and abiotic stresses, there is a call for more efficient and reliable phenotyping data to support modern genetic cultivars. Achieving this goal involves expertise from biological sciences, computer science, mathematics, and engineering in the field of phenotyping.

In recent years, high-throughput phenotyping platforms have been deployed in growth chambers or greenhouses (Granier et al., 2006; Deikman et al., 2012). These platforms utilize robotics, precise control of the surrounding environment, and visualization technologies (hardware and software) to assess plant growth and productivity (Hartmann et al., 2011; Yang et al., 2013).

Methods of plant phenotyping

To analyze the interactions between genotype and environment (G × E) and model phenotypic responses, the plant phenotyping scheme typically involves experimental design, quantitative measurements, and interpretation of results. The experimental design should account for different growth environments (controlled environments or field conditions). It also concurrently includes infrastructure for plant cultivation, monitoring of the surrounding environment, substrate processing, and biosafety installations. Quantitative measurement offers

significant advantages over new visualization technologies but requires standardized experimental protocols, including image sensor calibration and precise data preprocessing, as parts of best practices in plant phenotyping (White et al., 2012; Fiorani & Schurr, 2013). The interpretation of results necessitates the integration of experimental metadata into data frameworks for the measured phenotype, genomic data, and environmental data (Berger et al., 2010; Walter et al., 2012).

Modern visualization methods have high resolution and provide the visualization of multidimensional and multiparametric data. Visualization methods are used for the quantitative assessment of complex plant traits in the dynamic context of their growth in controlled environmenttal systems or field conditions (Mühlich et al., 2008). Image-analysis algorithms are the key drivers for advancing image-based research, which require the quantitative evaluation of plant phenotypes for components such as roots, stems, leaves, seeds, flowers, etc. (Biskup et al., 2007; Paproki et al., 2012).

Visible imaging is primarily used to measure parameters of plant architecture, such as predicted biomass based on images, leaf area, color, growth dynamics, shoot strength, seed morphology, root architecture, assessment of leaf disease severity, yield, and fruit number and distribution (Table 1) (Fiorani & Schurr, 2013; Araus & Cairns, 2014; Deery et al., 2014). Fluorescent imaging has been used to detect diseases in genetic disease resistance. Thermal infrared imaging can characterize plant temperature to detect differences in conductance as a measure of the plant's response to water status and transpiration rate for adaptation to abiotic stress.

Table 1
Visualization Methods Applied in Plant Phenotyping

Visualization Method	Sensor	Resolution	Processed Data	Phenotypic Parameters
Visible Light Imaging	Visible spectrum-sensitive cameras	Whole organs or organ parts, temporal changes	Grayscale or color images (RGB channels)	Geometric morphological dimensions, color, growth dynamics, architecture and shape, yield traits, germination rate (Granier et al., 2006; Ikeda et al., 2010; Joosen et al., 2010; Arvidsson et al., 2011; Clark et al., 2011; Duan et al., 2011; Golzarian et al., 2011; Joosen et al., 2012; Hoyos-Villegas et al., 2014)
Fluorescent Imaging	Fluorescent cameras	Entire shoot or leaf tissue, temporal changes	Pixel maps of emitted fluorescence in red and far-red regions	Photosynthetic status (variable fluorescence), quantum yield, non-photochemical quenching, leaf health, shoot architecture (Moshou et al., 2005; Jansen et al., 2009; Bürling et al., 2010; Harbinson et al., 2012; Mishra et al., 2012; Rousseau et al., 2013)
Thermal Imaging	Near-infrared cameras	Entire shoot or leaf tissue, temporal changes	Pixel-wise surface temperature maps in the infrared region	Crown or leaf temperature, insect infestations (Jones et al., 2009; Munns et al., 2010; Araus et al., 2012)
Near-Infrared Imaging	Near-infrared cameras, multispectral line-scan cameras, active thermography	Temporal changes or single-point analyses of shoots and crowns	Continuous or discrete spectra for each pixel in the near-infrared region	Seed water composition, leaf area index (Spielbauer et al., 2009; Munns et al., 2010; Bolon et al., 2011; Sakamoto et al., 2011; Shibayama et al., 2011; Cook et al., 2012)
Hyperspectral Imaging	Near-infrared instruments, spectrometers, hyperspectral cameras, thermal cameras	Continuous or discrete spectra	Crop vegetative cycles, indoor time-series experiments	Leaf and canopy water status, leaf and canopy health, crop growth, canopy coverage (Moshou et al., 2005; Liu et al., 2010; Huang et al., 2012; Matsuda et al., 2012; Yang et al., 2014)
3D Imaging	Stereocamera systems, time-of-flight cameras	Time-series full-frame capture with varying resolutions	Depth maps	Shoot architecture, leaf angle distribution, canopy structure, root architecture, height (Moshou et al., 2005; Klose et al., 2009; Van der Heijden, 2012; Busemeyer et al., 2013)
Laser Scanning	Wide-range laser scanning devices	Time-series full-frame capture with varying resolutions	Depth maps, 3D point clouds	Shoot biomass and structure, leaf angle distribution, canopy structure, root architecture, height, stem (Biskup et al., 2007; Fang et al., 2009; Paulus et al., 2014a, 2014b)
Magnetic Resonance Imaging	Magnetic resonance imaging (MRI) devices	200–500 μm; 1–600 s	Water imaging (1H)	3D morphometric parameters, water content (Rascher et al., 2011; Hillnhütter et al., 2012; Poorter et al., 2012)
Positron Emission Tomography	Positron emission detectors for short-lived isotopes (e.g., $^{11}CO_2$)	1–2 mm; 10 s–20 min	Radiotracer mapping and co-registration with positron emission signals	Transport partitioning, sectoriality, flow rate (Poorter et al., 2012)
Computed Tomography	X-ray computed tomography and digital radiography	100 μm and below; hours	Voxel and tissue slices	3D morphometric parameters, grain quality (Karunakaran et al., 2004; Flavel et al., 2012; Garbout et al., 2012)

Spectroscopy imaging can provide insights into the drivers of growth dynamics using tools such as measuring spatial-temporal growth patterns during experiments. It also aids in collecting plant spectroscopy data for quantitative assessment of vegetation indices, water content, seed-composition parameters, and more. Currently, visualization methods for plant phenotyping primarily include fluorescent imaging, thermal infrared imaging, visible light imaging, spectroscopy imaging, and other methods (magnetic resonance imaging, positron emission tomography, and computed tomography).
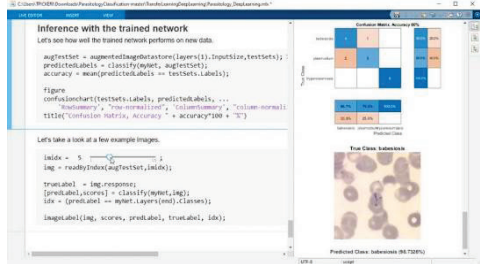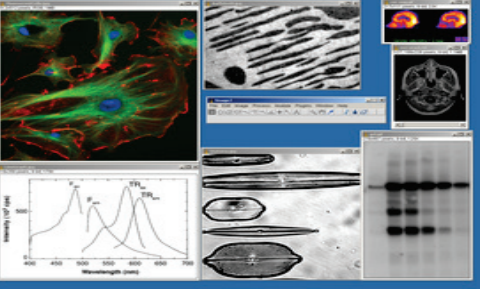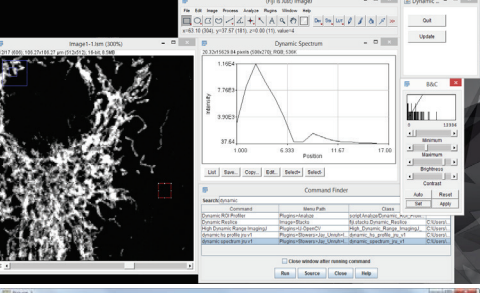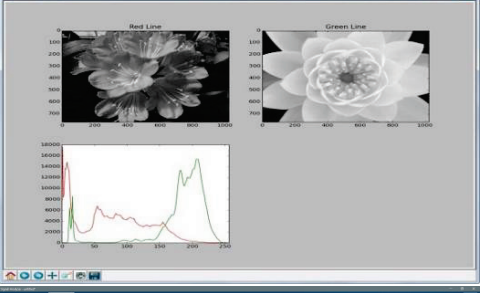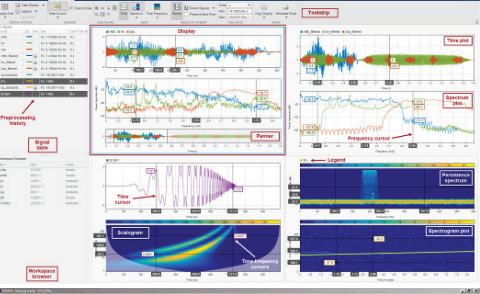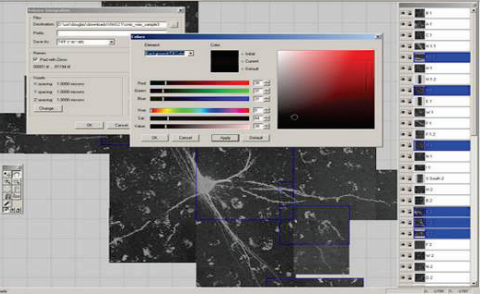
Visible light imaging is widely utilized in agriculture due to its low cost and ease of operation and maintenance (Barbagallo et al., 2003; Paproki et al., 2012). In controlled environments, visible light imaging is mainly used to analyze shoot biomass, yield traits, awn features, uptake and germination rates, leaf morphology, shoot strength, seed morphology, and root-system structure (Kozlov et al., 2007; Delagrange & Rochon, 2011; Eliceiri et al., 2012). Standard preprocessing and image analysis algorithms are employed to process the acquired images, often implemented in libraries and software packages (Table 2) (Abràmoff et al., 2004; Bradski & Kaehler, 2008; Schindelin et al., 2012). Working with image-analysis libraries like OpenCV requires programming skills. However, packages like ImageJ have a user-friendly graphical interface, sets of basic functions for solving common image-analysis tasks, and the capability to create computational pipelines from elementary operations for processing sets of images in a consistent manner. The advancement of image-analysis methods has led to the development of numerous programs aimed at determining phenotypic characteristics.

Analysis of the global experience in plant phenotyping

Let us analyze some of the most significant research on plant phenotyping. Studying the root system in the traditional sense is practically impossible. For instance, any disturbance to the roots during excavation can affect their arrangement and integrity. Therefore, scientists at the Jülich Research Center use positron emission tomography to study images of live roots in soil. Investigating 3D images of root architecture and the distribution of various substances in them allows for the examination of physiological characteristics of the root system.

Table 2

Image processing software

Name	Description	Interface
Matlab	A package of versatile applications	Command line
ImageJ	Expandable software for image analysis and processing	Graphical
Fiji	A software package based on ImageJ	Graphical
OpenCV	A library of computer vision algorithms, image processing, and general-purpose numerical algorithms	Programmatic
FARSIGHT	A set of tools for image processing and analysis	Command line
ProStack	A platform for managing image processing and analysis software modules	Graphical

In the studies conducted at the China Agricultural University, 3D models of 20 sugar beet genotypes were reconstructed using the Structure-from-Motion (SFM) method at three growth stages in field conditions (Xiao et al., 2020). An automated pipeline for data processing was developed, including processing point clouds of individual plants and extracting their distinctive features. Common features such as plant height, maximum plant canopy area, and the volume of the convex hull of numerous points were extracted based on the overall plant structure. Distinctive plant features were utilized to study their correlation with sugar-beet biomass. Such automated conveyor measurements can be effective for plant phenotyping in field conditions and provide a foundation for new breeding programs.

At the Jülich Research Center, the spatial-temporal dynamics of vegetation are mapped using image spectroscopy and three-dimensional reconstruction of plants. Utilizing unique tools for remote sensing of individual plants, it is possible to assess the condition of each plant or entire areas, select the best ones, and provide them with additional nutrition or necessary plant protection measures. Different colors of plants can indicate susceptibility to pests, diseases, inadequate growth conditions, or genetic variations and plant vulnerability. A method for seed phenotyping has been developed as a result of the research (Yang et al., 2021). The main advantages of this method novel synthetic method for generating and augmenting images, which works to prepare a large dataset of labeled images such as automatic segmentation, is that it reduces the manual annotation workload significantly. The proposed transfer-learning method, achieved by finely tuning the weight coefficients of a pre-trained model, can significantly reduce computational costs. The pipeline proposed in the research can be extended to segment specimens of other high-productivity objects and measure their morphology. Efficient seed germination is an important trait for both field and greenhouse crops. Large-scale germination experiments are labor-intensive and prone to observer errors, necessitating the use of automated methods. Researchers from the Earlham Institute (Colmer et al., 2020) introduced the SeedGerm system, which combines low-cost hardware and open-source software for seed germination experiments, automated seed imaging, and machine learning-based phenotypic analysis. The software can process multiple batches of images simultaneously and perform reliable analysis of traits related to similarity and viability, both in formats of comma-separated values (CSV) and processed image (PNG).

Experience of the Institute of Oilseed Crops of the NAAS in plant phenotyping for oilseed crops

As we can see, the global practice of quantitative plant phenotyping is evolving and becoming an essential component of the breeding process. Therefore, over the past 10 years, the Institute of Oilseed Crops of the National Academy of Agrarian Sciences (IOC NAAS) has conducted a series of relevant research projects involving renowned geneticists, breeders, and engineers.

For some applications of sunflower, particularly confectionery purposes, seed color analysis is of utmost importance. The Institute of Oilseed Crops has conducted a series of scientific studies on this trait. Visual analysis revealed that all the seeds from collection samples were categorized into 12 groups. In several lines, the inheritance of seed coat coloration was studied, and a collection of sunflower lines with defined genetic control of different color types was assembled. The collection included samples with specified seed coat coloration types and established genetic control. In total, three seed coat layers and ten alleles of four genes were described (Horokhivets & Vedmedieva, 2013). Based on the results of genetic research, a method for determining sunflower seed coloration has been developed (Vedmedeva & Poliakova, 2016). By visual assessment, direct scanning of sunflower seeds, and image analysis, there had been identified intensity ranges for four channels, and the genotypes were grouped, helping to avoid subjectivity in seed color assessment. For the development of a scale from the genetic collection of 700 lines, 120 samples were selected based on seed color characteristics. From each of the 120 samples, 100 seeds were selected. All seeds were divided into 10 groups of 5 colorations, which numerically confirmed the visual distribution of samples, and for which mean values and errors were calculated.

To automate the process of analyzing and selecting sunflower seed samples, a method and device for automatic sunflower seed phenotyping have been developed (Aliiev, 2019a, 2019b, 2019d). The novelty of the technical solution has been confirmed by the patent for invention and awarded the President of Ukraine's Prize (Decree of the President of Ukraine No. 595/2020 dated December 29, 2020). The method of automatic seed phenotyping includes the following stages (Fig. 1) (Aliiev, 2019c, 2019e, 2019f). The sequential irradiation of the seed region using electromagnetic radiation with different wavelengths, namely 465–470 nm (red spectrum – R), 515–520 nm (green spectrum – G), and 620–625 nm (blue spectrum – B), is carried out using a camera and software based on the OpenCV computer vision library, including the HighGui module. This allows for obtaining digital images of the seed batch in each of the three types of irradiation. Afterward, the cvtColor and inRange modules of the OpenCV library are applied to process the acquired images in the HSV color space (where Hue corresponds to the primary tone, Saturation to color saturation, and Value to the amount of light) and their subsequent transformation into black and white images. Next, the getStructurin-gElement and erode modules of the OpenCV library are used to perform morphological transformations of the obtained images.
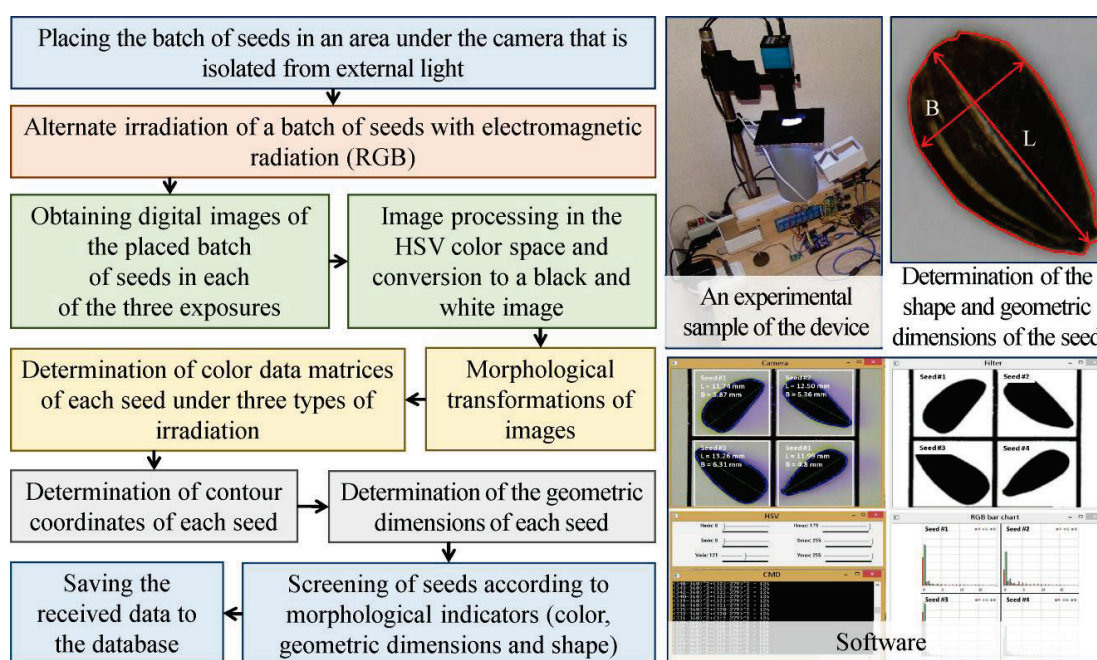

Fig. 1. Method and device for automatic sunflower seed phenotyping

The main goal of these transformations is to remove random speckles, noise, and merge areas that may be separated by shadows. Using the obtained images, a corresponding data matrix regarding the coloration of each seed from the batch is determined for three types of irradiation (Aliiev, 2019f, 2020). As a result of the conducted research, there were developed histograms of color distribution in sunflower seed areas in the RGB color space under different lighting conditions. The analysis of these histograms showed that the most distinct differences were under red illumination conditions in a uniform color environment. Additionally, seed color index C was introduced, represented as a matrix of frequencies f of the corresponding maxima (max) in the RGB color space under red seed illumination (Fig. 2) (Aliiev, 2020).

Similar work on studying seed coloration was conducted for oil flaxseed. The main types of colorations were evaluated, and a method for determining the coloration of flaxseed was developed and patented. A scale of digital indicators for the main types of colorations was developed: yellow, gray-brown, brown, and dark brown (Fig. 3). The use of the proposed method will contribute to the acceleration and standardization of the process of describing flaxseed samples and lines, allowing for their identification based on seed color (Yahlo, 2007; Shevchenko et al., 2017; Liakh et al., 2019).

For sunflower in various applications, the size and shape of seeds are important factors. At the IOC NAAS, a feature collection of sunflower lines based on seed size has been created and registered. Its main parameters and variability have been identified. A series of lines were studied in crosses to determine the inheritance pattern of seed size traits (Horokhivets & Vedmedieva, 2013; Vedmedeva & Poliakova, 2016). The results indicate a polygenic recessive mode of inheritance (Fig. 4).

The seed size trait is highly variable and depends on various factors. Even within a single head, seed sizes can vary significantly (Nosal et al., 2017; Nosal et al., 2018; Vedmedieva & Nosal, 2018, 2020). Research results have shown that seeds within the head are arranged in accordance with Fermat's spiral law (Fig. 5). In this spiral, seed sizes gradually decrease. The entire head can be divided into three zones. In the first zone, seeds are relatively large due to plant density in the sowing, the second tier also has a sufficiently high weight of 1,000 seeds and large seed size, while the third tier is either not developed or absent under unfavorable conditions. Figure 5 presents the research results of sunflower lines with large seeds based on their location within the head (Vedmedieva et al., 2017; Aliiev & Vedmedieva, 2023).

$$C=\begin{pmatrix} R_{1max} & f_{R1max} & R_{2max} & f_{R2max} \\ G_{1max} & f_{G1max} & G_{2max} & f_{G2max} \\ B_{1max} & f_{B1max} & B_{2max} & f_{B2max} \end{pmatrix}$$
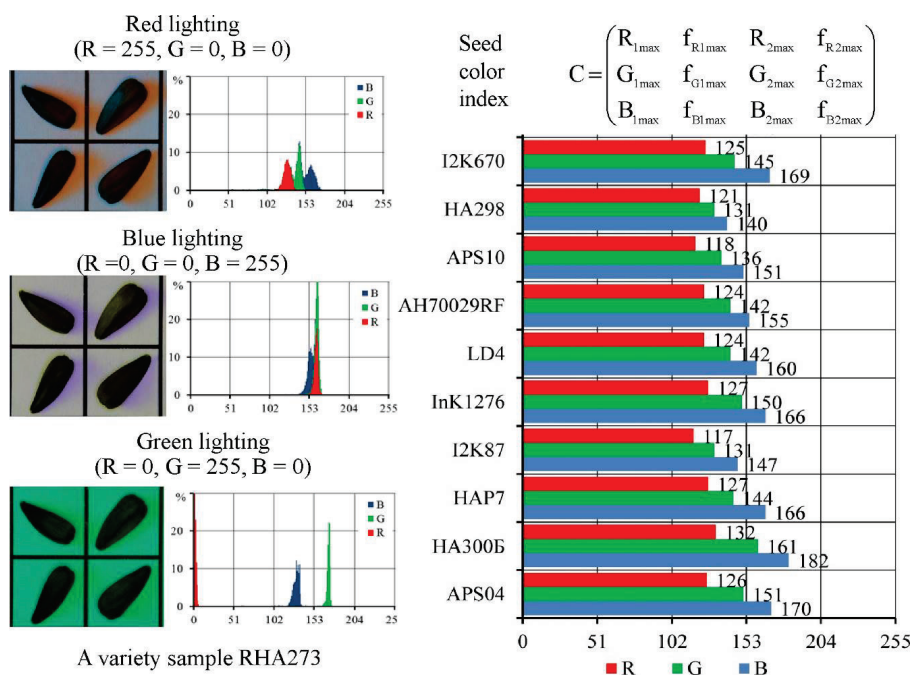

Fig. 2. Histogram of maximum channel values in the RGB color space under red illumination of sunflower samples
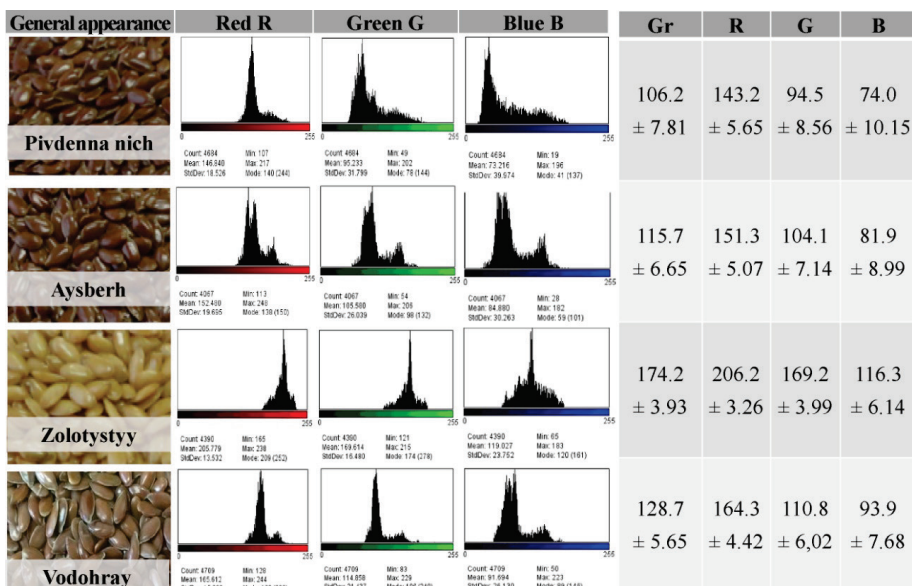
Fig. 3. Histograms of the distribution of colors in oil flaxseed

| Feature	Character expression	Mark	№	Name
	very small	1		
	small	3	UE0100326	L3069
1. Seed by size	average	5	UE0100556	BA4
	big	7	UE0100499	InK3159
	very big	9	UE0100642	ZKN51
2. Achene in thickness relative to width	thin	3	UE0101224	InK87
	average	5	UE0100473	L2079
	fat	7	UE0100509	MBG3
	very short (< 4.1 mm)	1		
	short (4.1 – 8.0 mm)	3	UE0100493	BK310
3. Seed length, score	medium (8.1 – 12.0 mm)	5	UE0100908	InK34
	long (12.1 – 16.0 mm)	7	UE0101221	M1048
	very long (> 16.0 mm)	9	UE0100642	ZKN51
	very narrow (< 2.1 mm)	1		
	narrow (2.1 – 4.0 mm)	3	UE0100467	L2090
4. Seed – width, point	medium (4.1 – 6.0 mm)	5	UE0100477	Sl179
	wide (6.1 – 8.0 mm)	7	UE0100485	Sl2177
	very wide (> 8.0 mm)	9	UE0100642	ZKN51
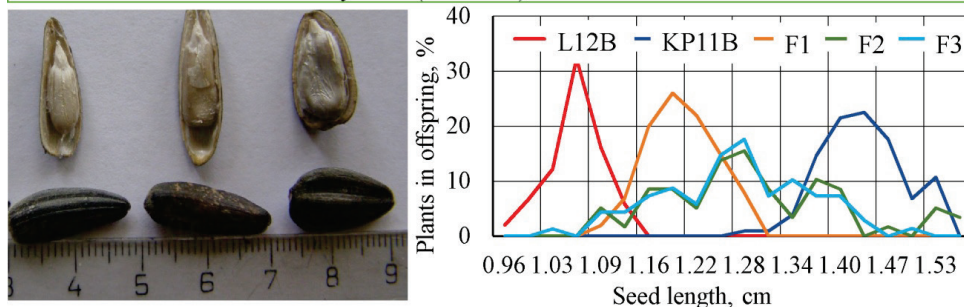
Fig. 4. Collection of sunflower lines based on seed size
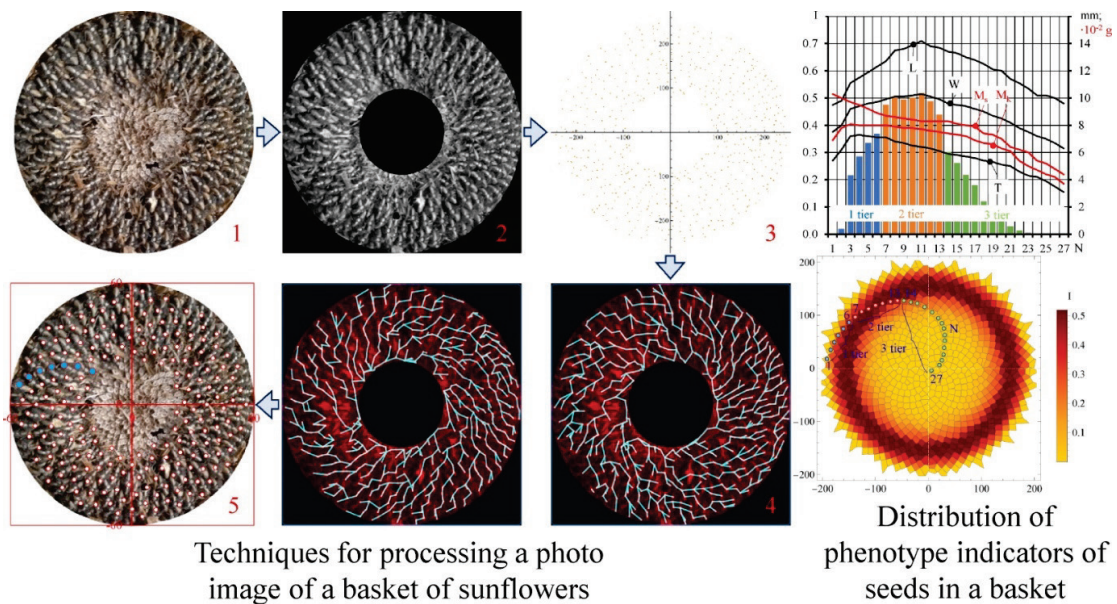

Fig. 5. Study of changes in phenotypic traits of sunflower seeds depending on their location within the head

The results of the research of changes in sunflower seed size within the head allow for evaluating plumpness. According to the studies of the impact of edge effects on large-seeded hybrids and varieties, it was found that the most significant effect was observed on the plumpness of the third layer (middle) of the head.

During the research, specialized software for seed composition analysis based on images was developed (Fig. 6). This software is used to transform full-color images with a 24-bit color depth into black and white images with a 1-bit depth. This process is carried out using segmentation. Subsequently, the images are processed using morphological operations and the Canny edge detector for automatic contour detection of each seed in the generated black and white image.

After determining the seed contours in the image, the software automatically calculates parameters for each seed, such as length (L), width (B), area (S), and perimeter length (P) (Shevchenko & Aliiev, 2022).

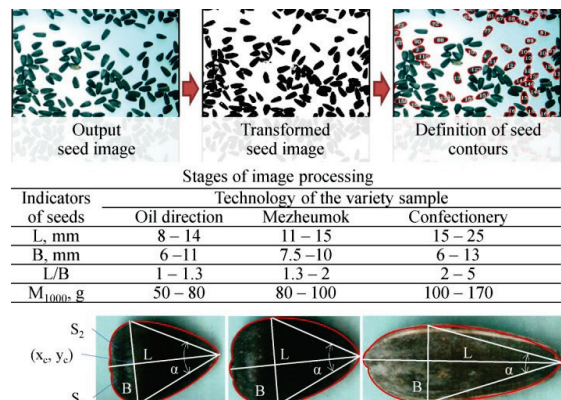| Indicators of seeds	Technology of the variety sample		
	Oil direction	Mezheumok	Confectionery
L, mm	8 – 14	11 – 15	15 – 25
B, mm	6 –11	7.5 –10	6 – 13
L/B	1 – 1.3	1.3 – 2	2 – 5
M_{1000}, g	50 – 80	80 – 100	100 – 170

Fig. 6. Research of the geometric dimensions of sunflower seeds

Research of the photosynthetic activity of safflower under the influence of agronomic practices was conducted in field conditions. To determine the net photosynthetic productivity, it was necessary to measure the leaf area of plants at three stages of development: budding, flowering, and physiological maturity. Leaf area was determined through the following steps (Fig. 7): selecting five random plants from each plot, separating the leaves from the plants, scanning the leaves using a Canon CanoScan LIDE 300 scanner with 1200 pixels resolution in the RGB color model, saving the files in .jpg format, converting the color model of the obtained files into raster images using Adobe Photoshop software, calculating the number of black pixels in the raster image using the ImageJ software package, calculating the leaf surface area by inputting calibration coefficients using the MS Excel software, and averaging the leaf surface area values. The research results revealed a correlation between safflower yield, water consumption, and net photosynthetic productivity (Aliieva et al., 2022; Vedmedieva et al., 2022).
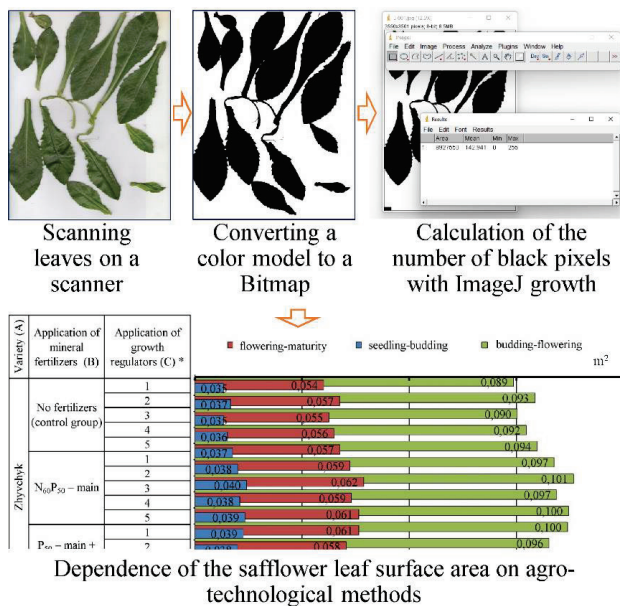

Fig. 7. Calculation algorithm of leaf surface area

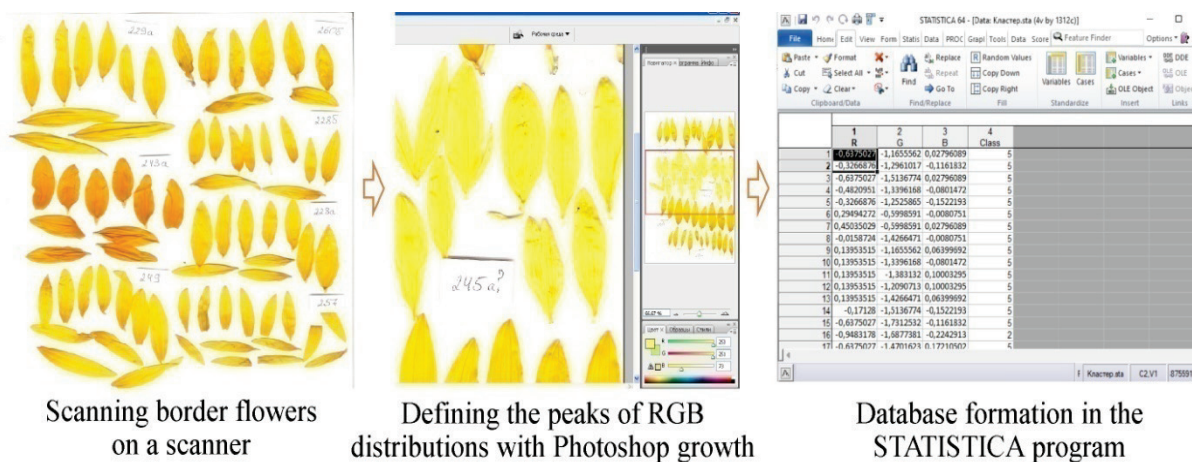Besides seed traits, it is also important to phenoty coloration in other plant organs. The types of coloration in the outer flowers of sunflower have been studied and a collection of 270 samples was created (Soroka & Lyakh, 2019; Soroka et al., 2020; Vedmedeva, 2020). It was studied based on coloration and the genetic control of the main color types. Through visual and genetic identification, the lines were classified into coloration classes. The patented method for determining coloration of the outer flowers of sunflower includes direct scanning of the flowers on a glass scanner and recording the results in jpg format. Subsequently, Photoshop is used to generate average RGB color values through a filter (Fig. 8) (Vedmedieva, 2014). Samples are categorized according to the proposed scale, and the primary flower color is determined. They are then grouped with further identification of sunflower line coloration types (Soroka et al., 2017b; Vedmedieva, 2019a, 2019b, 2020; Vedmedieva & Makhova, 2019).

The process of identifying types of coloration of the sunflower petal was carried out using the Statistica software. The identification steps include the following (Fig. 9): data summarization in the three-dimensional RGB color space; data clustering process; representation of clustering results in the three-dimensional RGB color space; development of a neural network algorithm for identification of a color group; application of the neural-network algorithm for grouping sunflower varieties by petal coloration; creation of diagrams illustrating genetic differences in petal coloration among the line groups.

Conclusions

Building upon the global experience and the research results of the Institute of Oilseeds Crops of the NAAS (IOC NAAS), the following advancement in plant phenotyping in Ukrainian agrarian science is proposed.

Integrated approaches from molecular to field-level methodologies are essential for the development of sustainable crop production, ensuring high yields, and optimizing limited resources. Despite significant progress in molecular and genetic approaches in recent years, the quantitative analysis and systematization of plant phenotypes (plant structures and functions) remain major challenges. Plant phenotyping is a science that links genomics, ecophysiology, and plant agronomy, utilizing modern automated methods for selection and systematization. The functional plant body (phenotype) develops during the growth and development of plants through dynamic interactions between the genotype and the surrounding environment in which the plants grow. These interactions determine the practical outcome of crop cultivation in terms of quantity and quality of production. This includes seed yield and its quality, such as oil content, seed size, shape, and density, among other factors.

Color indicators of groups of colors according to visual perception

Indexes	Groups by color				
	Yellow	Orange	Light yellow	Lemon	white
R (red)	248.7 ± 0,2	243.8 ± 0,5	249.6 ± 0,1	248.4 ± 0,2	251.8 ± 0.3
G (yellow)	205.0 ± 0,4	178.0 ± 0,8	212.0 ± 0,2	233.0 ± 0,2	241.0 ± 0.8
B (blue)	8.4 ± 0,2	8.5 ± 0,4	10.7 ± 0,1	52.9 ± 0,3	41.8 ± 1.5

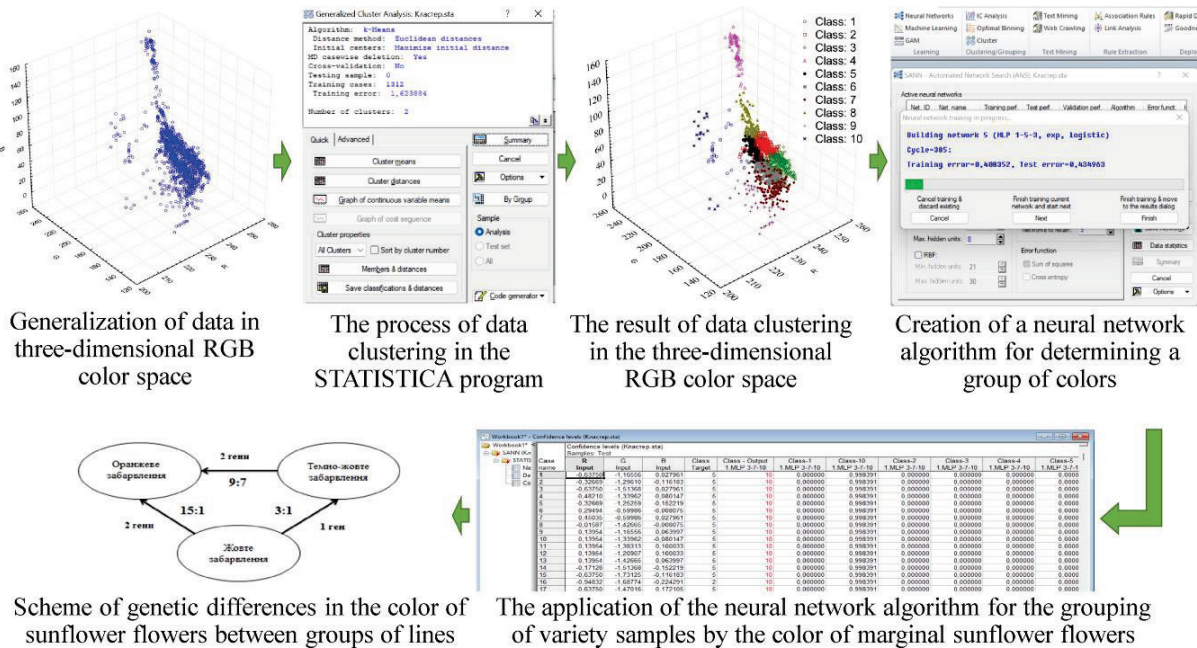Fig. 8. Method for determining the coloration of sunflower outer flowers

Fig. 9. The process of identifying types of sunflower petal coloration

Determining the coloration of plant organs in various crops allows for the expansion of collections of corresponding crop varieties, increasing genetic diversity, and serving various purposes. Coloration of flower petals is relevant for overall plant phenotyping, protection of plant breeders' rights, seed purity, and other needs. For instance, oil flax varieties exhibit different coloration of their corollas, and collections of safflower have already been studied for four types of corolla coloration. This enables the emphasis of authorship for plant varieties in the State Register of Plant Varieties Suitable for Distribution in Ukraine.

Systematizing oilseed crops based on a complex of phenotypic characteristics, considering gene penetrance and trait heritability, will facilitate decision-making, while mechatronic systems for material separation, selection, and classification using neural networks will significantly reduce costs. Therefore, one of the ways to address this challenge is the development of a methodology for systematizing sunflower genotypes based on their phenotypic expression using neural networks.

References

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

Aliiev, E. (2019a). Production testing of tape device for automatic penotyping of sunflower seeds. Scientific Horizons, 12(85), 75–83.

Aliiev, E. B. (2019b). Fizyko-matematychni modeli protsesiv pretsyzijnoji separatsji nasinnevoho materialu soniashnyku [Physical-mathematical models of the processes of precision separation of sunflower seed material]. Status, Zaporizhzhia (in Ukrainian).

Aliiev, E. B. (2019c). Patent Ukrajiny na vynakhid 120231, MPK (2006) A01C 1/00, G01B 11/00, G01B 11/02 (2006.01), G01N 21/25 (2006.01), G06T 7/00. Sposib avtomatychnoho fenotypuvannia nasinnia i prystrij dlia joho zdijsnennia [A method of automatic seed phenoltyping and a device for its implementation]. Instytut Oliiynykh Kultur Natsionalnoji Akademiji Ahrarnykh Nauk Ukrajiny, No. a201808708. Zaiavl. 25.10.2019. Opubl. 25.10.2019, biul. No. 20 (in Ukrainian).

Aliiev, E. B. (2019d). Prystrij dlia avtomatychnoho fenotypuvannia nasinnia soniashnyku [Device for automatic phenotyping of sunflower seeds]. Suchasni problemy zemlerobskoji mekhaniky: Materialy X Mizhnarodnoji naukovoji konferentsiji. Mykolajiv. Pp. 82–83 (in Ukrainian).

Aliiev, E. B. (2019e). Rezul'taty doslidzhen' protsesu avtomatychnoho fenotypuvannia nasinnia soniashnyku [Results of research into the process of automatic phenotyping of sunflower seeds]. Naukovi chytannia do 100-richchia vid dnia narodzhennia profesora Ivana Viktorovycha Yashovskoho: Materialy mizhnarodnoji naukovoji konferentsiji 14–15 serpnia 2019 roku. Chabany. Pp. 90–92 (in Ukrainian).

Aliiev, E. B. (2019f). Rozrobka prystroju dlia avtomatychnoho fenotypuvannia nasinnevoho materialu soniashnyku [Development of a device for automatic phenotyping of sunflower seed material]. Machinery and Energetics, 10(1), 11–17 (in Ukrainian).

Aliiev, E. B. (2020). Automatic phenotyping test of sunflower seeds. Helia, 43(72), 51–66.

Aliiev, E. B. (2022). Avtomatychne fenotypuvannia nasinnevoho materialu soniashnyku [Automatic phenotyping of sunflower seed material]. Ahrarna Nauka, Kyiv (in Ukrainian).

Aliiev, E. B., & Vedmedieva, K. V. (2023). Matematychna model rozmishchennia nasinnia soniashnyku u koshyku [Mathematical model of placement of sunflower seeds in the capitulum]. Scientific and Technical Bulletin of the Institute of Oilseed Crops NAAS, 34, 15–23 (in Ukrainian).

Aliieva, O., Polyakov, A., & Aliiev, E. (2022). Features of photosynthetic activity and water consumption of safflower. Zemdirbyste-Agriculture, 109(2), 123–130.

Araus, J. L., & Cairns, J. E. (2014). Field high-throughput phenotyping: The new crop breeding frontier. Trends in Plant Science, 19, 52–61.

Araus, J. L., Serret, M. D., & Edmeades, G. O. (2012). Phenotyping maize for adaptation to drought. Frontiers in Physiology, 3, 305.

Arvidsson, S., Pérez-Rodríguez, P., & Mueller-Roeber, B. (2011). A growth phenotyping pipeline for *Arabidopsis thaliana* integrating image analysis and rosette area modeling for robust quantification of genotype effects. New Phytologist, 191, 895–907.

Balachandran, S., Hurry, V., Kelley, S., Osmond, C., Robinson, S., Rohozinski, J., Seaton, G., & Sims, D. (1997). Concepts of plant biotic stress. Some insights into the stress physiology of virus-infected plants, from the perspective of photosynthesis. Plant Physiology, 100, 203–213.

Barbagallo, R. P., Oxborough, K., Pallett, K. E., & Baker, N. R. (2003). Rapid, noninvasive screening for perturbations of metabolism and plant growth using chlorophyll fluorescence imaging. Plant Physiology, 132(2), 485–493.

Bauriegel, E., Giebel, A., & Herppich, W. B. (2011). Hyperspectral and chlorophyll fluorescence imaging to analyse the impact of fusarium culmorum on the photosynthetic integrity of infected wheat ears. Sensors, 11, 3765–3779.

Bera, R. K. (2019). Synthetic biology, artificial intelligence, and quantum computing. IntechOpen. Pp. 1–28.

Berger, B., Parent, B., & Tester, M. (2010). High-throughput shoot imaging to study drought responses. Journal of Experimental Botany, 61, 3519–3528.

Biskup, B., Scharr, H., Schurr, U., & Rascher, U. (2007). A stereo imaging system for measuring structural parameters of plant canopies. Plant, Cell and Environment, 30, 1299–1308.

Bolon, Y.-T., Haun, W. J., Xu, W. W., Grant, D., Stacey, M. G., Nelson, R. T., Gerhardt, D. J., Jeddeloh, J. A., Stacey, G., & Muehlbauer, G. J. (2011). Phenotypic and genomic analyses of a fast neutron mutant population resource in soybean. Plant Physiology, 156, 240–253.

Bradski, G., & Kaehler, A. (2008). Learning OpenCV: Computer vision with the OpenCV library. O'Reilly Media, Inc.

Brewer, M. T., Lang, L., Fujimura, K., Dujmovic, N., Gray, S., & van der Knaap, E. (2006). Development of a controlled vocabulary and softwa-

re application to analyze fruit shape variation in tomato and other plant species. Plant Physiology, 141, 15–25.

Bürling, K., Hunsche, M., & Noga, G. (2010). Quantum yield of non-regulated energy dissipation in psii(y(no)) for early detection of leaf rust (*Puccinia triticina*) infection in susceptible and resistant wheat (*Triticum aestivum* L.) cultivars. Precision Agriculture, 11, 703–716.

Busemeyer, L., Mentrup, D., Möller, K., Wunder, E., Alheit, K., Hahn, V., Maurer, H. P., Reif, J. C., Würschum, T., & Müller, J. (2013). Breedvision – A multi-sensor platform for non-destructive field-based phenotyping in plant breeding. Sensors, 13, 2830–2847.

Clark, R. T., MacCurdy, R. B., Jung, J. K., Shaff, J. E., McCouch, S. R., Aneshansley, D. J., & Kochian, L. V. (2011). Three-dimensional root phenotyping with a novel imaging and software platform. Plant Physiology, 156, 455–465.

Cleland, J. (2013). World population growth: Past, present and future. En-vironmental and Resource Economics, 55, 543–554.

Colmer, J., O'Neill, C. M., Wells, R., Bostrom, A., Reynolds, D., Websdale, D., Shiralagi, G., Lu, W., Lou, Q., Cornu, T. L., Ball, J., Renema, J., Andaluz, G. F., Benjamins, R., Penfield, S., & Zhou, J. (2020). SeedGerm: A cost-effective phenotyping platform for automated seed imaging and machine-learning based phenotypic analysis of crop seed germination. New Phytologist, 228, 778–793.

Cook, J. P., McMullen, M. D., Holland, J. B., Tian, F., Bradbury, P., Ross-Ibarra, J., Buckler, E. S., & Flint-Garcia, S. A. (2012). Genetic architecture of maize kernel composition in the nested association mapping and inbred association panels. Plant Physiology, 158, 824–834.

Deery, D., Jimenez-Berni, J., Jones, H., Sirault, X., & Furbank, R. (2014). Proximal remote sensing buggies and potential applications for fieldbased phenotyping. Agronomy, 4(3), 349–379.

Deikman, J., Petracek, M., & Heard, J. E. (2012). Drought tolerance through biotechnology: Improving translation from the laboratory to farmers' fields. Current Opinion in Biotechnology, 23, 243–250.

Delagrange, S., & Rochon, P. (2011). Reconstruction and analysis of a deciduous sapling using digital photographs or terrestrial-LiDAR technology. Annals of Botany, 108(6), 991–1000.

Duan, L. F., Yang, W. N., Huang, C. L., & Liu, Q. (2011). A novel machine-vision-based facility for the automatic evaluation of yield-related traits in rice. Plant Methods, 7, 44.

Eliceiri, K. W., Berthold, M. R., Goldberg, I. G., Ibáñez, L., Manjunath, B. S., Martone, M. E., Murphy, R. F., Peng, H., Plant, A. L., Roysam, B., Stuurman, N., Swedlow, J. R., Tomancak, P., & Carpenter, A. E. (2012). Biological imaging software tools. Nat Methods, 9(7), 697–710.

Fang, S., Yan, X., & Liao, H. (2009). 3D reconstruction and dynamic modeling of root architecture in situand its application to crop phosphorus research. The Plant Journal, 60, 1096–1108.

Fiorani, F., & Schurr, U. (2013). Future scenarios for plant phenotyping. Annual Review of Plant Biology, 64, 267–291.

Flavel, R. J., Guppy, C. N., Tighe, M., Watt, M., McNeill, A., & Young, I. M. (2012). Non-destructive quantification of cereal roots in soil using high-resolution x-ray tomography. Journal of Experimental Botany, 63, 2503–2511.

Gaigbe-Togbe, V., Bassarsky, L., Gu, D., Spoorenberg, T., & Zeifman, L. (2022). World population prospects 2022. Summary of results. Department of Economic and Social Affairs, Population Division.

Garbout, A., Munkholm, L. J., Hansen, S. B., Petersen, B. M., Munk, O. L., & Pajor, R. (2012). The use of pet/ct scanning technique for 3D visualization and quantification of real-time soil/plant interactions. Plant and Soil, 352, 113–127.

Golzarian, M. R., Frick, R. A., Rajendran, K., Berger, B., Roy, S., Tester, M., & Lun, D. S. (2011). Accurate inference of shoot biomass from high-throughput images of cereal plants. Plant Methods, 7, 1–11.

Granier, C., Aguirrezabal, L., Chenu, K., Cookson, S. J., Dauzat, M., Hamard, P., Thioux, J. J., Rolland, G., Bouchier-Combaud, S., & Lebaudy, A. (2006). Phenopsis, an automated platform for reproducible phenotyping of plant responses to soil water deficit in *Arabidopsis thaliana* permitted the identification of an accession with low sensitivity to soil water deficit. New Phytologist, 169, 623–635.

Harbinson, J., Prinzenberg, A. E., Kruijer, W., & Aarts, M. G. (2012). High throughput screening with chlorophyll fluorescence imaging and its use in crop improvement. Current Opinion in Biotechnology, 23, 221–226.

Hartmann, A., Czauderna, T., Hoffmann, R., Stein, N., & Schreiber, F. (2011). Htpheno: An image analysis pipeline for high-throughput plant phenotyping. BMC Bioinformatics, 12, 148.

Hillnhütter, C., Sikora, R., Oerke, E.-C., & van Dusschoten, D. (2012). Nuclear magnetic resonance: A tool for imaging belowground damage caused by *Heterodera schachtii* and *Rhizoctonia solani* on sugar beet. Journal of Experimental Botany, 63, 319–327.

Horokhivets, N. A., & Vedmedieva, K. V. (2013). Uspadkuvannia pantsyrnoho sharu i zabarvlennia hipodermy v perikarpiji soniashnyku [Inheritance of the phytomelanin layer and coloration of the hypodermis in sunflower pericarps]. Visnyk Kharkivs'koho Natsional'noho Universytetu imeni V. N. Karazina, Serija Biolohija, 18(1079), 71–75 (in Ukrainian).

Hoyos-Villegas, V., Houx, J., Singh, S., & Fritschi, F. (2014). Ground-based digital imaging as a tool to assess soybean growth and yield. Crop Science, 54(4), 1756–1768.

Huang, J., Liao, H., Zhu, Y., Sun, J., Sun, Q., & Liu, X. (2012). Hyperspectral detection of rice damaged by rice leaf folder (*Cnaphalocrocis medinalis*). Computers and Electronics in Agriculture, 82, 100–107.

Ikeda, M., Hirose, Y., Takashi, T., Shibata, Y., Yamamura, T., Komura, T., Doi, K., Ashikari, M., Matsuoka, M., & Kitano, H. (2010). Analysis of rice panicle traits and detection of qtls using an image analyzing method. Breeding Science, 60, 55–64.

Jannink, J.-L., Lorenz, A. J., & Iwata, H. (2010). Genomic selection in plant breeding: From theory to practice. Briefings in Functional Genomics, 9, 166–177.

Jansen, M., Gilmer, F., Biskup, B., Nagel, K. A., Rascher, U., Fischbach, A., Briem, S., Dreissen, G., Tittmann, S., & Braun, S. (2009). Simultaneous phenotyping of leaf growth and chlorophyll fluorescence via growscreen fluoro allows detection of stress tolerance in *Arabidopsis thaliana* and other rosette plants. Functional Plant Biology, 36, 902–914.

Jones, H. G., Serraj, R., Loveys, B. R., Xiong, L., Wheaton, A., & Price, A. H. (2009). Thermal infrared imaging of crop canopies for the remote diagnosis and quantification of plant responses to water stress in the field. Functional Plant Biology, 36, 978–989.

Joosen, R. V. L., Arends, D., Willems, L. A. J., Ligterink, W., Jansen, R. C., & Hilhorst, H. W. (2012). Visualizing the genetic landscape of *Arabidopsis* seed performance. Plant Physiology, 158, 570–589.

Joosen, R. V., Kodde, J., Willems, L. A., Ligterink, W., van der Plas, L. H., & Hilhorst, H. W. (2010). Germinator: A software package for highthroughput scoring and curve fitting of *Arabidopsis* seed germination. The Plant Journal, 62, 148–159.

Karunakaran, C., Jayas, D., & White, N. (2004). Detection of internal wheat seed infestation by *Rhyzopertha dominica* using x-ray imaging. Journal of Stored Products Research, 40, 507–516.

Klose, R., Penlington, J., & Ruckelshausen, A. (2009). Usability study of 3D time-of-flight cameras for automatic plant phenotyping. Bornimer Agrartech Berichte, 69, 93–105.

Kozlov, K., Pisarev, A., Matveeva, A., Kaandorp, J., & Samsonova, M. (2007). Image processing package ProStack for quantification of biological images. In: Proceding of 4th International Symposium on Networks in Bioinformatics. Amsterdam. P. 204.

Kumar, P., Huang, C., Cai, J., & Miklavcic, S. J. (2014). Root phenotyping by root tip detection and classification through statistical learning. Plant and Soil, 380, 193–209.

Liakh, V. O., Yahlo, M. M., & Poliakov, V. O. (2019). Patent Ukrajiny na korysnu model 124398, MPK (2006): G01N 33/00, G01N 21/00. Sposib vyznachennia zabarvlennia nasinnia lionu [The method of determining the color of flax seeds]. Instytut Olijnykh Kul'tur Natsional'noji Akademiji Ahrarnykh Nauk Ukrajiny, No. u201709843. Zaiavl. 11.10.2017. Opubl. 10.04.2018, biul. No. 7 (in Ukrainian).

Liu, Z.-Y., Shi, J.-J., Zhang, L.-W., & Huang, J.-F. (2010). Discrimination of rice panicles by hyperspectral reflectance data based on principal component analysis and support vector classification. Journal of Zhejiang University-Science, 11, 71–78.

Matsuda, O., Tanaka, A., Fujita, T., & Iba, K. (2012). Hyperspectral imaging techniques for rapid identification of *Arabidopsis* mutants with altered leaf pigment status. Plant and Cell Physiology, 53, 1154–1170.

McMullen, M. D., Kresovich, S., Villeda, H. S., Bradbury, P., Li, H., Sun, Q., Flint-Garcia, S., Thornsberry, J., Acharya, C., & Bottoms, C. (2009). Genetic properties of the maize nested association mapping population. Science, 325, 737–740.

Menzel, M. I., Tittmann, S., Buehler, J., Preis, S., Wolters, N., Jahnke, S., Walter, A., Chlubek, A., Leon, A., & Hermes, N. (2009). Non-invasive determination of plant biomass with microwave resonators. Plant, Cell and Environment, 32, 368–379.

Mishra, K. B., Iannacone, R., Petrozza, A., Mishra, A., Armentano, N., la Vecchia, G., Trtílek, M., Cellini, F., & Nedbal, L. (2012). Engineered drought tolerance in tomato plants is reflected in chlorophyll fluorescence emission. Plant Science, 182, 79–86.

Monforte, A. J., Diaz, A. I., Caño-Delgado, A., & van der Knaap, E. (2014). The genetic basis of fruit morphology in horticultural crops: Lessons from tomato and melon. Journal of Experimental Botany, 65(16), 4625–4637.

Moshou, D., Bravo, C., Oberti, R., West, J., Bodria, L., McCartney, A., & Ramon, H. (2005). Plant disease detection based on data fusion of hyper-spectral and multi-spectral fluorescence imaging using kohonen maps. Real-Time Imaging, 11, 75–83.

Mühlich, M., Truhn, D., Nagel, K., Walter, A., Scharr, H., & Aach, T. (2008). Measuring plant root growth. In: Pattern recognition. Proceedings of 30th DAGM Symposium. Munich, Springer-Verlag. Pp. 497–506.

Munns, R., James, R. A., Sirault, X. R., Furbank, R. T., & Jones, H. G. (2010). New phenotyping methods for screening wheat and barley for beneficial responses to water deficit. Journal of Experimental Botany, 61, 3499–3507.

Newell, M. A., & Jannink, J.-L. (2014). Genomic selection in plant breeding. In: Crop breeding. Springer, Berlin, Heidelberg. Pp. 117–130.

Nosal, O. O., Vedmedieva, K. V., & Shkolova, S. V. (2017). Donorski vlastyvosti linij soniashnyku za oznakoju krupnoplidnosti [Donor properties of sunflower lines based on high fertility]. Scientific and Technical Bulletin of the Institute of Oilseed Crops, NAAS, 24, 110–121 (in Ukrainian).

Nosal, O. O., Vedmedieva, K. V., Makliak, K. M., & Leonova, N. M. (2018). Hospodars'ka otsinka krupnoplidnykh hibrydiv soniashnyku [Economic assessment of large-fruited sunflower hybrids]. Scientific and Technical Bulletin of the Institute of Oilseed Crops NAAS, 25, 83–95 (in Ukrainian).

Paproki, A., Sirault, X., Berry, S., Furbank, R., & Fripp, J. (2012). A novel mesh processing based technique for 3D plant analysis. BMC Plant Biology, 12, 63.

Paulus, S., Behmann, J., Mahlein, A.-K., Plümer, L., & Kuhlmann, H. (2014a). Low-cost 3D systems: Suitable tools for plant phenotyping. Sensors, 14, 3001–3018.

Paulus, S., Dupuis, J., Riedel, S., & Kuhlmann, H. (2014b). Automated analysis of barley organs using 3D laser scanning: An approach for high throughput phenotyping. Sensors, 14, 12670–12686.

Phillips, R. L. (2010). Mobilizing science to break yield barriers. Crop Science, 50, 99–108.

Pieruschka, R., & Schurr, U. (2019). Plant phenotyping: Past, present, and future. Plant Phenomics, 2019, 7507131.

Poorter, H., Bühler, J., van Dusschoten, D., Climent, J., & Postma, J. A. (2012). Pot size matters: A meta-analysis of the effects of rooting volume on plant growth. Functional Plant Biology, 39, 839–850.

Rao, N. K. S., & Laxman, R. H. (2013). Phenotyping horticultural crops for abiotic stress tolerance. In: Climate-resilient horticulture: Adaptation and mitigation strategies. Springer, New Delhi. Pp. 147–157.

Rascher, U., Blossfeld, S., Fiorani, F., Jahnke, S., Jansen, M., Kuhn, A. J., Matsubara, S., Märtin, L. L., Merchant, A., & Metzner, R. (2011). Non-Invasive approaches for phenotyping of enhanced performance traits in bean. Functional Plant Biology, 38, 968–983.

Rousseau, C., Belin, E., Bove, E., Rousseau, D., Fabre, F., Berruyer, R., Guillaumès, J., Manceau, C., Jacques, M.-A., & Boureau, T. (2013). High throughput quantitative phenotyping of plant resistance using chlorophyll fluorescence image analysis. Plant Methods, 9, 17.

Sakamoto, T., Shibayama, M., Kimura, A., & Takada, E. (2011). Assessment of digital camera-derived vegetation indices in quantitative monitoring of seasonal rice growth. ISPRS Journal of Photogrammetry and Remote Sensing, 66, 872–882.

Schindelin, J., Arganda-Carreras, I., Frise, E., Kaynig, V., Longair, M., Pietzsch, T., Preibisch, S., Rueden, C., Saalfeld, S., Schmid, B., Tinevez, J. Y., White, D. J., Hartenstein, V., Eliceiri, K., Tomancak, P., & Cardona, A. (2012). Fiji: An open-source platform for biological-image analysis. Nature Methods, 9(7), 676–682.

Shevchenko, I. A., Liakh, V. O., Poliakov, O. I., Soroka, A. I., Vedmedieva, K. V., Zhu-ravel, V. M., Makhno, Y. O., Tovstanovska, T. H., & Budilka, H. I. (2017). Lion olijnyj, hirchytsia. Stratehija vyrobnytstva olijnoji syrovyny v Ukrajini (maloposhyreni kul'tury) [Flax oil, mustard. Strategy for the production of oil raw materials in Ukraine (rare crops)]. Status, Kyiv (in Ukrainian).

Shevchenko, I., & Aliiev, E. (2022). Precise grading and sorting of sunflower plant materials in industrial facilities. Journal of Central European Agriculture, 23(2), 327–341.

Shibayama, M., Sakamoto, T., Takada, E., Inoue, A., Morita, K., Takahashi, W., & Kimura, A. (2011). Estimating paddy rice leaf area index with fixed point continuous observation of near infrared reflectance using a calibrated digital camera. Plant Production Science, 14, 30–46.

Soroka, A. I., & Lyakh, V. A. (2019). Polygenic inheritance of bracts number in sunflower. Helia, 42(71), 221–228.

Soroka, A. I., Boika, O. A., & Lyakh, V. A. (2020). Inheritance of the number of ray flowers in sunflower. Helia, 43(73), 123–131.

Soroka, A. Y., Pleshakova, E., Liakh, V. A. (2017). Nasledovanie kolichestva kraevykh tsvetkov i list'ev obertki u podsolnechnika [Inheritance of the number of marginal flowers and leaves of the involucrum of sunflower]. Scientific and Technical Bulletin of the Institute of Oilseed Crops NAAS, 24, 39–48 (in Ukrainian).

Spielbauer, G., Armstrong, P., Baier, J. W., Allen, W. B., Richardson, K., Shen, B., & Settles, A. M. (2009). High-throughput near-infrared reflectance spectroscopy for predicting quantitative and qualitative composition phenotypes of individual maize kernels. Cereal Chemistry, 86, 556–564.

Van der Heijden, G., Song, Y., Horgan, G., Polder, G., Dieleman, A., Bink, M., Palloix, A., van Eeuwijk, F., & Glasbey, C. (2012). Spicy: Towards automated phenotyping of large pepper plants in the greenhouse. Functional Plant Biology, 39, 870–877.

Vedmedieva, K. V. (2020). Genetic affinity of sunflower lines and cluster analysis by morphological traits. Helia, 43(73), 113–122.

Vedmedieva, K. V., & Poliakova, N. A. (2016). Patent Ukrajiny na korysnu model' 107096, MPK (2006) A01C 1/00, A01M 11/00, G01N 21/00, B07C 5/10 (2006.01). Sposib vyznachennia zabarvlennia simianok soniashnyku [The method of determining the color of sunflower seeds]. Instytut Olijnykh Kul'tur Natsionalnoji Akademiji Ahrarnykh Nauk Ukrajiny, No. u201510357. Zaiavl. 23.10.2015. Opubl. 25.05.2016, biul. No. 10 (in Ukrainian).

Vedmedieva, K. V. (2014). Patent Ukrajiny na korysnu model 87462. MPK (2014.01): A01G 7/00. Sposib vyznachennia zabarvlennia krajovykh kvitiv soniashnyku [The method of determining the color of marginal sunflower flowers]. Instytut Olijnykh Kul'tur Natsionalnoji Akademiji Ahrarnykh Nauk Ukrajiny, No. u201309730. Zaiavl. 05.08.2013. Opubl. 10.02.2014, biul. No. 3 (in Ukrainian).

Vedmedieva, K. V. (2019a). Henetychnyj kontrol' zabarvlennia krajovykh kvitok mutantnykh linij soniashnyku [Genetic control of color of marginal flowers of sunflower mutant lines]. Visnyk Kharkivs'koho Natsional'noho Universytetu imeni V. N. Karazina, Serija Biolohija, 33, 21–27 (in Ukrainian).

Vedmedieva, K. V. (2019b). Uspadkuvannia oznaky abrykosovoho zabarvlennia krajovykh kvitok soniashnyku (Helianthus annuus L.) [Inheritance of the characteristic apricot color of marginal flowers of sunflower (Helianthus annuus L.)]. Plant Varieties Studying and Protection, 15(2), 118–123 (in Ukrainian).

Vedmedieva, K. V. (2020). Uspadkuvannia oranzhevykh zabarvlen' krajovykh kvitok soniashnyku [Inheritance of the orange colors of marginal sunflower flowers]. Visnyk Lvivskoho Universytetu, Seriia Biolohichna, 81, 41–49 (in Ukrainian).

Vedmedieva, K. V., Makhova, T. V., & Kyrpychova, N. M. (2017). Rezul'tat doboru na krupnoplidnist' u liniji ta sorti soniashnyku [The result of selection for large fertility in the line and variety of sunflower]. Zbirnyk Naukovykh Prats Selektsijno-Henetychnoho Instytutu – Natsionalnoho Tsentru Nasinnieznavstva ta Sortovyvchennia, 29(69), 26–34 (in Ukrainian).

Vedmedieva, K. V., & Makhova, T. V. (2019). Vplyv markernykh morfolohichnykh oznak linij na hospodarski jakosti hibrydiv (Hellianthus annuus L.) [The influence of marker morphological traits of lines on economic qualities of hybrids (Hellinthus annuus L.)]. Scientific and Technical Bulletin of the Institute of Oilseed Crops NAAS, 27, 27–34 (in Ukrainian).

Vedmedieva, K. V., & Nosal, O. O. (2018). Uspadkuvannia oznaky krupnoplidnosti nasinnia soniashnyku (Hellianthus annuus l.) v kombinatsiji skhreshchuvannia L12B kh KP11B [Inheritance of the characteristic of large-fruited sunflower seeds (Hellianthus annuus L.) in the combination of crossing L12B x KP11B]. Scientific and Technical Bulletin of the Institute of Oilseed Crops NAAS, 26, 21–29 (in Ukrainian).

Vedmedieva, K. V., & Nosal, O. O. (2020). Otsinka krupnoplidnykh linij soniashnyku za kil'kisnymy kharakterystykamy morfolohichnykh oznak [Evaluation of large-fruited sunflower lines by quantitative characteristics of morphological traits]. Scientific and Technical Bulletin of the Institute of Oilseed Crops NAAS, 29, 46–55 (in Ukrainian).

Vedmedieva, K. V., Poliakov, O. I., Leus, T. V., Aliieva, O. Y., & Nikitenko, O. V. (2022). Saflor [Safflower]. Ahrarna Nauka, Kyiv (in Ukrainian).

Von Mogel, K. (2013). Taking the phenomics revolution into the field. CSA News, 58, 4–10.

Walter, A., Silk, W. K., & Schurr, U. (2009). Environmental effects on spatial and temporal patterns of leaf and root growth. Annual Review of Plant Biology, 60, 279–304.

Walter, A., Studer, B., & Kölliker, R. (2012). Advanced phenotyping offers opportunities for improved breeding of forage and turf species. Annals of Botany, 110, 1271–1279.

White, J. W., Andrade-Sanchez, P., Gore, M. A., Bronson, K. F., Coffelt, T. A., Conley, M. M., Feldmann, K. A., French, A. N., Heun, J. T., &

Hunsaker, D. J. (2012). Field-based phenomics for plant genetics research. Field Crops Research, 133, 101–112.

Xiao, S., Chai, H., Shao, K., Shen, M., Wang, Q., Wang, R., Sui, Y., & Ma, Y. (2020). Image-based dynamic quantification of aboveground structure of sugar beet in field. Remote Sensing, 12, 269.

Yahlo, M. N. (2007). Markernye priznaki l'na [Marker signs of flax]. Scientific and Technical Bulletin of the Institute of Oilseed Crops NAAS, 12, 86–91 (in Ukrainian).

Yang, S., Zheng, L., He, P., Wu, T., Sun, S., & Wang, M. (2021). High-throughput soybean seeds phenotyping with convolutional neural networks and transfer learning. Plant Methods, 17, 50.

Yang, W., Duan, L., Chen, G., Xiong, L., & Liu, Q. (2013). Plant phenomics and high-throughput phenotyping: Accelerating rice functional genomics using multidisciplinary technologies. Current Opinion in Plant Biology, 16, 180–187.

Yang, Y., Chai, R., & He, Y. (2014). Early detection of rice blast (*Pyricularia*) at seedling stage in nipponbare rice variety using near-infrared hyper-spectral image. African Journal of Biotechnology, 11, 6809–6817.