Ontological Model of Helianthus Cultivation in Ukrainian Conditions

Anna Bakurova[1], Kateryna Vedmedeva[2], Stanyslav Vedmedev[1], Elina Tereschenko[1]

[1] National University «Zaporizhzhia Polytechnic», Zhukovskogo Street 64, Zaporizhzhia, 69063, Ukraine
[2] Institute of Oilseed Crops of the National Academy of Agricultural Sciences, Instytutska Street 1, Soniachne Village, Zaporizhzhia District, Zaporizhzhia Region, 69055, Ukraine

Abstract
The paper presents a subject ontology of agricultural technology for growing sunflowers in Ukraine. Experts from the Institute of Oilseed Crops of the National Academy of Agricultural Sciences were involved in the work. The experts identified Objectives and influencing factors on sunflower yield and formulated issues of ontology competence. The results of the work include the substantiation of the need to create an ontology of sunflower cultivation in Ukraine and its integration into the pan-European community. Based on the results of ontology modeling, it is recommended to use an ontological approach to manage the created data repositories on sunflower cultivation, its selection, genetics, and phenotyping. The ontology was built in the Protégé editor.

Keywords
Ontology, Relations, Protégé, Ontograph, Ontology Quality Evaluation, Sunflower, Agricultural Technology, Selection, Genotype

1. Introduction

Ukraine is a full member of the European community for improving the conditions for maintaining and improving agribusiness technologies. In pre-war 2021, the share of agriculture in Ukraine's GDP was the highest among all sectors of the economy and amounted to more than 10%. Agri-food products also accounted for the largest percentage of Ukraine's total exports - about 41% for 2021 and 53% for the war year 2022 [1]. The contribution of Ukraine is equivalent to the nutrition of about 400 million people, so Ukraine claims to be one of the largest World Food Security guarantors, set as the number two goal of sustainable development of mankind [2]. International cooperation is aimed at the development and improvement of three areas: agricultural technology, breeding and genetics. The international project ECPGR European Evaluation Network (EVA) for Plant Genetic Resources for Food and Agriculture (PGRFA) aims to increase the use of numerous accessions of crops and landraces [3]. It is of strategic importance for Europe and provides an opportunity to promote the sustainable use of PGRFA to promote the adaptation of European agriculture to climate change EVA, creates standardized estimated phenotypic and genotypic data for agricultural plants stored in European genebanks [4]. The retrieval catalog for plant genetic resources (EURISCO) provides passport and phenotypic data on more than 2 million accessions of cultivated plants and their wild relatives held by about 400 institutes. The catalog includes a network of national inventories of 43 member countries [5]. The catalog also includes collections from Ukraine and the Institute of Oilseed Crops of the National Academy of Agricultural Sciences, in particular from the Donor institute code UKR012. Ukraine is an active member of The International Union for the Protection of New Varieties of Plants (UPOV), which unites 75 states. UPOV provides access to the PLUTO Plant Variety Database [6].

COLINS-2023: 7th International Conference on Computational Linguistics and Intelligent Systems, April 20–21, 2023, Kharkiv, Ukraine
EMAIL: email1@mail.com (A. Bakurova); email2@mail.com (K.Vedmedeva); email3@mail.com (S.Vedmedev); email3@mail.com (E.Tereschenko)
ORCID: 0000-0001-6986-3769 (A. Bakurova); 0000-0003-4571-2960 (K.Vedmedeva); 0009-0005-9635-8879 (S.Vedmedev); 0000-0001-6207-8071 (E.Tereschenko)

Large volumes of heterogeneous data create an obvious problem with their active and effective application in practice by farmers, breeders, and scientists. The need to develop common protocols for providing the information is due to the presence of different protocols for fixing the experiments results or describing a culture, a multitude of measurable phenotypic traits, and the dependence of these traits on culture-growing conditions. Accessibility for review and the opportunity to present the research results allows using the already known necessary requirements for the method of storing information.

It is common practice to organize large interconnected arrays of information in the form of ontologies [7]. The purpose of building an ontology is the possibility of obtaining new knowledge and application. For example, in the work [8] the method of intellectual agent action is based on the task field ontologies. This model defines not only explicit but also implicit knowledge. Ontologies serve as a common standard for the semantic integration of a large body of plant genomic, phenomic, and genetic data [9,10], for example, PATO – Phenotype and Trait Ontology [11].

Sunflower culture is among the most important and economically profitable in the world, Europe and Ukraine. This is confirmed by the creation of the INTERNATIONAL SUNFLOWER ASSOCIATION. The goal of the association is to develop research and strengthen national cooperation at the agronomic, technical, and legal levels [12].

This work is devoted to the actual topic of building an ontology of sunflower cultivation and its integration into international information resources. The experts are the Institute of Oilseed Crops of the National Academy of Agricultural Sciences, Ukraine. The purpose of the study is to build an ontological model of sunflower cultivation with a focus on the agricultural technology of sunflower cultivation in Ukraine and to analyze the need of creating such an ontology and its integration into the world agro-ontology system.

2. Related works

The problem of unified collection and provision of diverse and multidimensional information about research in agricultural sciences is solved by creating ontologies. The Planteome project [9] provides a set of reference and species-specific ontologies for plants and annotations for genes and phenotypes [13]. PATO is phenotype and trait ontology, and ontology is the phenotypic quality (properties, attributes, or characteristics) [14]. PATO is based on the phenotype model, which is created by the EQ method, i.e. an appeal to an “entity” that has a “quality” as properties or attributes of an entity [15, 16]. When using the EQ method to describe phenotypes, an object will usually be assigned to a class either by an anatomical ontology or by an ontology of processes and functions, such as GO [17], and the "quality" is taken from PATO. This provides a level of interoperability between these ontologies and facilitates the integration of data annotated to them, as well as the automation of inference. The ability to describe "direct" observations of the phenotype and "comparative" ones has been developed. It is also important that the PATO construction structure allowed information on phenotypes, which is in text publications inaccessible to computer analysis, integrated with information in genetic and phenotypic databases using anatomy and phenotype ontologies [18].

The culture's ontology [11] is based on the metadata schema and is called Minimum Information About a Plant Phenotype Experiment [19, 20]. The conceptual model defines a phenotypic variable as a combination of traits, agricultural practices, and measurement methods. This allows you to create unified protocols for fixing the results of the experiment - field journals. It also allows you to create a description of the results of the study, which can be repeated, to build a model of the reference result of selection work. This model allows you to combine agronomic, morphological, physiological, and qualitative traits and information about research and geodata. Sunflower Ontology [10] is the Crop Ontology part with number 359 contains 351 records of sunflower phenotypes.

Phenotypes are the manifestation of a genotype under certain growing conditions, that is, environmental conditions are necessary to understand the mechanisms leading to the phenotype. In the future, the number of studies about the environment's influence on the phenotype will increase and lead to a deeper understanding of the mechanisms leading to the phenotype [21-23]. To date, the sunflower genome reference has not been constructed. The organization and structure of the sunflower genome are poorlyl understood due to its large size. This hinders the study of sunflowers as a representative of

Compositae, and also complicates the apply molecular approaches to sunflower breeding and improvement [24,25].

It is necessary to link the information of evolutionary and genomic databases, to solve the problems of evolutionary development analysis concerning the genetic basis of evolutionary changes, genetic and evolutionary basis of interrelated traits simultaneously with the process of independent evolution. One of the directions of the research development is the use of information through general phenotypic and anatomical ontologies [26]. The German Crop BioGreenformatics Network (GCBN) as part of the German Network for Bioinformatics Infrastructure (de.NBI) is working in this direction. The mission of this resource is to provide transparent access to germplasm seeds, improve plant gene annotation, and implement bio-informatics services linking genotypes and phenotypes. GCBN integrated data resources that address common research problems in the plant genomics community provide data and software infrastructure [27]. PlabiPD is a central portal provided by FZJ that provides integrated access to plant genomes, protein family data, and protein-coding gene sequences.

The analysis of Related works allows us to conclude that it is necessary to create structured sources of information with the ability to store the scientific results and practical results in the domestic agricultural sector and the ability to integrate into existing European and world data and knowledge banks.

3. Our approach

The most relevant form of organizing the representation of concepts of a certain field of knowledge is an ontology, which contains the basis for modeling this field of knowledge and determines the attitude and agreement on the representation of the theoretical foundations of this field of knowledge. Ontologies are agreements about shared conceptualizations [29]. The ontology is an ordered triple of the form: O=(T,R,F), where T is a finite non-empty set of terms (concepts, notions, classes) of the field of knowledge, which is represented by the ontology O; R is a finite set of relations between the concepts of the field of knowledge; F is a finite set of interpretation functions (axiomatization) defined on the concepts and/or relations of the ontology O. According to [30], ontology design includes the collection of knowledge of the subject area, specification of ontology terms, competence questions formulation, ontology formalization, ontology evaluation, and ontology evolution.

In modern agriculture, there are many opportunities to improve the external growing conditions, taking into account financial possibilities and economic feasibility. Typically, growing conditions include the supply of moisture, minerals in an appropriate mechanical composition, temperature, sunlight, oxygen, and carbon monoxide. By studying collections of specimens with different levels of trait expression due to the internal environment of the plant (genotype), genotypic conditioning can be established. Most scientific studies determine the strength of influence of the factor, including the genotypic one [31]. Thus, based on the results of scientific studies involving a variety of samples, it is possible to obtain information on each sample and each genotype about the strength of influence of this genotype on the manifestation of a particular trait. In sunflower, about 50 genes and trait manifestations have already been identified. In particular, the seed colouring genes are important for the quality of production.

The involvement of experts is a priority compared to the automatic method of ontology construction [32,33]. The experts of the Institute of Oilseed Crops of the National Academy of Agricultural Sciences identified objectives and influencing factors on sunflower yield (fig.1). The sunflower yield (productivity) is affected by a system of factors for the year, for the growing season and the distribution of factors over the growing season and calendar year, as well as the quality of the sunflower plant genotype (variety, hybrid) and adaptability to environmental conditions. In addition, the yield is also affected by soil conditions, climatic conditions, diseases, pests, technologies, and timely control of factors [34].

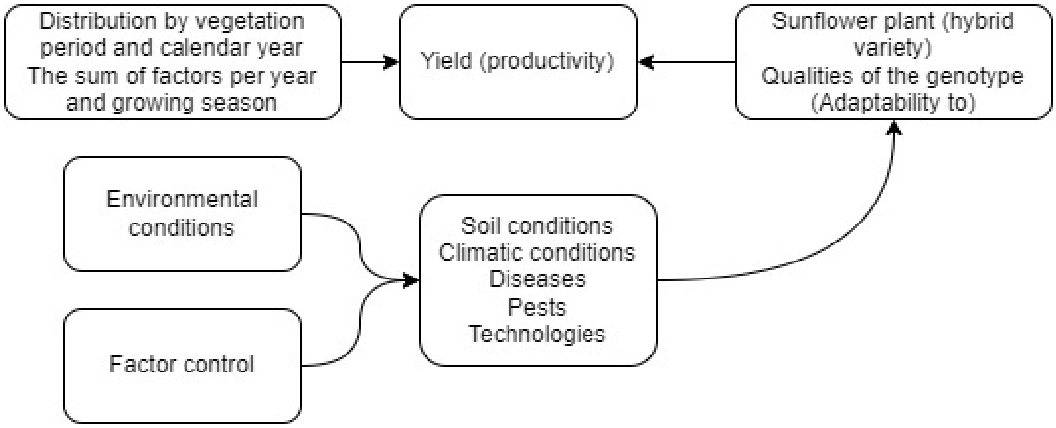

Figure 1: Objectives and influencing factors on sunflower yield

Based on the information provided by the experts of the Institute of Oilseeds of the National Academy of Sciences of Ukraine, at the first step, the subject area of knowledge about sunflower, soil, fertilizers and weather conditions, irrigation technologies, and other agricultural technologies was determined, and the terminological concepts provided by the experts were defined (Table 1). GOST and catalogs of fertilizers, pesticides, herbicides, and technologies were also used [35]. At the second step of ontology building, based on the information determined at the previous step, structures are laid that provides a unified interpretation of terminology by all participants in working with the ontology, namely experts, developers, and users. At this stage, the main classes and subclasses of the ontology were determined on the basis of factors affecting the harvest: soil, climatic conditions, and laboratory research.

Table 1
The influencing factors on sunflower yield

Soil conditions	Climatic conditions	Diseases	Pests	Technology
Mechanical composition of soils (sand, clay, humus, etc.) Chemical composition (major elements (NPK), minor elements (boron, zinc, magnesium, selenium, etc.) Water-holding capacity (aggregate state, colloidality) The living component of the soil (bacteria, worms, symbionts, etc.)	Temperature Precipitation Solar radiation Wind Altitude or latitude	Fake Mildew Plasmopara halstedii Sclerotinia (white rot) Sclerotinia sclerotiorum Phomopsis (stem cancer) Diaporthe helianthi Sunflower rust Puccinia heliantha Coal rot Macrophomina phaseolina Phomosis Phoma macdonaldii Verticillosis (vascular wilt) Verticllium dahliae Alternariosis Alternariaster helianthi, Alternaria zinniae Phomopsis sunflower (Phomopsis helianthi) Fusarium Fusarium species	Barbel or sunflower agapanthia Agapanthia dahli Richt Wireworms: Black boletus Athous niger L Sowing bollard Agriotes sputator L. Sand tarragon Opatrum sabulosum (L., 1758) Sunflower spikenose Mordellistena parvula Gyll. Fruit flies Strautia longipennis Bow butterfly Margaritia sticticalis L	Crop rotation Type of technology (classical, no rear, intensive, herbicide type, irrigation) Available cultivation equipment

	Septoria leaves of Septoria helianthi Bacterial rot (soft rot) Pectobacterium carotovorum, subsp. carotovorum and P. atrosepticum Rhizopus (Gray rot) R. stolonifer, R. oryzae (syn. R. arrhizus) and R. microsporus Powdery mildew Erysiphe cichoracearum Bacterial leaf spot of Pseudomonas syringae pv. Helianthii White rust Albugo tragopogonis / Albugo candida Viral diseases: Ring spot virus, Sunflower foliar mosaic virus Spinning top parasite plant (Orobanche cumana Wallr.)	Thistle Vanessa cardui (Linnaeus, 1758) Leaf-eating cutworms A number of species of the family Noctuidae Sunflower moth Homoeosoma nebullum (Den. and Schiff.)

At the next stage, the model of the subject ontology HELIANTHUS was built in the Protege editor [36], and represented by the ontograph in Fig.2. To determine the three root classes of the ontology, the expert's statement on the main directions of research on sunflower culture at the Institute of Oilseeds, namely: agricultural technology, breeding, genetics, was used. The basic concepts of these directions form subclasses that form the third level of the hierarchy, which correspond to certain types of class diversity. For example, the class "soil" contains three subclasses: "mechanical composition", "chemical composition", and "living component of the soil". In turn, the classes of the lowest level of the hierarchy have a corresponding set of instances, for example, for the class "Mechanical composition of the soil" instances are considered: "sand", "clay", and "humus". All classes are disjoint, which follows from the definitions of the basic terms. The experts emphasized the need for such a factor as the timely implementation of agrotechnological processes. It is important to note that the definition of "on time" can take place according to different indicators, namely soil temperature, solar activity level, start of vegetation, the prevention of pests and diseases, and the total amount of precipitation for a certain period.

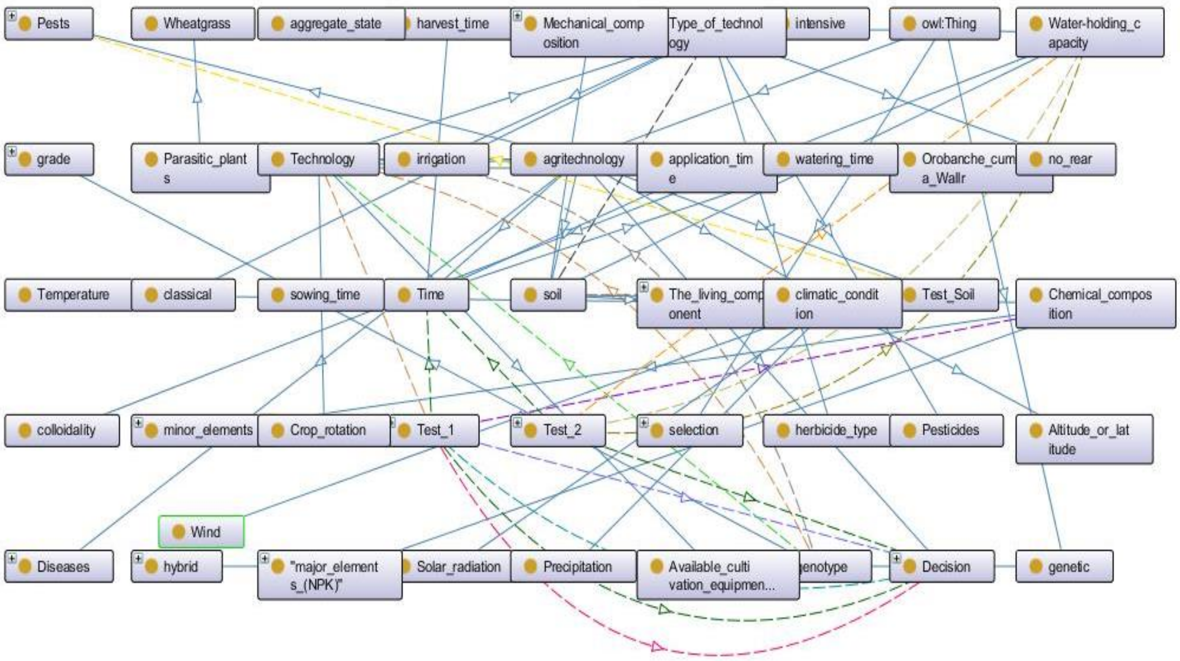

Figure 2: Ontology graph HELIANTHUS

Therefore, we introduce the "Time" class into the ontology, which has subclasses related to the main issues of growing practitioners (farmers) who seek advice from the institute's employees from different regions of Ukraine. The example of presenting the main results of ontology development is shown in Fig. 3.

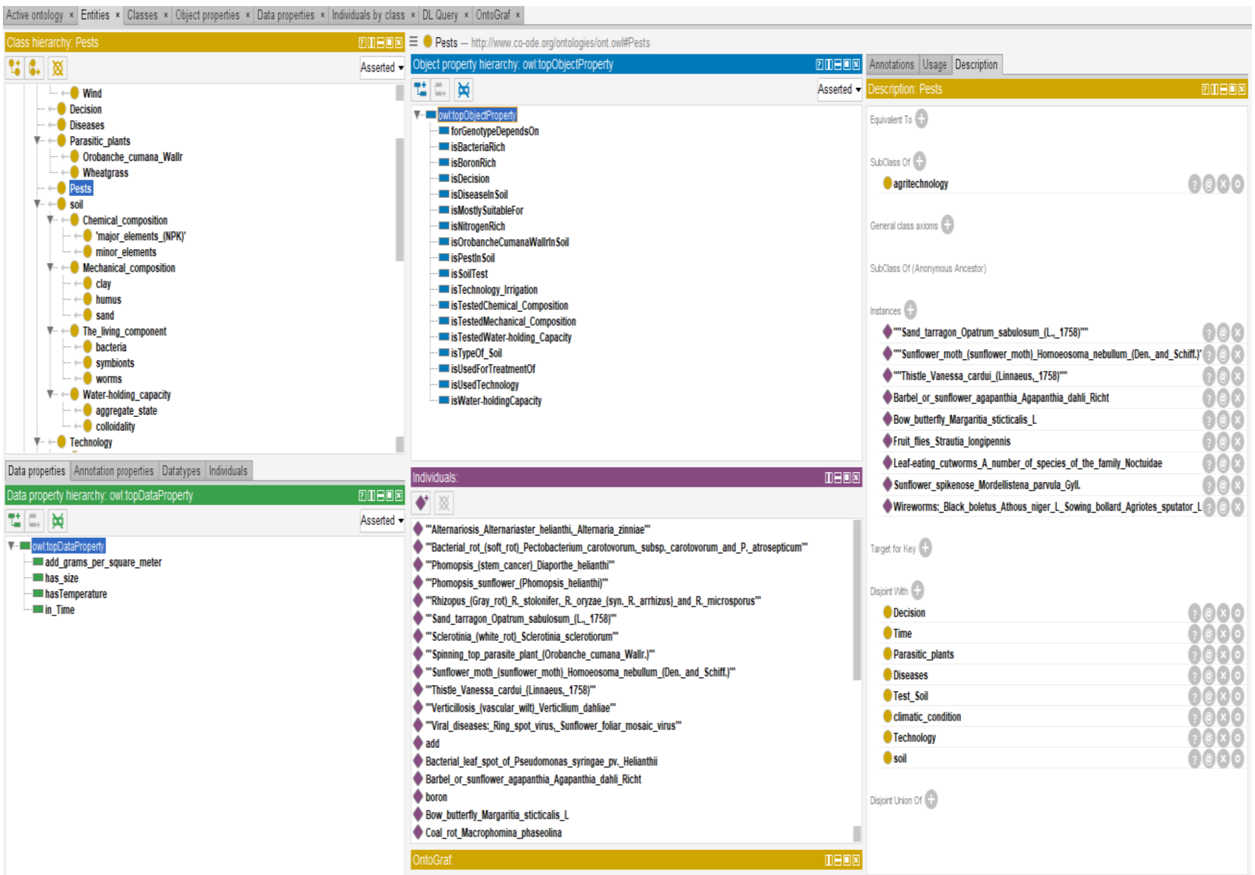

Figure 3: The example of presenting the main results of HELIANTHUS ontology development

The ontologies are created for further use in decision support systems and should allow to contain nested and form new knowledge that meets the needs of users. To ensure semantic content between the components of the ontology, the corresponding relationships are set, partially shown in Table 2.

4. Experiments: ontology quality evaluation

We have two types of ontology quality evaluation and reliability assessment: semantic evaluation is based on competence questions formulated by an expert, and structural evaluation is quantitative metrics of the ontograph.

The assessment of the semantic quality of the ontology was carried out with experts, as a result of which many competency-based questions were formulated [32]. The first column of Table 2 gives an informal expert representation of the questions, the second column gives a formal representation using ontology class names and using first-order predicate logic, and the last column lists the relationships between classes in queries.

Table 2
What should I do to get the best sunflower crop in my field?

Competence questions (informal)	Competence questions (formal)	List of Relations
How can you determine the state of soil fertility for the sunflower crop?	There exists Time t AND exists Soil Test y (1m–1.5m) for any Soil Sample x AND Chemical Composition (NPK or minor elements (boron, zinc, magnesium, selenium, etc.)) and Water-holding Capacity (aggregate) state, colloidality) OR Living Component soil (bacteria, worms, symbionts, etc.) OR Mechanical Composition of soils (sand, clay, humus, etc.), then the decision is made Decision d about Application YES / NO and Time t	isSoilTest(y,x); isTestedChemical_Composition (x,y); isTestedWater-holding_Capacity(x,y); isTestedMechanical_Composition(x, sand, clay, humus); isDecision(Application, Time t)
How much and when to apply fertilizers per hectare of sunflower?	There exists Decision d AND exists Fertilizer f for any Sunflower s AND exists Soil Test y (1m–1.5m) for any Soil Sample x AND Chemical Composition (NPK or minor elements (boron, zinc, magnesium, selenium, etc.)) AND Living Component soil (bacteria, worms, symbionts, etc.), then the amount of litter or the amount of NPK or the amount of urea.	isNitrogenRich(f, y); isBoronRich(f, y); isBacteriaRich(f, y); isMostlySuitableFor(f, y)
Should I water the sunflower?	There is Time t AND exists Soil Test y (1m–1.5m_ (y) AND Water-holding capacity (aggregate state, colloidality) OR Mechanical composition of soils (sand, clay, humus, etc.), then Irrigation Technology w	isTypeOf_Soil(Loam ∨ Clay ∨ Sandy, x); isWater-holdingCapacity (aggregate_state,colloidality); isTechnology_Irrigation(w,x)
When and with what to treat from pests?	There is a pest z and there is a Genotype G and a pesticide p such that include pest z species x and Time t, as well as Pesticide treatment p and there is a technology Agricultural chemical treatment with pesticide p	isPestInSoil(z,x); forGenotypeDependsOn(G,z); isUsedForTreatmentOf (G,p)

When and how to treat diseases?	There is disease w AND there is Genotype G AND Pesticide p including Disease w and TIME t and Pesticide treatment p and there is a technology Agricultural chemical treatment with Pesticide p then Pesticide p is used to treat Disease w.	isDiseaseInSoil(w,x); forGenotypeDependsOn(G,w); isUsedTechnology(G,p)
How to get rid of Orobanche cumana Wallr in sunflower crops?	There is a parasite Orobanche cumana Wallr (OCW) and Genotype G with the trait resistant to Orobanche cumana Wallr, then do not process OR There is a parasite Orobanche cumana Wallr. AND Genotype G with trait resistant to Orobanche cumana Wallr AND resistant to Herbicide g and Time t AND there is a technology Agricultural chemical treatment with Herbicide g, then treat Herbicide g OR There is a parasite Orobanche cumana Wallr. AND Genotype G with the trait resistant to Orobanche cumana Wallr AND TIME t, then Technology CropRotation is resistant to Orobanche cumana Wallr	isOrobancheCumanaWallrInSoil(OCW,x); forGenotypeDependsOn(G,OCW); isUsedTechnology((G,g)(G,Crop rotation))

The presented results of the formalization of competency issues were studied and confirmed by experts in this field.

To perform a structural evaluation of the constructed HELIANTHUS ontology, we compare its structural estimates with the average and median values for existing OWL ontologies, according to the source [32], and the same structural estimates for the SUNFLOWER ontology with number 359 in [10] (Table 3). The SUNFLOWER ontology includes 273 classes and 81 classes in the HELIANTHUS ontology with an average value of 36 and a median of 6. The numbers of first-level superclasses are 8 and 3, respectively, with the median value of 5 and the average of 6.69 for existing OWL ontologies. The number of individual object properties are 353 and 36, respectively, with the median value of 6 and the average of 28.13 for existing OWL ontologies. The ontology schema deepness is a measure of reliability and is calculated as the ratio of the number of subclasses to the total number of classes. Depths of 0.98 for SUNFLOWER and 0.96 for HELIANTHUS characterize ontologies as deep. Therefore, metric estimates confirm the reliability of the proposed ontology. Summarizing the results of the analysis of the received evaluations, we emphasize that the proposed ontology is in the development stage and certain classes will be filled when working with expertise.

Table 3
Comparison of structural scores with average and median values of existing OWL ontologies and SUNFLOWER ontology and HELIANTHUS ontology

Structural metrics	Average	Median	SUNFLOWER	HELIANTHUS
Number of classes	36.11	6	273	81
Number of individuals	28.13	6	353	36
Number of root classes	6.69	5	8	3
Schema deepness	0.34	0	0.98	0.96

5. Discussions, Conclusions and Further Research

The scientific achievement is the creation of an ontological model of the subject branch of sunflower cultivation in Ukraine. The experience of national experts in breeding, genetics, and agricultural technology of sunflower cultivation, as well as the state standards of Ukraine, were taken into account. The ontological model allows further integration of national resources and knowledge bases in this area, as well as the development of a unified presentation of the results of scientific research and experiments. The practical value lies in expanding the possibilities of collecting experimental data, extracting new knowledge, promptly consulting practitioners, and integrating into the global scientific community. With large collections of national and global genebanks and their agricultural value, there is a problem with the systematic application of these genetic resources due to the lack of phenotypic information about individual accessions, which is necessary to assess variability at the trait level. It is this information that the Institute of Oilseed Crops of the National Academy of Agricultural Sciences collects. Therefore, integration into international systems may become a necessary link in the comparison of phenotypic observations between different laboratories or different species [26]. The first step towards this goal is the creation of a common vocabulary in the form of standardized ontologies describing the nuances of phenotype and environmental data, and the development of new methods for the automatic combination of phenotype and genotype, which will allow more complex models to be built for users. All this implies the evolution of ontology, in particular, in connection with the emergence of new varieties and hybrids, with phenotyping.

In the course of the study, it was found that the representation of knowledge embedded in questions of competence faces the task of formalizing poorly structured concepts and fuzzy relationships. The solution of this problem constitutes the next stage of research and development of ontological approaches in decision support.

6. Acknowledgement

The work was performed as part of the research work "Mathematical modelling of socio-economic process and systems", registration number SR 0121U113264, in the Department of System Analysis and Computational Mathematics of National University "Zaporizhzhia Polytechnic", Ukraine.

7. References

[1] Ministry Of Agrarian Policy And Food Of Ukraine, 2022. URL: https://minagro.gov.ua/.
[2] Our Work on the Sustainable Development Goals in Ukraine. URL: https://ukraine.un.org/uk/sdgs.
[3] The European Cooperative Programme for Plant Genetic Resources (ECPGR). URL: https://www.ecpgr.cgiar.org/.
[4] The ECPGR European Evaluation Network (EVA) for Plant Genetic Resources for Food and Agriculture (PGRFA) URL: https://www.ecpgr.cgiar.org/european-evaluation-network-eva.
[5] The European Search Catalogue for Plant Genetic Resources (EURISCO). URL: https://eurisco.ipk-gatersleben.de/apex/eurisco_ws/r/eurisco/home.
[6] The International Union for the Protection of New Varieties of Plants (UPOV). URL: https://www.upov.int/portal/index.html.en.
[7] A. Ch. Khadir, H. Aliane, A. Guessoum, Ontology learning: Grand tour and challenges, Computer Science Review,Volume 39 (2021). URL: https://doi.org/10.1016/j.cosrev.2020.100339.
[8] V. Lytvyn, D. Dosyn, V. Vysotska, A. Demchuk, L. Demkiv and I. Lytvyn, Intellectual Agent Construction Method Based on the Subject Field Ontology, in: 15th International Conference on Computer Sciences and Information Technologies 2020 (CSIT), Zbarazh, Ukraine, 2020, pp. 40-46. doi: 10.1109/CSIT49958.2020.9322032.
[9] Planteome. URL: http://www.planteome.org.
[10] Crop ontology for agriculture data. URL: http://www.cropontology.org.
[11] PATO - the Phenotype And Trait Ontology. URL: https://www.ebi.ac.uk/ols/ontologies/pato.
[12] International Sunflower Association. URL: https://www.isasunflower.org/about-us/statutes.

[13] L. Cooper, A. Meier, M. A. Laporte, J. L. Elser, C. Mungall, B. T. Sinn, D. Cavaliere, S. Carbon, N. A. Dunn, B.Smith, B. Qu, J. Preece, E. Zhang, S. Todorovic, G. Gkoutos, J. H. Doonan, D. W. Stevenson, E. Arnaud, & P. Jaiswal, The Planteome database: an integrated resource for reference ontologies, plant genomics and phenomics. Nucleic acids research, 46(D1), D1168–D1180 (2018). https://doi.org/10.1093/nar/gkx1152.
[14] RL. Walls, L. Cooper, J. Elser, et al. The Plant Ontology Facilitates Comparisons of Plant Development Stages Across Species. Front Plant Sci. 10:631 (2019). doi:10.3389/fpls.2019.00631.
[15] C. Mungall, G. Gkoutos, C. Smith, et al. Integrating phenotype ontologies across multiple species. Genome Biol 11, R2 (2010). https://doi.org/10.1186/gb-2010-11-1-r2.
[16] A.E. Thessen , R.L. Walls , L. Vogt , J. Singer, R Warren , et al. Transforming the study of organisms: Phenomic data models and knowledge bases. PLOS Computational Biology 16(11): e1008376(2020). https://doi.org/10.1371/journal.pcbi.1008376.
[17] P.D.Thomas, , D.P Hill,., H. Mi, et al. Gene Ontology Causal Activity Modeling (GO-CAM) moves beyond GO annotations to structured descriptions of biological functions and systems. Nat Genet 51, (2019) 1429–1433. https://doi.org/10.1038/s41588-019-0500-1.
[18] P.M. Mabee, M. Ashburner, Q. Cronk, et al. Phenotype ontologies: the bridge between genomics and evolution. Trends Ecol Evol 22(2007) 345–350. doi: 10.1016/j.tree.2007.03.013.
[19] Minimum Information About Plant Phenotyping Experiments, 2019. URL: https://www.miappe.org/.
[20] Pommier C, Michotey C, Cornut G, et al. Applying FAIR Principles to Plant Phenotypic Data Management in GnpIS. Plant Phenomics.(2019):1671403. doi:10.34133/2019/1671403.
[21] M.Ringwald, J.E Richardson, R.M. Baldarelli, et al. Mouse Genome Informatics (MGI): latest news from MGD and GXD. Mamm Genome 33, 4–18 (2022). https://doi.org/10.1007/s00335-021-09921-0
[22] D. Arend, et al. . From Genotypes to Phenotypes: A Plant Perspective on Current Developments in Data Management and Data Publication. In: Chen, M., Hofestädt, R. (eds) Integrative Bioinformatics. Springer, Singapore (2022). https://doi.org/10.1007/978-981-16-6795-4_2.
[23] P. Larmande, K. Todorov, Revealing Genotype–Phenotype Interactions: The AgroLD Experience and Challenges. In: Chen, M., Hofestädt, R. (eds) Integrative Bioinformatics. Springer, Singapore (2022): 321–342. https://doi.org/10.1007/978-981-16-6795-4_16.
[24] C. Ranathunge, M.E Chimahusky, M.E Welch,. A comparative study of population genetic structure reveals patterns consistent with selection at functional microsatellites in common sunflower. Mol Genet Genomics 297, (2022) 1329–1342. https://doi.org/10.1007/s00438-022-01920-3
[25] Joon Seon Lee, Mojtaba Jahani, Kaichi Huang, J.R. Mandel, L. F. Marek, J. M. Burke, N. B. Langlade, G. L. Owens, L. H. Rieseberg, Expression complementation of gene presence/absence polymorphisms in hybrids contributes importantly to heterosis in sunflower, Journal of Advanced Research,V. 42 (2022) 83-98. https://doi.org/10.1016/j.jare.2022.04.008.
[26] M Kulmanov , R Hoehndorf DeepPheno: Predicting single gene loss-of-function phenotypes using an ontology-aware hierarchical classifier. PLOS Computational Biology 16(11): e1008453(2020). https://doi.org/10.1371/journal.pcbi.1008453.
[27] M. Oppermann, St. Weise, M. Lange, M. Spannagl, B. Usadel, K.F.X. Mayer, U. Scholz, Bioinformatics in the plant genomic and phenomic domain: The German contribution to resources, services and perspectives, Journal of Biotechnology, Volume 261 (2017) 37-45, https://doi.org/10.1016/j.jbiotec.2017.07.006.
[28] E. H. Mahood, L. H. Kruse, G. D.Moghe,. Machine learning: A powerful tool for gene function prediction in plants. Applications in Plant Sciences 8(7), e11376 (2020). https://doi.org/10.1002/aps3.11376
[29] Thomas R. Gruber,Toward principles for the design of ontologies used for knowledge sharing?,International Journal of Human-Computer Studies,V. 43, Issues 5–6(1995) 907-928, https://doi.org/10.1006/ijhc.1995.1081.
[30] E.F. Aminu, I.O. Oyefolahan, M.B. Abdullahi, M.T. Salaudeen, A review on ontology development methodologies for developing ontological knowledge representation systems for

various domains, in: International Journal of Information Engineering and Electronic Business, 12 (2) (2020), pp. 28-39, 10.5815/ijieeb.2020.02.05.
[31] K. Vedmedeva, Genetic affinity of sunflower lines and cluster analysis by morphological traits, Helia 43, no. 73 (2020): 113-122. doi: 10.1515/helia-2020-0014.
[32] E. F. Aminu, I. O. Oyefolahan, M. B. Abdullahi, M. T. Salaudeen, MaCOnto: A robust maize crop ontology based on soils, fertilizers and irrigation knowledge, Intelligent Systems with Applications, Volume 16(2022). https://doi.org/10.1016/j.iswa.2022.200125.
[33] Rafal Rzepka, Daiki Shirafuji, Akihiko Obayashi, Limits and Challenges of Embedding-based Question Answering in Export Control Expert System, Procedia Computer Science, V. 192(2021) 2709-2719.https://doi.org/10.1016/j.procs.2021.09.041.
[34] V. S. Kudrina, Formation of sunflower productivity depending on the elements of cultivation technology in the Southern Steppe of Ukraine (Agricultural Sciences) Ph.D. thesis. - Mykolayiv National Agrarian University of Ministry of Education and Science of Ukraine, Mykolayiv, 2021.
[35] Soil quality, 2004. URL: https://zakon.isu.net.ua/sites/default/files/normdocs/dstu_4362_2004.pdf
[36] A free, open-source ontology editor and framework for building intelligent systems, 2020. URL: https://protege.stanford.edu/