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DECIPHERING THE NEW-AGE INNOVATIVE TECHNOLOGIES FOR FUTURISTIC BREEDING & GLOBAL FOOD SECURITY

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ABSTRACT

Sustainable agriculture and global food security are the two important concerns of the mankind. The elaborate understanding of emerging bio-physical, biochemical and bio-computational technologies could assist the agriculturist to achieve sustainable future. In the present paper the innovative technologies presented in 39 research publications were extracted by application of Voyant tools. The discoveries highlighting automates seed germination, soil-health monitoring devices, bench mark HSP database, cell-free disease detection, 3D-nano-needles, infra-red thermal imaging, machine driven mass spectroscopy, AI-integrated precision breeding and customized crop-web interface were discussed with an aim of using those technologies in enrichment of current agricultural scenario of the world. The innovative technologies could be integrated by the researchers for cropimprovement program.

Keywords: innovative technologies, precision breeding, thermal imaging, voyant tool

Introduction:

The genetic material nucleic acid applies a four letter alphabet for the genesis of a complex life-form on earth. The linear nucleic acid as ruler depended on cellular soldiers known as proteins for the construction of our vast three dimensional worlds. The twenty letter alphabet of amino acids with the property of folding and association executes the order given by the nucleic acid. The plethora of phenotypes accounted by different life forms are reflection of the genetic code decoded by cellular protein synthesizing machinery known as ribosome present inside the cytoplasm along with diverse forms of ribonucleic acids. On the contrary, Machine language operates on the basis of numerical codes understood by the CPU of machines. Assembly language is one order higher than machine language that uses short mnemonic codes for instructions and allows the programmer to introduce names for blocks of memory that holds the data. Algorithmic languages are designed to express mathematical or symbolic computations. They can express algebraic operations in notably similar manner as mathematics and allow the use of subprograms that are commonly provided by the package for operations. In trans-disciplinary field of bio-computation a cognizance about both genetic code and programme code is required for successful development of a novel tool.

The discovery of central dogma involving the interplay of DNA, RNA and protein and decoding of the genetic code in biological science was the basis in the delicate designing of Omic computational tapestry by interweaving the threads of biological and machine language. The availability of huge amount of wet laboratory research data in public domain with simultaneous progress in theoretical computer modelling led to the emergence of trans-disciplinary study of bio-computation. The plant biologist with lesser knowledge of computer programming prefers a graphical display based systemic operations for their daily research compared to the bioinformatics experts (Bartocci and Lio, 2016).

At the beginning, the available standard algorithmic techniques were adopted by computational biologists while dealing with biological problems but later an intricate insight into biological systems improved the extant algorithms (ChellyDagdia et. al. 2021). The designing of a biological model is equivalent to developing a computer program for the operation of a toy. The syntax of the language defines the ways of combining symbols to create well-formed sentences or instructions. In bio-computational system the model development integrates experimental data, research questions and process calculus or rule-based system to develop a complete model with workflow integration and final output generation (Liu et al. 2019). The dynamic recent advances in omic field research has generated huge amount of wet laboratory data that could be explored by the scientists before initiation of their research. The genomic complexity of the higher organisms with presence of huge amount of quantitative phenotypes in biological world has opened a new area where integration of machine language with genetic algorithm could develop predictive phenotypic models. The enormous demand of the biologists for integration of the modelling approach in experimental studies motivated the computer engineers to critically thinking about the enrichment of the sector. This need has changed in the pattern of strings in dry lab leading to discovery of new algorithm for the wet biologists.

In the field of omic studies the intimidating challenges were solved by the introduction of representative discoveries including Smith–Waterman algorithm for local sequence alignment, the Lander–Waterman model for physical mapping, and the De Bruijn graph approach for sequence assembly (Pavzner et. al. 2022). These models in an inclusive manner assisted the biologists to crack complicated genome intricacies. In this paper an attempt is taken to highlight the most prominent discoveries of computational biology that could assist the beginner's from the computer science background to identify the most important areas were programming could be implemented for developing new models for future crop security of the world. Additionally attempt is taken to simultaneously identify the gaps in the trans-disciplinary research domain where future research could be focused for improvement in the field of synthetic biology. The application of computational algorithm and software in plant science has augmented the agriculture sector. The computational method has played a vital role in the integration of vast amount of data as well as comparison of diverse plants and their metabolic pathways in less time. The discovery of a gene in one plant expanded the horizon for application of the same information for unique discoveries in all associated species.

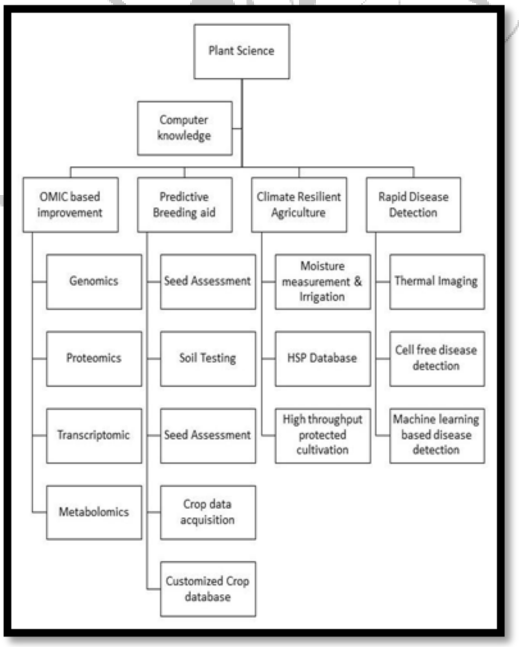

Fig 1: Bio-computational applications utilized for multiple sector of agricultural research

Method:

In this paper a data-mining was done on the available information on computational biology papers covering last 30 years. The search was categorized into three timelines 1992-2002, 2003-2013 and 2014-2023. 50 papers were initially screened under each category with a search tab using computational biology + application + translational research in

Google Scholar. The text-mining was done with the application of voyant tool (https://voyant-tools.org/) for selection, screening of the papers with apparent relevance with the domain of the manuscript. In each segment the most relevant and prominent research papers were screened on the basis of their abstract and key words. The research papers with seminal bio-computational findings were included for further study with selective liquidation of redundant papers, grey articles, news reports. During this selection the authentication of the papers were made involving other robust academic web platform (ResearchGate, Springer, PLOS, MDPI, Agricola, Biocola, ARCC) web platform. Research paper with full text was selected, read, examined for generation of metadata for developing this article.

Fig 2: Text mining of bio-computational papers with the application of Voyant Tool for making the inventory for systematic review

Result and Discussion: The hybridization of plant science and computational biology has given rise to new resource computational-botany with appreciable benefit to the human life. The performance of a plant essentially depends on its internal structure and the environment on which it is being grown. The exogenous factors including agronomic, ecological and environmental dynamics modulate the function of a plant. The endogenous factors involving the omic interface intrinsically harmonize the overall performance of a plant. The evolution of computer and enrichment of virtual research database has made the plant science research more liberal with substantial applicability of the computational models and software in better crop management practices. Furthermore, the cutting-edge molecular research strengthens advance breeding approaches. The pioneering discoveries in the field of soil performance, seed germination, thermal imaging, disease database, nano-injecting devices and AI based predictive breeding create equivalent influence in acceleration of agricultural research. In future the advancement of innovations in the field of soil-science, ecological modeling and environmental kinetics could play pivotal role in assessment of plant performance in unstable climatic condition. A precise plant-computational research requires precise understanding of the critical inventions of the field. The *prima facie* research findings having significant influence in futuristic plant biological sectors were selected and discussed in the subsequent paragraphs.

Table 1: The prominent bio-computational research relevant to the improvement of agricultural research ensuring futuristic applications

Sl No.	Field	Advancement	Paper Title	Year	Reference
1	Soil analysis	Soil engineering software	LoRaWan- IoT based soil health tool	2021	Ramson et. al. 2021
2	Automated germination kinetics	Seed screening software	Seed Screen: Automated phenotyping system with real time imaging and software assisted calculation of germination kinetics	2021	Merieux et. al. 2021
3	Climate resilience	Benchmark HSP database	Recent Advances in Machine Learning Methods for Predicting Heat Shock Proteins	2019	Chen Wei et. al. 2019
4	Biotic Stress	Customized Disease database	Transforming big data into computational models for customized disease detection	2010	Pradhan et. al. 2010, Soroushmehr & Najarian, 2016
5	On-spot disease detection	Cell free disease detection	PLANT-Dx: A Molecular Diagnostic for Point-of-Use Detection of Plant Pathogens	2019	Verosloff et. al. 2019
6	Yield forecast	Automated infra-red Thermal imaging	A non-destructive adjunctive enthalpimetric screening tool	2015	Barin et al. 2015
7	Bio-sensor	3DNano needle	Simulation and fabrication of a new novel 3D injectable biosensor for high throughput genomics and proteomics in a	2013	Esfand yarpour et. al. 2013

			lab-on-a-chip device		
8	Metabolome Analysis	Machine driven Mass Spectroscopy	Machine Learning Applications for Mass Spectrometry-Based Metabolomics.	2020	Leibal et. al. 2020
9	AI based plant breeding	Precision breeding	iGEP: Smart breeding driven by big data, artificial intelligence, and integrated genomic-environmic prediction	2022	Xu et. al. 2022
10	Dynamic crop web interface	Customized database	OrysPSSP: a comparative platform for small secreted proteins from rice and other plants	2012	OrysPSSP, 2012

1. **Influence of Soil Health software:**

The crop environment relationship is the most important tool in assessment of the ultimate performance of a plant. The plant performance has direct relation with the soil in which it is being grown and the subsequent intake of water and diverse nutrients by the plant. The assessment of soil health before the crop planning provides idea about the varietal selection and subsequent forecast about resource management, labor engagement, investment and ultimate production. Multiple soil specific software provides information about various aspects of soil related parameters automatically along with an accurate calculation of the cost-benefit ratio of crop cultivation. SWRC is a basic software used for a long period of time for detection of soil water retention capacity of the soil (Dourado-Neto et. al. 2000). Likewise SOILPAR2 is a programme useful for soil data storage and hydrological analysis of soil (Acutis and Donatelli, 2003). Several field scale software such as LEACHC, SWAP, SOWACH, HYDRUS and UNSATCHEM were appreciated and applied by the soil engineers for detection of soil parameters and downstream decision making (Mondal et. al. 2022). The progress in soil health analysis has led to the development of an innovative software LoRaWAN (Ramson et. al. 2021). Likewise, PARIO software could be used for soil texture analysis. It assists in the analysis of particle size, porosity, charge, bulk density, crystallinity, powder flow, water-solid interaction and determination of sorption, desorption isotherms. Diverse soil centric software played crucial role in the cropping pattern determination, farm performance estimation and mitigation of abiotic stresses with optimization of crop production.

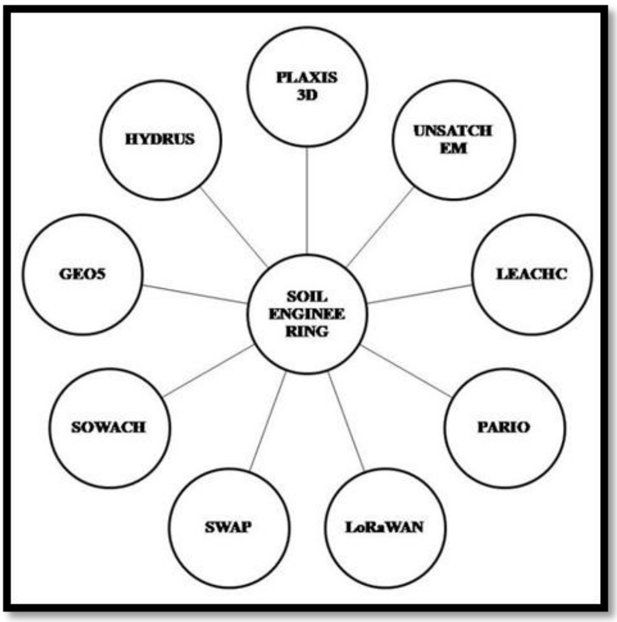

Fig 3: Software related to soil engineering and health monitoring

2. **Automated Seed Technology:**

In agriculture the genetic purity and pathogen-free seeds are the basis for successful cultivation and production. The food security of the rising global population depends on the performance of the seed industry. The global seed industry is depending on the automated technologies for monitoring of germination kinetics and germination related metrics. The examination of physio-biochemical kinetics of germinating seeds and their response to external stimuli is essential for the assessment of seed lots collected from vast and multiple places. The automation of these standard techniques could rapidly validate the quality of the newly introduced varieties with comparison to local check varieties. Jacobson germination table, Germinator, SeedGerm software integrates computer vision in monitoring germination kinetics of sprouting seeds. Another advanced technology is presented by ScreenSeed that enables high-throughput screening of germination kinetics of large number of seeds at a time. The ScreenSeed technology facilitated with pipetting robots notably increases the efficiency of screening of large amount of chemical libraries and subsequent identification of new seed treatment or priming agents (Merieux et. al. 2021). Additionally some new technologies support monitoring of seed rate in large-scale sowing in large area. An effective method for seed rate determination at field level was conducted by integration of a high-speed camera software with another software for estimating the efficiency of an electric-driven variable seed-planter (Mangus et. al. 2017). In recent times precision farming is aided with deep learning for direct estimation of seed yield. Mask-R-CNN could be utilized for seed yield prediction in spinach plants involving two phenotypic variables, plant area and canopy coverage with the number of harvested seeds and seed weight. The research was able to interpret 77.4% of the variation expressed in thousand seed weight on the basis of number of plants. Mask-RCNN trained with UAV images and orthomosaic tiles has evolved as an effective algorithm for ultimate spinach plant calculation and prediction of seed yield. This kind of algorithm could be effective for seed companies for prediction of cost: benefit ratio (Ariza-Sentis et. al. 2023). Customized seed software may assist in the future food security of the world.

3. **Abiotic Stress Management (Bench Mark Dataset for HSP):**

The seeds after germination produce tender seedlings that encounter several biotic and abiotic stresses. In this process the performance of the plants under climatic atrocities is regulated by the presence and performance of the heat shock proteins (HSP). The Heat Shock Proteins not only play a pivotal role in protein folding and stability but it also assist in detection of some diseases and survival of plants under biotic and abiotic stresses.The Heat shock protein information resource (HSPIR http://pdslab.biochem.iisc.ernet.in/hspir/) contains 9902 manually curated proteins covering 277 genomes and sHSPdb (small Heat Shock Proteins database). The website http://forge.info.univangers.fr/~gh/Shspdb/index.php) provides information about sHSP from all kingdom with 4800 curated sHSP for the development of Bench Mark Dataset for HSP. The efficient BenchMark dataset was able to decrease the sample redundancy problem by application of CD HIT program with removal of HSPs with pairwise sequence identity ≥40% in HSPIR. This dataset has been used to train computational models for classifying the six major families of HSPs.HSPMdb is also another manually curated database of web-accessible Hsp modulator with 10,223 entries extracted from 176 research articles. The database provides idea about the enzymatic and cellular activity of the modulators with information on chaperone biology and protein mis-folding associated diseases. HSPMdb is freely accessible at http://bioinfo.imtech.res.in/bvs/hspmdb/index.php. HSP family is essential for response to environmental stresses and maintenance of cellular homoeostasis. The ir-HSP is recommended as an improved proteome based web interface aided with auto-correlation feature and Support Vector Machine (SVM) based prediction feature. The software is able to differentiate HSP from non-HSP more accurately and classify diverse J-proteins. A robust HSP database is important for designing experiments related to plant stress. Additionally, the resource could effectively predict HSPs found in other organisms. In humans the defective protein folding leads to neuro-degenerative diseases Alzheimer's, Parkinson's as well as cancer and cardio-vascular problems (Meher et. al. 2018). This Swissprot based web server is freely accessible at http://cabgrid.res.in:8080/ir-hsp, with 97% accuracy to classify HSPs, 94% for DNAj and overall efficiency of 84% with its bench mark datasets. The knowledge of HSP is essential in climate resilient breeding strategies. The development of new HSP specific dedicated software with regular data integration and enrichment will assist plant scientist in futuristic agricultural research.

Table 2: Heat Shock Protein present in important crops of the world (NCBI)

Organism	Gene	Protein	Nucleotide	Protein Structure
Rice	197	8227	2047	6
Wheat	542	3076	892	2
Maize	164	1723	523	0
Oat	38	86	459	0
Ragi	0	21	2	0
Soybean	148	4098	1341	0
Groundnut				
Pearl millet	0	30	38	0
Chickpea	69	3621	345	0
Pea	233	703	386	2
Mung	0	1763	81	0
Kidney bean	52	176	92	0
Lentil	4	11	6	0
Sunflower	197	2291	500	0
Mustard	93	340	151	0
Rapeseed	0	337	18	0
Olive	203	694	527	0
Cotton	315	2275	1184	0
Jute	0	234	44	0
Coconut	2	140	36	0
Palm	202	1371	873	0

4. Biotic Stress Mitigation (Customized Disease Database):

The biological organisms suffer from challenges from their own domain. The plant community experiences several threat from multiple biotic factors. In human specialized databases are available for several diseases. Though the data sharing on diseases remain incomplete due to scarcity of information on published and reported cases and creates gap in holistic disease management. In case of humans several fragmented repositories are available such as the Alzheimer's database maintained by the National Alzheimer's Coordinating Center (NACC). NACC developed a robust database of patient information collected from the 29 Alzheimer disease centers (ADCs) funded by the National Institute on Aging. The network is maintained by the advanced networking system of Oracle (Beekly et. al. 2004). Indian Genetic Disease Database (IGDD) is an integrated and curated repository of reported genetic mutations leading to diseases in the Indian population. IGDD navigated through three major query options: (a) disease category, (b) disease name and (c) gene name. IGDD(1.0) covers 52 genetic diseases entries and 63 related genes collated from 123 reports (Pradhan et. al. 2010). DiseaseMeth version 2.0 is an oncogene repository covering a major expansion and update of the human disease methylation database.

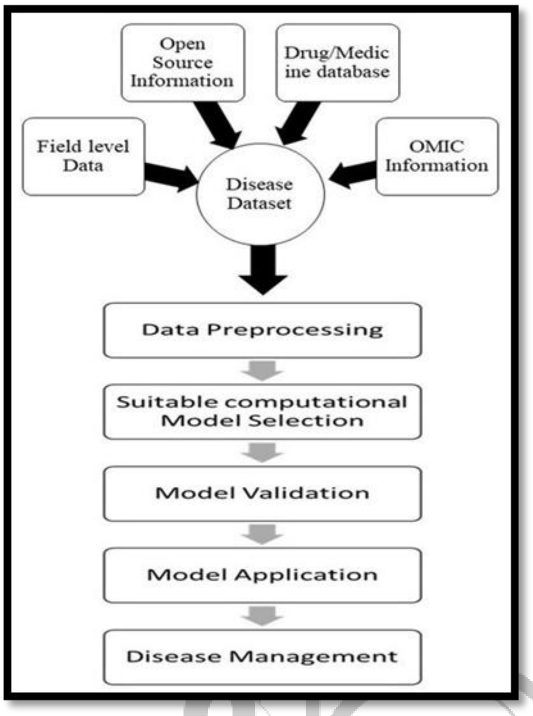

Fig 4: Development of advance disease management system

In plants the available information on global diseases are scanty and opportunities lies in construction of curated databases. In potato a study was done on the construction of a capsule network database including diverse species of potato with association of pre-trained CNN models. Coloured images of diseased and non-diseased leaves were extracted from Plantvillage database. The model acts with 91.83% accuracy involving pre-trained transfer learning models such as ResNet18, VGG16 and GoogleNet. A Multi-level CapsNet based algorithm in horticultural crop was found useful in early detection of diseases with 98.5% accuracy in disease characterization (Janakiramaiah et. al. 2021). Similar type of network is used in peanut (Dong et. al. 2019), DenseNet-121 for apple leaf disease detection (Zhong and Zhao, 2020), SVM model for major disease detection in alfalfa (Qin et. al. 2016). The information may help the farmers in adoption of IPM practices and accurate calculation of budget before initiating a farming business.

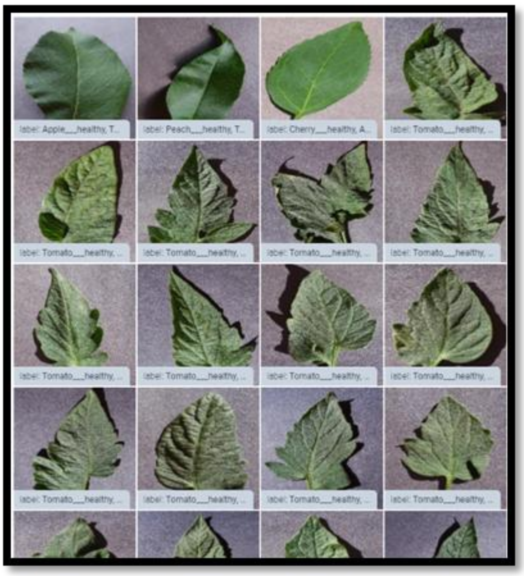

Fig: PlantVillage (free, open source repository of mobile disease diagnosis) accessed on 14.06.2023

5. **Low cost Plant Disease Detection (Cell free disease detection):**

With the increase in climatic irregularities a substantial elevation is detected in disease and pest infestation in crop fields of different parts of the world. In remote places the collection and transport of the diseased samples to laboratory and further elaborate culturing and molecular analysis becomes a cumbersome task. The invention of low cost field based disease detection and diagnostic kit provides sufficient scope for on the spot disease mitigation. These devices accelerate early disease detection and large scale crop protection. One such device is the loop mediated iso-thermal amplification (LAMP), which is a simple, ready to use disease diagnostic technique that could be used both in field condition and laboratory setup. In Indonesia the LAMP assay was integrated with portable fluorometer-based field detection method to efficiently detect begomovirus infection at a very early stage and subsequent treatment of plants belonging to Cucurbitaceae and Solanaceae family (Wilisiani et. al. 2019). RT-LAMP assay was used for detection of Apple chlorotic leaf spot virus (ACLSV) and stem pitting virus (STV) in pear trees. The method has a direct application in the pear certification programme (Lu et. al. 2018). LAMP assay was used for the detection of *Sclerotinia sclerociorum* (Duan et. al. 2014), investigation of pathogenic oocytes in lettuce (Feng et. al. 2019), large scale early screening of Indian Citrus ring spot virus (ICRSV) a devastating pathogen in kinnow mandarin (Kokane et. al. 2021), identification and quarantine of necrotic fungal pathogen in temperate legumes (Bilkiss et. al. 2019).

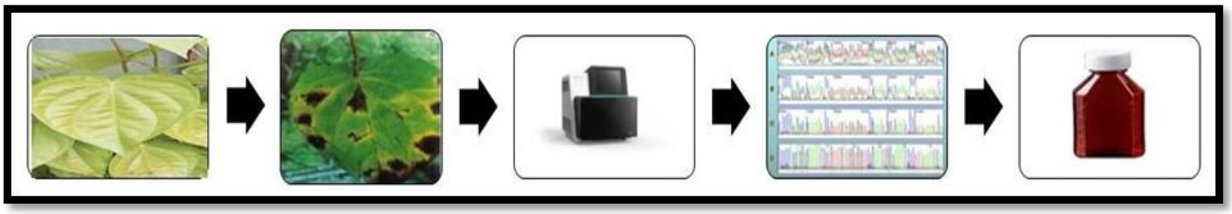

Fig 3: Disease detection through High-throughput DNA based technologies (Field visit, identification of diseased plants, Genotyping, Sequencing, application of precision medicine

6. Computer driven thermal imaging:

Thermal imaging has emerged as a potent tool for several fields of agriculture including nursery monitoring, orchard management, bruise detection in tree crops, irrigation requirements, disease pathogen infestation, soil analysis, maturity prediction, measurement of stomatal conductance, stress determination and yield forecast. In a research conducted on the measurement of canopy temperature by infrared thermal imaging, the method was proved useful for automatic measurement of canopy temperature. A low-cost thermal camera and AI based image segmentation model was efficient in monitoring crop water stress index (CWSI) over wide area and multiple replications. The model provided comparable result at per with commercial thermal imaging system (Giménez-Gallego et. al. 2021). The AI based thermal imaging is a fast, non-destructive on-field method with immense prospect in precision agriculture. High throughput field phenotyping (HTFP) system could be utilized in breeding of forest and tree species. In a study of the drought tolerance trait of full sib F2 partially inbred poplar population with a sample size of 4603, high throughput thermal field phenotyping proved efficient in complementing the forest breeding program. The un-manned drone based thermal imaging was successful in detection of homogeneous drought tolerant genotypes in an apparent phenotypically heterogeneous population.

Fig 4: Multiple applications of thermal imaging in agriculture sector

7. **3D injectable Nano Biosensor:**

Biosensors are used for the detection of biochemical molecules related to omic study such as proteins and nucleic acids. Enzyme-linked immuno-sorbent assay (ELISA), are sensitive but traditional technique requires time to yield a result and usually require the attachment of a fluorophore molecule to the test molecule. Micro-level biosensors apply electrical detection and are ultrasensitive, real-time, labelling free and customized.

Micro-nano-needle (MNN) is a comparatively new technology progressing rapidly with huge demand in health care and Pharma sector. MNN is a firm technology ensuring non-invasive, efficient drug deposition. The MNN technology outperformed the conventional oral drug administration or topical cream application. The delivery of the nano-needle depends on mechanical or magnetic forces and electric field or thermal delivery of the nano-cargo to targeted site (Meng et. al. 2020). Golden rice was developed with the foreign DNA micro-injection with carbon nano-fibers (Abd-Elsalam and Alghuthaymi, 2015). Nanotechnology is an emerging field of science and could revolutionize sub-cellular research experiments in bio-computational research.

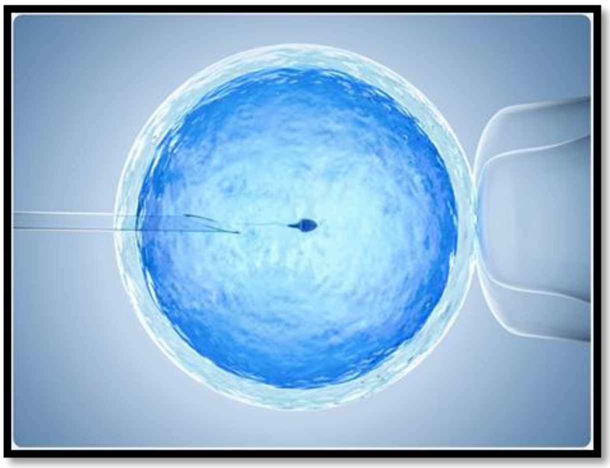

Fig: Micro-manipulation at cellular level at News-medical.net accessed on 19.06.2023

8.

Integration of Omic approaches in crop improvement:

With progress of biology the discovery of numerous compounds are taking place mainly from available plant communities and extensive inventory of microorganisms. The universal compound database offers more than 120 million available representations with less than 20% were annotated to detected peaks of non-targeted metabolomes. The peak picking becomes easy with the knowledge of retention time of the metabolite compounds with its molecular fingerprints. In recent days along with artificial neural network (ANN), genetic algorithm (GA) is integrated for omic data exploration and novel biomarker generation. Mutual conversion of spectrum to molecular fingerprint and *vice versa* is possible through the application of modern annotation tools (Liebal et. al. 2020). In large scale quantitative analysis after annotation the normalization is achieved through quality control based on non-linear regression. In an interesting study of ovarian cancer detection, the comparative metabolome profiling of control and patient groups were able make to early diagnosis of the disease with 100% accuracy employing SVM model with potent biomarkers such as phosphatidylinositol, lysophospholipids, lysophosphatidyl ethanolamine and lysophosphatidylinositol (Gaul et al. 2015). Likewise, the ML driven metabolome has huge prospect in chemical, pharmacy and agro-industry. The comparative chemical profiles of plant and microbial diversity along with prospect analysis of novel compound could be efficiently initiate metabolomics led pharmaceutical production. Targeted and untargeted metabolomics aid pharmacokinetic research and drug development and supports the drug efficacy and therapy sector (Phapale, 2021).The machine aided statistical approaches include MetScape or Mummichog tools aid in metabolite correlation network construction

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	Proteome Size	Sequences Modelled	Models	Seq Coverage	Metadata (Homology models and experimental structures)	Coordinates (Homology models only)
Homo sapiens	20,593	17,084	41,172		13.4 MB	5.3 GB
Mus musculus	21,957	18,621	41,800		7.4 MB	3.7 GB
Caenorhabditis elegans	19,827	12,374	22,308		3.4 MB	1.6 GB
Escherichia coli	4,403	3,646	6,074		1.9 MB	475.3 MB
Arabidopsis thaliana	27,498	19,872	36,363		5.2 MB	2.4 GB
Drosophila melanogaster	13,821	9,799	18,951		2.9 MB	1.6 GB
Saccharomyces cerevisiae	6,060	4,538	8,320		2.1 MB	575.8 MB
Schizosaccharomyces pombe	5,122	4,129	7,754		1.1 MB	538.5 MB
Caulobacter vibrioides	3,720	2,909	4,907		675.7 KB	378.9 MB
Mycobacterium tuberculosis	3,995	3,199	5,104		874.7 KB	373.8 MB
Pseudomonas aeruginosa	5,564	4,724	8,461		1.2 MB	701.3 MB
Staphylococcus aureus	2,889	2,322	3,694		563.4 KB	246.6 MB
Plasmodium falciparum	5,372	3,531	6,335		921.8 KB	371.2 MB

Fig: Examination of TOR protein 3D annotated model repository available in SWISS-MODEL accessed on 19.06.2023

9.

AI based predictive breeding:

In modern era high throughput technologies along with AI were integrated to develop predictive breeding system. High throughput phenotyping (HTP) involves several factors, measurement, source, collection, processing, storage, sharing, analysis and mining for designing a molecular plant through Smart breeding. Field phenomics are based on 9 'V's covering volume, velocity, variety, veracity, variability, validity, visibility, value and vexing. iGEP is a smart AI tool that integrates multi-omic, multi-environmic data for predicting multiple traits in plants. The iGEP system could enable integration of large sample data covering hundred millions of information of genotypes and ten million genetic x environment interactions (Ansari et al. 2025).

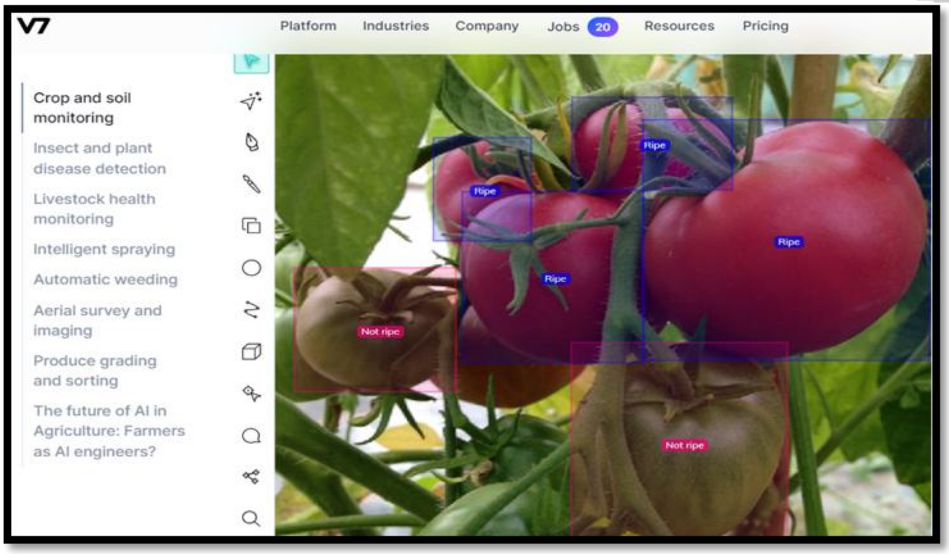

Fig: V7 – online AI based plant performance tool used for detection of apple harvest accessed on 19.06.2023

10

. **Web Interface for Crop plants:** The plant based field data collection at ground level along with integration of various new-age technologies discussed in previous sections could assist in the construction of crop related databases. The database could be wide or specific in nature. Phytozome, Plaza, PlantDB, Plant GDB, Gramene, EBI are generic databases covering multiple crops with huge information coverage applicable for wider population and floral community. OrysPSSP (http://www.genoportal.org/PSSP/index.do), involving more than 100 000 SSPs from rice and 25 related plant species. OrysPSSP is a hybrid database composed of a core SSP database and a dynamic web interface including a variety of user tools and resources. The total 101048 SSPs of core database were generated through a rigid computation/curation pipeline. The web interface contains eight different modules, providing users with rich resources/functions for browsing SSP by chromosome, searching and filtering SSP, validating SSP with omics data, comparing SSP among multiple species and querying core SSP database with BLAST. OrysPSSP serves as a comprehensive resource to explore SSP on the genome scale and across the phylogeny of plant species. OrysPSSP platform assist in advance understanding of the essential roles by SSP and provide information on the processes of development, differentiation, stress response and symbiosis in plants. The emergence and evolution of web platform witnessed development of several generic databases such as Plant-O-Matic (Goldsmith et. al. 2016), a dynamic and mobile guide to all plants of the American subcontinent and SHPIS (Syed 2017) database covering medicinal plants of Saudi Arabia. Whereas TFGD, RAP-DB, GrainGenes, wheatgenome, MaizeDIG, MaizeDB, SoyGD are customized databases developed with genus or species specific information only confirming cross-transferability of omic information in tailored breeding in concerned or allied taxa. Soybean genome database (http://soybeangenome.siu.edu/) is a publicly available physical map of the crop displaying numerous genetic markers with 1053 microsatellites and 2111 gene models. The availability of open source research articles along with crop databases aided futuristic agriculture research and accurate modeling of research program with ease in precise time-frame with less expenditure of time for survey of review and literature.

Conclusion

In this paper the author has discussed about the most significant innovative techniques emerged as potent tool for enriching agricultural research and future plant breeding programs. The application and integration of these new-age technologies could revolutionize agriculture sector securing global food security and a toxin-free sustainable future.

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