CLIMATE CRISIS AND AGRICULTURAL RESPONSE: CLIMATE RESILIENT CROPS FOR SUSTAINABILITY IN FOOD PRODUCTION SYSTEMS

Abstract

Climate change encompasses altered levels of temperature and humidity, variability in the rainfall pattern, fluctuations in weather parameters, rise in ambient CO_2 levels, emission of greenhouse gases, global warming, etc. that results in extreme events and disasters as cyclones, floods, droughts, salinity, nutrient and heavy metal stress, change in arthropod diversity and emergence of new invasive pests. This results in un-usual effects in agro-ecosystems leading to changes in cropping patterns, crop diversity, and their interaction with biotic and abiotic stress factors, threatening livelihood, food, and nutritional security. Population displacement, declining food productivity, and vulnerable agro-ecosystems are the major consequences of altered meteorological events that occur due to climate change. Therefore, substitution of traditional crops with crops that exhibit resilience to climate crisis is the need of the hour. Smart breeding approaches and precision farming technologies as remote sensing and spectral analysis, artificial intelligence, machine learning, speed breeding, genome analysis, genetic manipulation, gene drive systems, system biology study, omics approaches, etc can make agricultural production climate resilient and sustainable. Response of biofortified crops under changing climate must also be assessed to improve the crop productivity and output.

Keywords: Climate change, Agro-ecosystem, Malnutrition, Climate resilient crops, Food

1.1 Introduction

Rising CO_2 levels, fluctuating temperatures, and relative humidity and melting of polar ice leading to rise in water levels are the direct impacts witnessed due to Climate change. The indirect impacts include the changes in the precipitation patterns that challenges the future fresh water availability, ensuring water quality, maintenance of hydrological cycles and groundwater recharge. This further aggravates the disasters as droughts, floods, salinity, heat and heavy metal stress and disease and pest occurence. The most significant impact will be witnessed by the agro-ecosystems that will threaten the food productivity and agricultural sustainability (Bibi and Rahman, 2023). Agriculture, dependent on soil characteristics, weather patterns, and biodiversity, is vulnerable to climate change (EEA, 2019, 2020). The direct impacts include abiotic stress due to altered temperature and rainfall patterns. The indirect effects include biotic stresses, outbreak of invasive pests and diseases, detrimental effects on pollinator species ultimately threatening crop production. The major challenges faced by world today are greenhouse gases, soil and water acidification, soil erosion, land degradation and nutrient leaching that hamper the agricultural production system (Bermúdez et al., 2020). Consequently, livelihoods dependent on agriculture are threatened and global and national food security and nutrition is compromised.

Further in marginal environments, the biodiversity loss and genetic erosion becomes more pronounced due to changing climate (Yazdandoost et al., 2021). Species richness and abundance of pestiferous insects change leading to more adverse situations (Bocci & Smanis, 2019). Population explosion and Climate change together will disdain the agro-ecosystems resulting in human miseries and huge distress among the farmers (Ceglar et al., 2019).

Therefore, climate resilient crops are a urgent need. Crop improvement technologies mitigating the biotic and abiotic stress must be developed. Development and selection of suitable varieties, enhancing the water and nutrient use efficiency, better buffering to heat and cold stress, and biotic and abiotic stress is desired. In this chapter, we summarised the strategies to be followed for mitigating biotic and abiotic disasters. Using revolutionary tools as biotechnology and molecular biology, genome engineering, genome editing, nanotechnology etc can help us to deal with serious repercussions that climate change possess. The adaptation cycle is represented in (***Figure 1***).

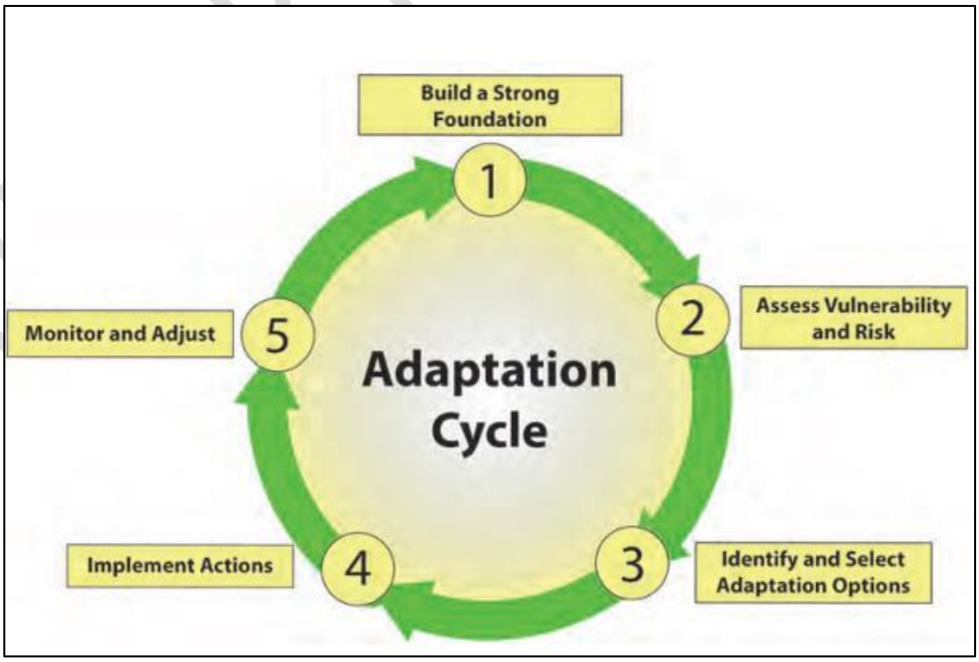

Figure 1: Adaptation cycle of Climate change

1.2 Climate change impairing food security

Anthropogenic actions led to emission of greenhouse gases that raised the average temperature of Earth. Raising CO_2 levels and fluctuating temperatures have resulted in worser weather events that changed the timing of the seasons (Nelson et al., 2009). Therefore, climate change added to population explosion will have detrimental effect on food security and sustainability of the agricultural production systems (Singh et al., 2023). Higher temperatures will result in proliferation of weed and insect populations and encourage emergence of new races of pathogens and biotypes of insects (Kamezi et al., 2023). Absence of rains lead to crop failures and will increase cases of farmers suicides. Increased temperatures also maximise evapotranspiration losses from the soil and plant surface (Tomlinson, 2013). Higher CO_2 emissions may improve the crop yields to a certain extent, beyond which the situation is unpredictable (Sultan & Gaetani, 2016). However, the net impact of climate change on food production systems will be negative, threatening nutritional security. Price volatility will have a significant impact on the global trades and provincial markets, leading to an unrest amongst the public (***Figure 2***).

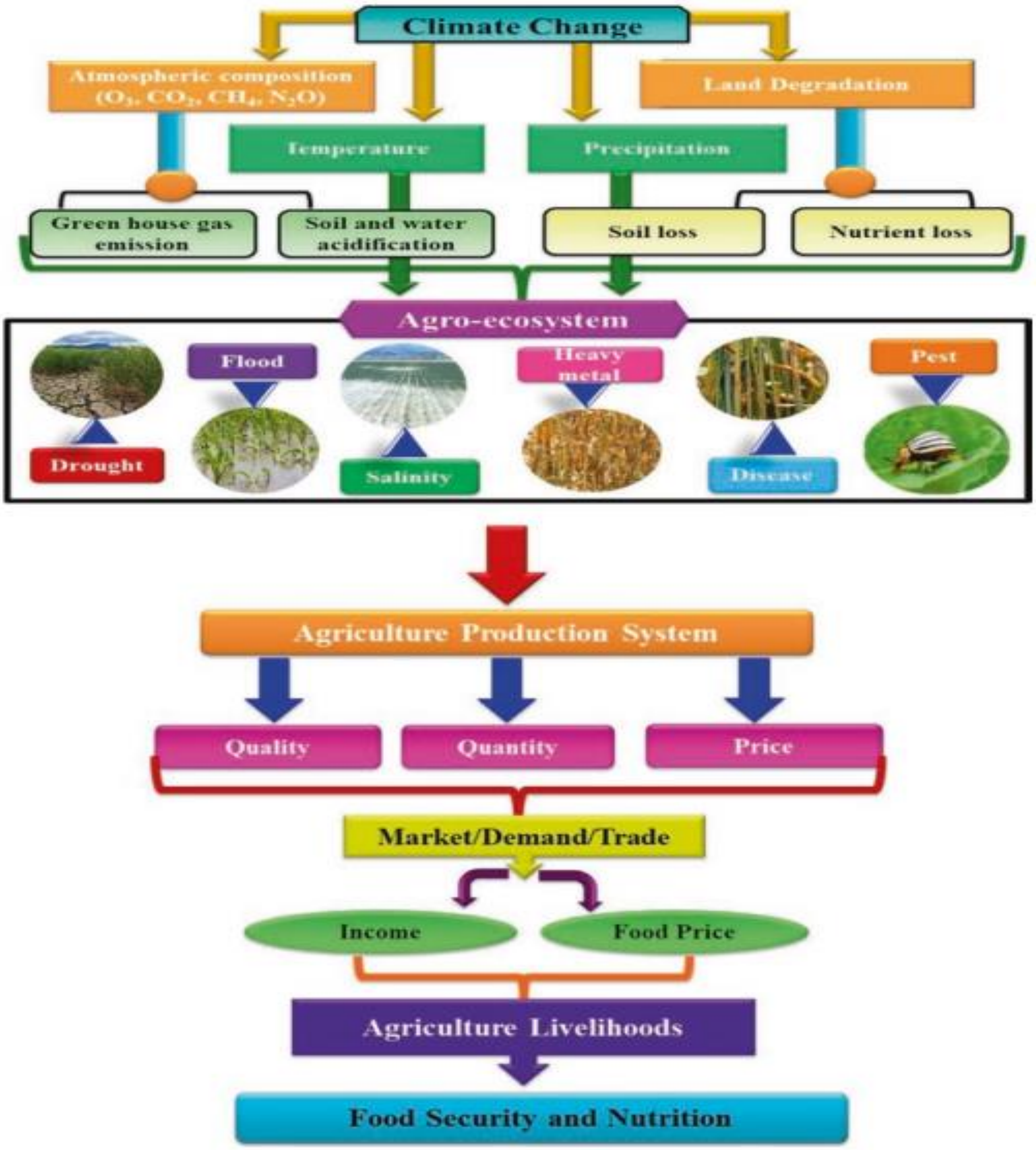

Figure 2: Climate change threatens food security

Climate change questions the stability and sustainability of food production systems. Food availability, accessibility to safe and nutritious food, utilisation, and processing to meet the dietary demands and food preferences and stability is necessary to lead a healthy life (Renzaho & Mellor, 2010) (***Figure 3***). Agricultural production indices, balance sheets for food project the food availability. Similarly, accessibility refers to the possession of appropriate resources to access nutritious diets and utilisation refers to food consumption for nutritional well-being (FAO, 2016). These three dimensions all together sum up food stability and sustainability. Thus, climate change has environmental, social and economic impacts that can favour hunger and malnutrition. To sum up, climate change will lead to decline in rural income and threaten rural livelihoods, create havoc in aquatic and coastal ecosystems, inland water and terrestrial ecosystems and ultimately break the global food security (FAO, 2015b). Developing countries and poor targets will be the easy targets in this line. Trade flows and price stability will decline (Hope, 2009). Human health and livelihood will be compromised because of climate change.

Figure 3: Four pillars of food security

1.3 Strategies to mitigate climate change

Considering the huge risks and vulnerabilities that will be projected by climate change shortly, agriculture risk management strategies must be focussed to generate 60-100% more food by 2050 (Tilman et al., 2011). Strategies to double the agricultural output and intensify agricultural production without scope for horizontal expansion is the prime focus at present times (Bibi and Rahman, 2023). Therefore, development of climate resilient varieties and those that can ensure sustained yields in resource constraint environments must be stressed (Begna, 2021). Crops and varieties that tolerate the biotic and abiotic stress factors imposed by climate change must be encouraged.

1.4 Climate resilient crops against abiotic stress

Adaptation to climate change and devising mitigation strategies are the major tools to fight a war against climate change (Satterthwaite et al., 2010). Adaptation involves the development of climate resilient crops that culminate the negative impacts of climate change. The various abiotic stress affecting crops are represented in ***Figure 4***.

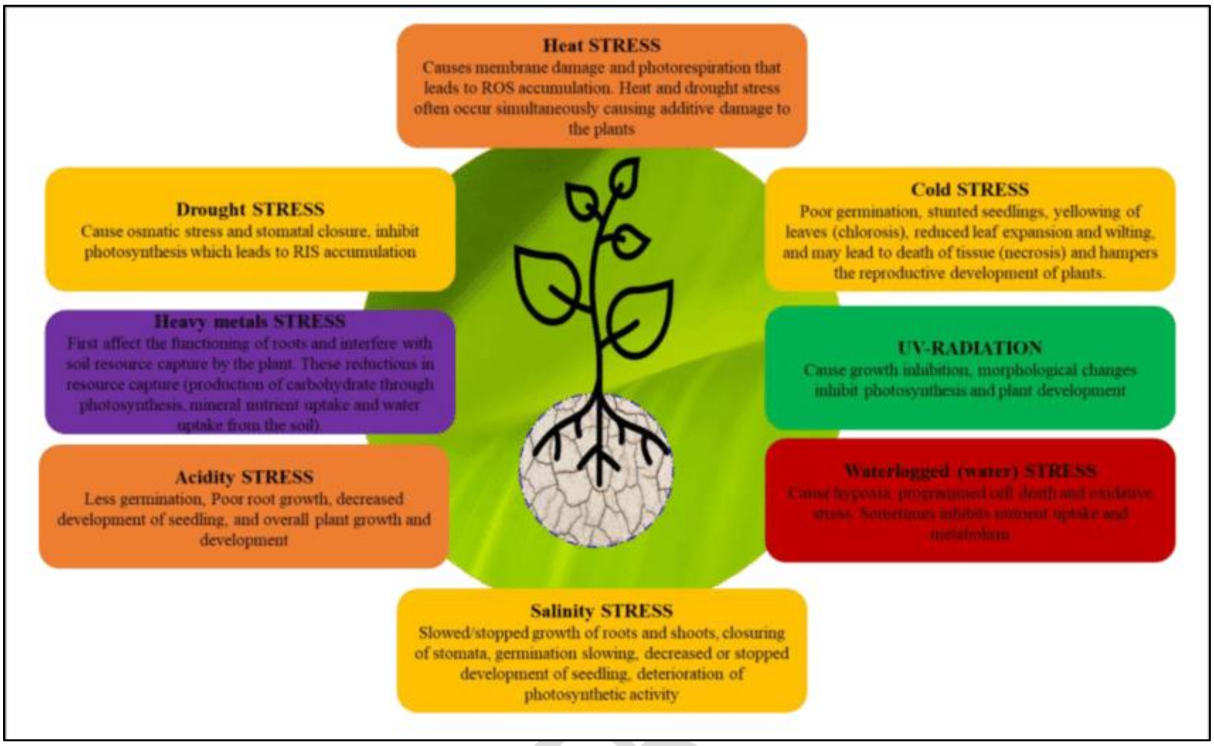

Figure 4: Abiotic stress impacting crop yields

Mitigation on the other hand, aims to cut down the potential effects of climate change (Zhou et al., 2017). Crop genetic improvement is thus aimed at to devise crops that can withstand the vagaries of climate change (von der Gathen et al., 2021). A multidisciplinary approach (***Figure 5***) must be encouraged to expert engagement from disciplines as genetics and breeding (Marker assisted backcross breeding), molecular biology and biotechnology (system biology, bioinformatics, genome selection, genome sequencing, genome editing, omics approaches), plant physiology (signal perception, transduction and chaperon function), entomology (transgenic approaches, improving host plant resistance, IPM, gene cloning strategies), nematology, plant pathology (gene pyramiding, RNA interreference, agro-infiltration), agronomy (balanced nutrient, seed priming and balanced nutrient application), and soil science (chemical amendment, Phyto-filtration and ion exclusion). All the dimensions of the problem must be understood to devise solutions that will be effective and practical (Ali et al., 2020).

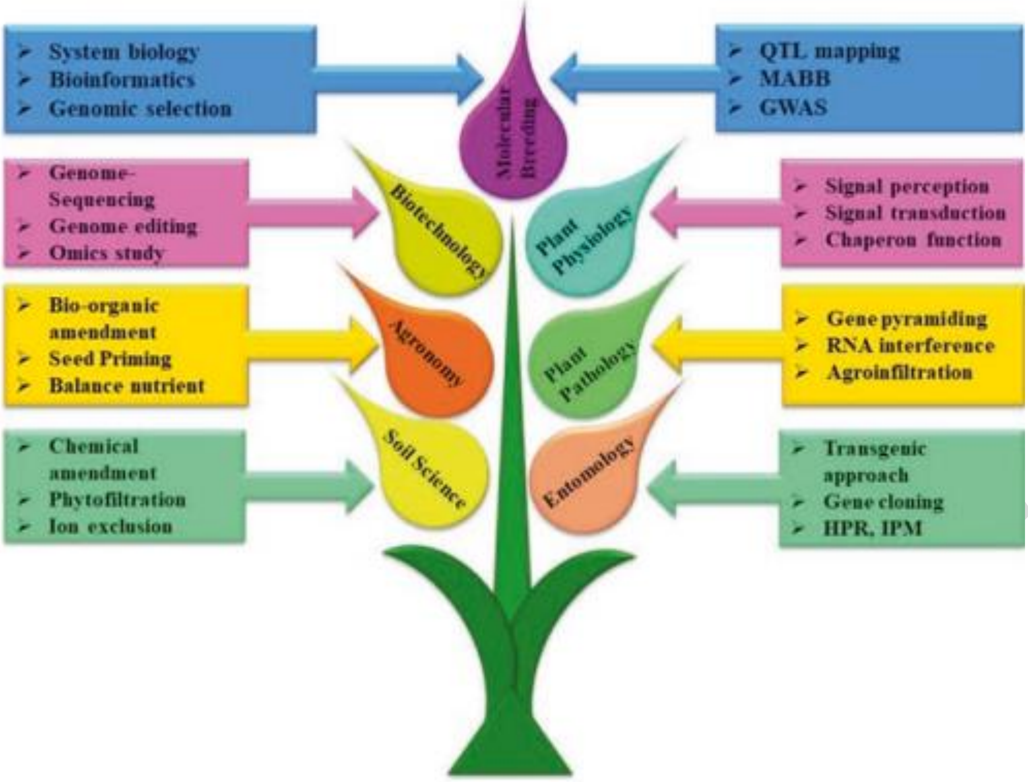

Figure 5: Multidisciplinary approach for developing climate resilient crops

The multifactorial nature of climate change jeopardizes global food supply. Therefore, breeding or designing plants that have optimum yield under changing environmental situations may be smart strategy to fight climate change.

1.4.1 Developing plants with drought tolerance

A thorough understanding of the morphological and the physiological responses, drought related molecular pathways and genetic factors controlling drought at various plant life stages is a pre-requisite for improving drought tolerance character (Osakabe et al., 2014). Droughts can be mitigated by drought tolerance, escape and enhancing plant resistance for drought (Kumar *et al.,* 2023). For this purpose, classical breeding approaches must be integrated with marker assisted breeding and genomic technologies including allele mining, genome wide association studies, genome selection, etc (Babar et al., 2023).

1.4.1.1 Crop management and conventional breeding approaches

Slight alteration in the conventional crop and soil management practices can be done to mitigate drought conditions. Altering the action of stomata to activate metabolic pathways that maintain higher water potential in the tissues can be done by application of vital micronutrients as B, Se, Mn etc (Waraich et al., 2012). Hormonal formulations as ABA are employed to induce drought resistance in plants. This prevents the occurrence of wilting. At times protective and lifesaving irrigation targeting the critical stage of the crop can be given. Similar measures can be adopted to prevent harsh drought like situations (Kumar et al., 2008).

The ability of a plant to withstand drought is determined by the depth, thickness, and branching pattern of the roots (Comas et al., 2013). Therefore, varieties having good root distribution and penetration must be selected and bred. Exploiting heterosis to boost stress performance is another strategy (Tester & Langridge, 2010). Hybrids tolerating stress better and ensuring higher yields under stressful situations must be selected. Selection of plants under stress helps to identify useful alleles that confer drought tolerance to the plant (Des Marais et al., 2014). Limitations that conventional breeding approaches confer are lowered accuracy, labour intensive and time consuming and selection based on morphology makes if impractical to screen large number of genotypes. In this line, modern breeding approaches as Single seed descent (SSD) must be adopted for Rapid generation advance.

1.4.1.2 Mining for beneficial alleles

Land races and wild relatives of the crop are the significant sources that can help developing climate resilient plants. Using hybridisation wheat lines were selected from the progenitors and new drought resistant alleles were identified (Calleja-Cabrera et al., 2020). Varieties or cultivars with improved root architecture and drought resistance must be mined for alleles that confer such characters. The pathways and mechanisms involved in drought resistance protein production and expression must be targeted for overexpression of the genes that will make plants drought tolerant (Cossani & Reynolds, 2015). Tropical land races and genomic pools must be screened thoroughly for plants, genes and alleles that confer better water use efficiency and drought tolerance (Xue et al., 2013). However, identifying germplasms that confer resistance to multiple stress and have improved yield is the need of the hour.

1.4.1.3 Mutagenesis

Explants are exposed to physical and chemical mutagens to induce genetic variations at a very stage. Therefore, molecular mutation aims to create changes in useful traits like drought tolerance and yield parameters. High throughput DNA technologies, EcoTILLING (Eco-targeting induced local lesions in genomes, HRMA (High resolution melt analysis) can enhance the efficiency of mutation breeding approaches. Similarly, de-TILLING or deletion TILLING was attempted in rice and Arabidopsis to develop deletion mutants (Rogers et al., 2009). For example, LRD (Lateral root density) gene was identified in wild wheat *Agropyron elongatum*, promoting lateral root growth (Placido et al. 2020).

1.4.1.4 Improvising root architecture

Root length, branching, root density and distribution can tolerate water stress better. A desirable root architecture should be predisposed genetically with mechanisms that allow root plasticity for water and nutrients (Voss-Fels et al., 2018). The DRO1 locus in paddy controls root architecture without any trade-off on yield related parameters (Arai-Sanoh et al., 2014). Ideal root ideotypes must be designed by gene stacking and pyramiding. For example, stacking QUICK ROOTING genes with DRO genes, plants with proliferated roots can be designed (Kitomi et al., 2018). Phenotypes with reduced tillering, reduced transpiration, delayed senescence, and maximised yield must be selected and bred.

1.4.1.5 RNA interference

MicroRNAs (miRNAs) are the non-coding dsRNAs that modulate gene expression during transcription, translation, and post- transcriptional events. Research directed to the screening of drought induced miRNAs must be encouraged. For example, a long non-coding miRNA was shown to improve rice yield by diminishing FT/SQS enzyme activity that was involved in the production of b-diketone wax. Artificial micro-RNAs that are more selective and transgenerational silencing activity are more valuable approaches in these lines (Pieczynski et al., 2013).

1.4.1.6 Development of transgenics

Transformation of gene regulators involved in vital processes is required for development of transgenics. Careful integration of genes encoding transcription factors, useful stress related metabolites, and modifying or altering proteins develops drought tolerance character in plants. Drought tolerance in plants as rice, wheat, Arabidopsis, potato, maize etc was developed overexpression of *DREB1/CBF* (Bhatnagar-Mathur et al., 2014).

Similarly, over expression of genes and enzymes involved in ABA synthesis pathway, 9-cis-epoxycarotenoid dioxygenase (NCED) was done to induce drought tolerance in petunias (Estrada-Melo et al., 2015). Development of plants with stay-green phenotype, delayed leaf senescence, and high temperature tolerance must be done (Abdelrahman et al., 2017). Further, enhanced production of solutes as glycine betaine in plants enhances drought tolerance (Fan et al., 2016). Also, integrating systems biology and synthetic approaches, plants with C3 mechanisms can be converted to C4 pathways, improving photosynthetic yield (Wang et al., 2014). However, large scale use of transgenics must be evaluated as per the safety guidelines.

1.4.1.7 Mapping quantitative trait loci (QTL)

QTLs can be used to map areas or genes or gene combinations linked to complex characters like drought tolerance. For instance, drought related high economic yield QTL were mapped and selected in rice for stress management and yield enhancement. The QTLs *qDTY3.2* and *qDTY1.1* (Vikram et al., 2011) were strongly associated with grain yield during drought. Similarly, QTL, *qtl12.1* in rice was associated with higher plant height, biomass yield and early blooming (Venuprasad et al., 2012). Similarly, SSR markers were used screen gene pool of rice for drought tolerance (Verma et al. 2019). Similar interventions were also adopted for wheat and other crops.

1.4.1.8 Marker assisted selection (MAS)

Robust genes and genetic combinations in desired cultivars can be identified using molecular or genetic markers. As drought tolerance is a complex trait involving interactions of genes and environment, and thus conventional breeding is not so successful (Jiang et al., 2012). Thus, genes responsible for drought tolerance are usually introgressed from wild to the domesticated population through map-based cloning and marker assisted backcross breeding.

1.4.1.9 Epigenetic factors

Epigenetics changes as DNA methylation and modification of histone proteins are under chromatin control. These are reversible and heritable changes that are brought in without any variation in the sequence of the genome (Lister et al., 2009). It includes processes as methylation, phosphorylation, acetylation, ubiquitination that modifies the regulatory gene expression. This in turn alters the production of hormones and stress related proteins (Kim et al., 2012). CRISPR/Cas technology and tissue specific chromatin profiling under drought stress improves the single base pair resolution (Li et al., 2015). Therefore, the usage of epigenetics in breeding programs is crucial for ensuring drought tolerance in modern day cultivars.

1.4.1.10 Omics approaches

It involves the study of multi-dimensional data including genomics, transcriptomics, proteomics, and metabolomics (Jing et al., 2014). The mining and analysis of such data will provide a deep insight about the mechanism that govern drought resistance in plants. They use desiccation and drought tolerant or resurrection plants as models to study drought tolerance (Giarola et al., 2017). Genomics assisted breeding and QTL pyramiding was developed to stack genes resulting from derived trait specific introgression lines (Ali et al., 2020). GWAS (Genome wide association analysis), gene mapping and high-throughput field-based data accumulation techniques have aided in improvement in the accuracy and the selection efficiency. Using CRISPR based targeted high precision genome editing, drought related polymorphisms can be restored (Mega et al., 2019). Genes involved in development of better root architecture can be targeted and over expressed (Bray & Topp, 2018).

Similarly, transcriptomics can unravel the pathways that are involved in the regulation of the plant stress responses. It involves the use of RNA sequencing, microarrays, suppression subtractive hybridisation, and EST (Expressed sequence tags). Moreover, transcription factors involved in drought stress may be used in the development of transgenic crops based on previous functional gene analysis. For example, transcriptomics has revealed various drought responsive genes in cereal, pulse, fruit, and vegetable crops (Barbosa et al., 2013). Further, this is aided by proteome analysis that reveals the whole set of the proteins necessary to make plant resistance to drought. Comparative proteomic analysis identifies the proteins and subsequently genes that get up or down regulated during stress. Proteins that are responsible for protein, carbohydrate and protein metabolism vary in levels on exposure to stress (Arc et al., 2011). Similarly, metabolomics can be used to identify the metabolites that are responsible for plant stress tolerance. There are various tools like GCMS (Gas Chromatography Mass Spectrometry) (Semel et al. 2007), LCMS (Liquid Chromatography Mass Spectrometry) and FTIR (Fourier Transform Ion Resonance) etc that aid in profiling and identification of metabolites. For example, proline was detected as metabolite developing in the plants in response to drought stress using GCMS.

1.4.2 Developing plants with flood tolerance

Flooding is an abiotic stress that results in water stagnation in the root zone restricting gaseous exchange, root development and the absorption of the nutrients. Severe and frequent floods primarily devastate crops (Bailey-Serres et al., 2019). Thus, there is an urgent need to develop crops that can tolerate water stagnation up to certain periods. In this line, to elongation factor lines (ef1 and ef2) were identified that help in internode elongation (Ramiah, 1940). Coupling traditional plant cross breeding approaches with strategies as SSD and Marker assisted back cross breeding or selection is not sufficient. Therefore, germplasm pools must be thoroughly screened for flood tolerance using efficient molecular markers and effective phenotyping technologies. Fine mapping, QTL analysis and adopting diverse cloning strategies for flood and submergence tolerant genes is promoted. Markers closely linked to submergence trait must be used for development of introgression lines (Toledo et al., 2015). Marker assisted back cross breeding retains all suitable characteristics of the recurrent parent along with the useful traits from the donor parent. For example, three QTLs (*qAG1b* + *qAG1a* + *qAG8*) for enhanced submergence tolerance in rice were integrated (Kim and Reinke, 2018). The introgression of SUB1 QTL into the popular cultivar Swarna was successful by IRRI (Dar et al., 2017). Similarly, C9285, a deep-water rice cultivar was seen to have two ethylene response factor genes *SNORKEL1* and *SNORKEL2* necessary for shoot elongation in floating rice (Kato et al., 2019).

Similarly, development of cultivars that have good aerenchyma tissues in the root must be done to facilitate proper gaseous exchange and oxygen transport and accumulation in the root tissues. It is believed that thick roots can tolerate flooding better as compared to thin roots (Pedersen et al. 2021). A higher cortex to stele ratio is desired in the roots to promote aerenchyma development and avoid anoxia during submergence (Yamauchi et al., 2019). Similar techniques must be investigated for development of root architecture ideotype, including cultivars which have surface rooting and develop adventitious roots. In this line, recently Bulu rice types were also identified having QTL *SOIL SURFACE ROOTING 1* (*qSOR1*) that helps these rice types to tolerate flooding conditions (Kitomi et al., 2020). Similarly, *DLR2* gene was associated with root growth angle was identified (Kitomi et al., 2020). Other genes to be targeted for submergence tolerance can be *SUB1A-1, SK1/2,* and *OsTPP7* may be used in genome editing for better submergence tolerance (Kitomi et al., 2020).

1.4.3 Developing plants with heat tolerance

High temperature induced stress, pollen sterility and altered crop phenological patterns are the major concerns projected due to climate change (Nguyen et al., 2013). Heat stress contribute to high levels of yield loss due to its complex inheritance patterns. A broad germplasm pool with high levels of genetic diversity with precise genomic and phenomics tools is the necessity of the hour. Correlating genetic variation on stomatal density with transpiration efficiency under heat stress conditions can help developing plants with enhanced photosynthetic rate. The whole set of germplasm can be screened for genes or QTLs responsible for heat stress. More emphasis must be given for selection from wild landraces and crop relatives. For example, N22 cross line has heat stress tolerance and high yield (Manigbas et al., 2014). In climatic scenarios that are expected in 2050, it was observed that delayed crop maturity and extension of crop cycle improved yields in crops as wheat and maize (Parent et al., 2018). Further, physiological traits relating to canopy structure, delayed senescence, photosynthetic efficiency, lower respiration rates, reproductive qualities, and harvest index should be used to develop heat stress cultivars (Gupta et al., 2012). QTLs necessary to prevent loss of membrane integrity and yield was identified and selected. Further, heat susceptible restorer lines are used in three-line breeding in rice breeding approaches to maintain economic yields. Also, a dominant locus, OsHTAS (*Oryza sativa* heat tolerance at seedling stage) was identified that confer heat stress tolerance at 48^0C during the seedling and the grain filling stages (Wei et al., 2013). The STAY-GREEN trait was similarly identified in many loci that maintained optimum yields under heat stress. Genomic selection helps in the prediction of phenotype based on genomic estimated breeding value using complex and reliable markers and phenotyping techniques (Rutkoski et al., 2016).

1.4.4 Developing plants with salinity tolerance

1.4.4.1 Impact of salinity stress on crops

Asia, Australia, and Pacific regions have most of the salt affected soils in the world. These are basically the low-lying areas that have shallow water table. They have high evaporation to precipitation ratios. Salinity imposes osmotic, ionic, and oxidative stress on crops disturbing the cellular homeostasis, denaturing proteins, and nucleic acids, enhancing development of reactive oxygen species, and causing lipid peroxidation (Isayenkov & Maathuis, 2019). The ROS so generated interacts with the working of electron transport chain in chloroplast and mitochondria. This leads to higher lipid peroxidation, electrolyte leaching, enhanced photorespiration and reduced photosynthetic efficiency (Alkharabsheh et al., 2021). There is alteration in the Na^+ and K^+ balance in the cell, affecting nutrient absorption and plant development. This results in low germination rates, dry matter production, low nutrient intake, and consequently lower yields. High salinity damages the photosynthetic machinery in the plants by degrading chloroplasts and hindering plant photosynthetic growth (Ha-Tran et al., 2021). Therefore, lowering the Na^+ absorption, maintaining cellular osmotic balance, more apoplastic acidification, higher levels of osmolyte production and storage, producing anti-oxidants and hormonal regulation are necessary to diminish the negative impacts of high salinity stress in the plants (Negrão et al., 2017).

1.4.4.2 Overcoming salinity stress

1.4.4.2.1 Traditional approaches

In traditional approaches the nutrients that were deficit were added and water was used to leach out excess salts present in the soil. Therefore, under traditional agronomic approaches, reclamation and amendment of the soil holds the central place. It included leaching of the salts away from the root zone, replacement of the Na^+ ions from the soil exchange sites, using good quality water for reclamation. Further, physical, hydro-technical, and chemical amelioration methods can be adopted for reclaiming soils from salinity effects.

1.4.4.2.2 Modern breeding approaches

It is an integrated approach and includes modern techniques to reduce salinity effects. The techniques are listed below.

Bio-organic amendments

It refers to the combined use of organic sources and beneficial micro-organisms to enhance crop yields. They ensure availability of soil water and nutrients to the plants. It includes PGPR (plant growth promoting rhizobacteria), VAM (Vesicular arbuscular mycorrhiza), nutrient solubilising and fixing bacteria. These microbes maintain a harmony and symbiotic association with plants and favour them under stressful situations. They promote the uptake of nutrients and minerals. For example, double inoculation with PGPR and VAM is known to enhance salt tolerance by enhancing nutrient accumulation and proline production (Krishnamoorthy et al., 2016). Further, it helps to maintain the ionic homeostasis, prevents ROS mediated cell damage, and regulate plant hormones mitigating salt stress (Kapoor et al., 2019). For instance, Glomalin, a heat shock protein is produced in plants in response to salt stress, that helps the plants to overcome the cellular damage induced by Na^+ ions (Gadkar & Rillig, 2006). Plants associated with mycorrhiza exhibit higher osmolyte production and higher osmotic potential imparting salinity tolerance (Navarro et al., 2014). Therefore, salt tolerant PGPR show remarkable success in enhancing agricultural productivity. It is known to influence the expression of aquaporins that promote plant water uptake. Association of *Azospirillum brasilense* with barley roots improve salt tolerance in barley (Zawoznik et al., 2011). Similarly, effects were observed upon association of *Pantoea agglomera* with maize roots. To maintain Na^+ ions homeostasis and prevent excessive uptake of Na^+ ions plants employ SOS (salt overly sensitive) signalling pathways, the genes of which are known to be upregulated by the PGPR (Mishra et al., 2021). They also reduce ethylene stress via production of ACC deaminase conferring stress tolerance (Kumar et al., 2020). The halophilic organisms that preserve protein structure and functions must be investigated to unravel mechanisms and pathways that mitigate salinity induced stress in plants (Ruppel et al., 2013).

Exogenous application of essential phytohormones

Hormones are endogenous molecules that regulate various biochemical and physiological processes and determine plant resistance or susceptibility to stressful situations. Exogenous application of hormones mitigates salinity stress. For instance, exogenous application of ABA at 100M improves survival of rice indica seedlings by 20% and upregulate *OsP5CS1* gene that enhance proline build up in the plants (Sripinyowanich et al., 2013).

Seed priming

Seed priming with auxin reduce the damaging potential of salinity stress. Hormo-priming is done to treat the seeds with hormones before planting (Sahab et al., 2021). For example, seed priming with cytokinin reduce the negative effects of salt stress and promote seedling germination and development (Amjad et al., 2014). Several types of priming viz. hydro-priming, halo-priming, osmo-priming, thermo-priming, bio-priming, and solid matrix priming can be adopted to enhance seed germination and seedling growth under adverse environmental stress conditions, in this case, salinity (Banerjee & Roychoudhury, 2018; Farooq et al., 2019; Sahab et al., 2021).

Nanoparticles

Nanoparticles help plants to cope with salt stress and salinity (Abdoli et al., 2020). They are applied at various doses depending on the salinity level of the soil. For example, use of chitosan NPs for priming *Vigna radiata* reduced ROS generated in plants due to salt stress (Sen et al. 2020). This improved growth, chlorophyll development and metabolism. Utilisation of NPs increase K^+ ion absorption, more production of anti-oxidant enzymes, trapped energy flow, enhance morphological characteristics and proline and phenolic content (Abdoli et al., 2020).

1.4.5 Developing plants that tolerate Heavy metal stress

1.4.5.1 Heavy metal pollution

Metals that have an atomic number more than 20, the atomic mass more than 23, and density more than 5g/cc are regarded as heavy metals (Koller & Saleh, 2018). However, it is considered misnomer, as many non-metals and metalloid elements also fit this category. Industrial activities, mining, or oil exploration activities lead to heavy metal pollution (Duruibe et al., 2007). Because these elements are non-biodegradable, their disposal must be well managed by industries to maintain their concentration below critical limits. Heavy metal pollution is more common in agricultural lands and water bodies. It includes arsenic (As), cadmium (Cd), chromium (Cr), copper (Cu), lead (Pb), nickel (Ni), and mercury (Hg). Primary sources (natural sources) of heavy metal pollution are igneous and sedimentary rocks, and the anthropogenic factors include industries and establishments (Garrett, 2000). They are present in various forms as hydroxides, sulphates, oxides, sulphites, phosphate, and silicates. They are added due to volcanic eruptions, forest fires, weathering of rocks, and other biogenic sources (Alloway, 2012).

1.4.5.2 Role of phytoremediation in mitigating heavy metal pollution

It involves the use of plants to extract harmful substances from soil as heavy metals, radionucleotides, harmful pesticides and other aliphatic and aromatic hydrocarbons. It thus helps us to transform harmful substances to relatively safer molecules, safeguarding human health and environment. Phytoremediation includes phytoextraction (or phyto-accumulation), phyto-stabilization, phyto-filtration, phyto-volatilization, and phyto-degradation (Alkorta et al., 2004) (***Figure 6***). Phyto-extraction, also known as, phyto-accumulation or absorption refers to the movement of toxic elements from the soil and water via plant roots, following accumulation of these substances in the plant system, following which plants are incinerated. Hyperaccumulator plants maintain high metal concentration in their cell cytoplasm, which is an evolutionary mechanism to deter herbivores and pathogens. A hyperaccumulator must has high bioconcentration and translocation factor. They should have high biomass generation potential, high transpiration, deeper root penetration and fast-growing potential. For example, plants like Salix and Populus are excellent hyperaccumulators for Cd and Zn (Pulford & Watson, 2003).

Similarly, phyto-filtration is the process of removal of toxic elements from wastewaters. It involves blasto-filtration (use of seedlings), caulo-filtration (use of excised plant parts/shoots) and rhizo-filtration (use of plant roots) for removal of harmful heavy metals from water, which safeguards the quality of ground water (Sangeeta & Maiti, 2010).

Phyto-stabilisation similarly, refers to the use of plants that stabilise the pollutants in the harmful elements in the soil. This is possible by reducing the valences of the metals in the rhizosphere zone of the plants (Singh, 2012). Conversion of Cr (IV) to Cr (III) is essential is Cr (III) is less mobile and less toxic (Wu et al., 2010). Plants also secrete certain enzymes that act to immobilise the harmful heavy metals.

Phyto-volatilisation is the process in which plants absorb the heavy metals and convert them to volatiles to be released into the environment. For example, mercury and selenium are phyto-volatilised (Padmavathiamma & Li, 2007). In direct phytovolatilization, the process occurs through root pressure, transpiration stream or through the aerenchyma tissues formed through the death of the parenchymal cells. The volatiles are mostly released to the atmosphere via stomata and lenticels. In indirect phyto volatilisation the plant rhizosphere is modified for volatilisation of organic pollutants. In this mechanism the plants use the water and result in development of thick vadose zone, that makes volatilisation faster (Wang et al., 2017). Therefore, the chemistry of the boundary between the vadose zone and the soil water is necessary for the volatilisation of the pollutants.

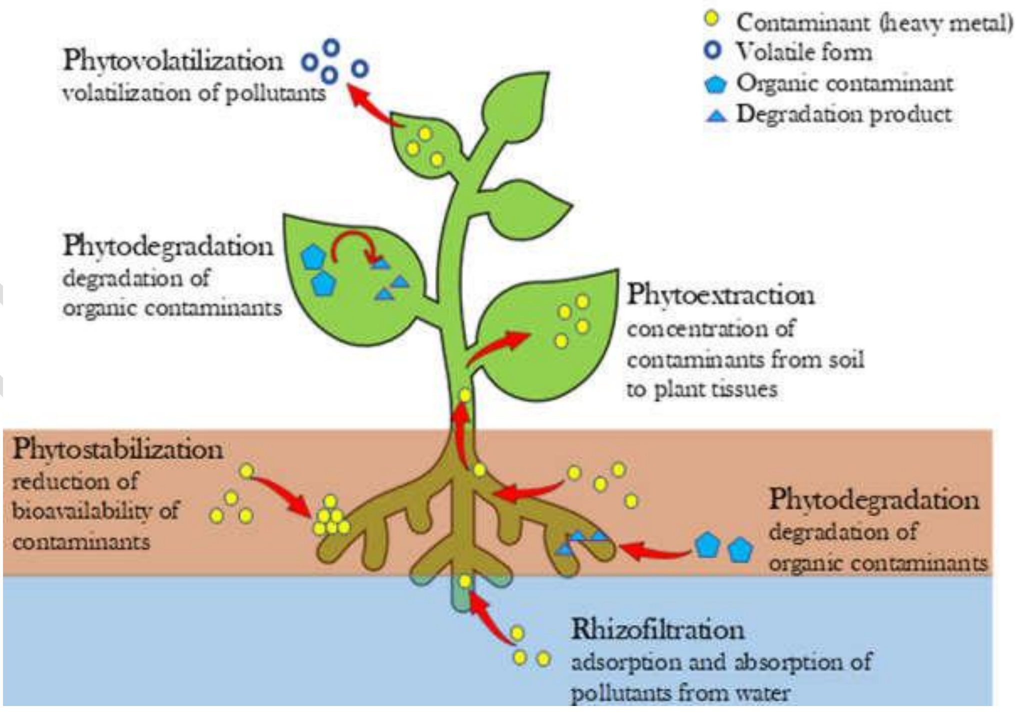

Figure 6: Potential of phyto-remediation in mitigating heavy metal pollution

1.4.5.3 Role of microbes in mitigating heavy metal pollution

Organic pollutants serve as carbon source for the microbes, which they take up and convert into less toxic forms. However, the inorganic pollutants are sequestered through mechanisms as oxidation, methylation, enzymatically, metal-organic complexation, metal-ligand degradation, metal efflux pumps, intracellular and extracellular metal sequestration, and metal exclusion (Ramasamy & Banu, 2007). Similarly, microbes that are tolerant adopt mechanisms as extrusion, bio-transformation, exo-polysaccharide production (Wu et al., 2010). The redox reactions convert heavy metals to non-toxic forms and some microbes also convert inorganic pollutants to organic form. Volatiles that formed during the methylation processes by microbes lead to complete phase change from solid to gas and helps in proper amelioration of heavy metal contaminants.

Endophytes residing in the plants share a mutualistic relation with plants and favour bioremediation processes (Huo et al., 2012). *MerB* gene is expressed by endophytic bacteria that are resistant to mercury and encode organomercuriallyase enzyme that converts organomercurials to mercury ion (Brown et al., 2003). Similarly, *Serratia* sps. of bacteria remediate 65% Cadmium and 35% zinc that making plants and soil free from heavy metal stress (Luo et al. 2011).

1.4.5.4 Role of genetically engineered microbes in mitigating heavy metal pollution

Microbes can be modified genetically to tolerate stress caused due to heavy metals, over-express proteins that bind and inactivate metals and have high accumulation potential (Dash et al., 2014). These transgenic organisms can be used to treat inorganic heavy metal contaminated wastes. For example, engineering microbes to convert Cr (IV) to Cr (III) is beneficial Frederick et al. (2013). Similarly, *Alcaligenes eutrophus* AE104 (Srivastava et al. 2010) and *Chlamydomonas reinhardtii* (Ibuot et al., 2017) was used for the removal of Cr from wastewaters. Engineered *Corynebacterium glutamicum* (Mateos et al., 2017) and *Rhodopseudomonas palustris* (Deng & Jia, 2011) help in remediation of arsenic and mercury respectively.

1.4.5.5 Role of nanoparticles in mitigating heavy metal pollution

Green synthesis of nanoparticles is a popular approach in which plant or microbial extracts can be used as stabilisers or reducing agents. This makes the production of NPs ecofriendly and cost effective (Chandra et al., 2020). The nano zero valent iron and copper is more affinity towards pollutants particularly chromium, thus helping in effective remediation of heavy metals from soil and water (Zhu et al., 2018).

1.4.6 Developing plants that tolerate nutrient stress

The nutrient use efficiency (NUE) of the plants can be improved by nutrient losses and at the same time by prolonging the duration for the availability of the nutrients to the plants. Additives that favour the controlled release of nutrients from the soil, along with synchrony between peak nutrient demand of the crop and the release of the nutrients from the fertiliser formulations must be investigated (Baligar & Fageria, 2015). Fertiliser application methods are also crucial. Controlled and slow-release formulations must be promoted to reduce losses due to volatilisation, leaching, and fixation and immobilisation in unavailable forms (Srivastava et al., 2016). Conservation tillage, organic manure application and band placement of fertilisers are among the other strategies to improve the NUE. Organic manures promote microbial growth that favour proper occurrence of nutrient cycles and help in the release of the plant nutrients that are hooked to them. Substitution of the chemical fertilisers with bio-fertilisers (Vessey, 2003) and formulations can promote the NUE, are cost effective and reduce environmental pollution (Son et al., 2001). Further biofertilizers are known to reduce the levels of chemical fertilisers applied by 50-60% (Naher et al., 2016).

1.5 Conclusion and future direction

Climate change is a global phenomenon characterised by abrupt changes in the climatic parameters that has serious consequences in long run. They are caused by natural or artificial causes. Agriculture is the prime target of climate change phenomena that threatens nutritional and food security globally. Thus, it suffers from various stress like drought, flood, heat, salinity, nutrient, and heavy metal stress accompanied by high rates of disease and pest infestation. Therefore, genetic diversity of the crop must be thoroughly investigated for devising effective solutions for stress management. Thus, focus must be shifted towards climate smart breeding approaches that will produce enough food for growing population. Horizontal contraction on the land availability for agricultural use calls for an improvement in agricultural productivity ensuring availability of safe and healthy food. Multidisciplinary approaches involving high throughput genotyping and precision phenotyping, machine learning, big data analysis, artificial intelligence, remote sensing, system biology, bioinformatics, speed breeding, haplotype breeding, genome engineering and genome editing must join hands to develop variety and crops that provide optimum yield under adverse conditions (***Figure*** *7*).

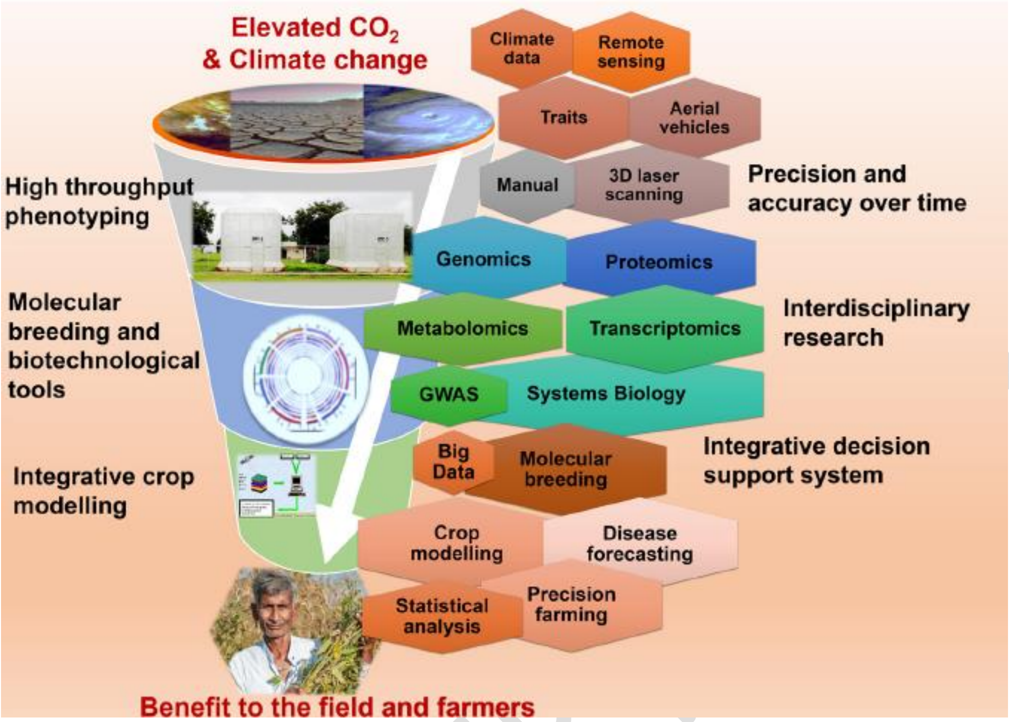

Figure 7: Integrated approach against climate change

Only integrated and continuous efforts in this direction can assure quality and healthy food in sufficient quantities, outperforming the vagaries imposed by climate change.

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