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Growing seed

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MORPHO-PHYSIOLOGICAL UNDERSTANDING OF NITROGEN USE EFFICIENCY IN INDIA

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Nitrogen (N) is one of the most critical inputs that define crop productivity and yield under field conditions, and must be supplemented to meet the food production demands of an ever-increasing population. Efficient utilization of fertilizer N is essential to ensure better value for investment as well as to minimize the adverse impacts of the accumulation of reactive N species in the environment. The current average nitrogen use efficiency (NUE) in the field (Abrol, *et al.*, 1999) is approximately 33% and a substantial proportion of the remaining 67% is lost into the environment, especially in the intensively cropped areas (Abrol, Raghuram & Sachdev, 2007). The form and amount of N available to the plant can be improved by managing fertilizer-soil-water-air interactions; the innate efficiency of the plant to utilize this available N has to be tackled biologically. The biological processes involved include nitrogen uptake, translocation and assimilation, and their optimal contribution towards a desirable agricultural outcome, such as biomass growth and/or increased grain/leaf/flower/fruit/seed output, depending on the plant/crop involved. Identification of appropriate phenotypes, genotypes, molecular markers and target candidates for improvement of NUE poses a formidable challenge.

Nitrogen use efficiency

NUE can be defined as yield obtained per unit of N available in the soil (Kant, Bi and Rothstein, 2011). NUE is quantified based on apparent nitrogen recovery using physiological and agronomic parameter. Therefore, it can also be defined as physiological NUE and agronomic NUE. Physiological NUE is the efficiency with which the plant uses N from acquired available N to total plant dry matter. Agronomic NUE is the N imported from the field to the crop product/ N applied. Nitrogen use efficiency required in all environmental

condition where yield is required, because it is reported that NUE is directly proportional to crop yield. For abiotic stress improvement in crops, NUE has become the second priority after drought both in the private and in the public sector. It is required to minimize N loss, maximize N uptake & reduce environmental pollution.

Needs for the improvement of NUE

Nitrogen (N) must be supplemented to meet the food production demands of an ever-increasing population. The cost of mineral nitrogen fertilizer accounts for a major portion of the total cost of production. N recovery by crops is only 30% to 35% of that applied and remaining 65% to 70% is lost into the environment through a combination of ammonia volatilization, denitrification, leaching, immobilization and runoff. Therefore, Physiologist and plant breeders need to develop cultivars that can exploit N more efficiently in order to minimize loss of N, reduce environmental pollution, decrease input cost and make more economic use of the absorbed N.

Physiological basis of NUE

There may be two components of NUE i.e. nitrogen uptake efficiency and nitrogen utilization efficiency. Young developing leaves and roots behave as sinks for inorganic N uptake, synthesis and storage of amino acid via the nitrate assimilation pathway. The amino acids are further used in synthesized in the synthesis of proteins and enzymes involved in different biochemical pathway and the photosynthetic machinery governing plant growth and architecture development.

(a) Nitrogen uptake efficiency: N uptake efficiency is the amount of absorbed N/quantity of available N. It derives biomass produced from and depends on amount of nitrogen uptake, storage and assimilation into amino acid and other nitrogenous compound during the vegetative stage.

Nitrogen uptake: Plants take up N primarily as nitrate and ammonium, with nitrate being the predominant form in most agricultural soils (Crawford and Forde, 2002). The function of several structural genes involved in N uptake and assimilation have been studied extensively in the past decade. In Arabidopsis, there are three families of nitrate transporters NRT1, NRT2, and CLC with 53 NRT1, 7 NRT2, and 7 CLC genes identified. The NRT2 are high-affinity nitrate transporters while most of the NRT1 family members characterized so far are low-affinity nitrate transporters, except NRT1.1 which is a dual-affinity nitrate transporter. NRT1.1, NRT1.2, NRT2.1, and NRT2.2 are involved primarily in nitrate uptake from the external environment (Miller *et al.*, 2007; Tsay *et al.*, 2007; Ho *et al.*, 2009).

Amongst the CLC family members, CLCa is known to mediate nitrate accumulation in the plant vacuole (De Angeli *et al.*, 2006).

Nitrogen assimilation: Nitrate, after entering the plant cell, is reduced to nitrite by nitrate reductase and further to ammonium by nitrite reductase. The ammonium derived from nitrate or from direct ammonium uptake by AMT transporters (Crawford and Forde, 2002) is further assimilated into amino acids via the glutamine synthetase (GS) and glutamate synthase (GOGAT). This pathway was termed as Glutamate synthase cycle by Rhodes, Sims and Folkes, 1980.

Nitrate is not only the predominant source of N supply to plants, but also acts as an important signal for several developmental processes. This regulation includes a rapid change in expression pattern of genes involved in carbon (C) and N metabolism and other metabolic pathways.

(b) Nitrogen utilization efficiency: N utilization efficiency is the efficiency of a plant to utilize N from acquired available N in the plant for production of biomass. It involves N remobilization i.e. the proportion of N that is partitioned in the seed, result in final yield.

At the reproductive stage the increased supply of nitrogenous compound is necessary for optimum flowering & grain filling. At this stage both nitrogen assimilation & remobilization became crucial. Leaves and shoot acts as the source for providing N₂/amino acid (80% in the form of amino acid) to the reproductive and storage organ. Up to 80% of grain N content are derived from leaves in rice/wheat plant gave efficient method and mechanism that releases N via protease activities during leaf senescence. In the presence of protease activities stored protein reduces to amino acid. Then these reduced amino acid load in to the phloem and transported to developing grain (Figure 4). The prominent gene family which might be involved in the phloem-loading process are the amino acid permeases (AAP). In Arabidopsis, eight AAP genes are present (Liu and Bush, 2006). AAP1, AAP2, AAP6, and AAP8 have been characterized for their varied roles in amino acids transport (Okumoto *et al.*, 2004; Tilsner *et al.*, 2005; Schmidt *et al.*, 2007; Sanders *et al.*, 2009).

What happens to the rice crop when nitrogen level is low?

Plant with nitrogen deficiency often has spindly stems and their growth is stunted. In addition, their leaves turn yellowish from lack of chlorophyll and flowering is delayed. Nitrogen deficiencies first appear on the lower leaves because it is a mobile element within

the plant and is often transferred from older to younger tissues when uptake is limiting. As harvested plant parts such as seeds are high in nitrogen content and require sufficient supplies for optimal growth, nitrogen deficiency is particularly damaging to crop yields. The low nitrogen availability in rice leads to decline in leaf N allocation, photosynthesis and water uptake, due to decreased demand by the plant. Similar patterns are observed in most other studies (Chapin 1980; Clarkson 1985). It has been observed that Nitrogen-limited plants have high carbohydrate status, and light-limited plants have high tissue-nitrogen concentrations (Evans 1989).

Conclusion

Nitrogen must be supplemented to meet the food production demands of an ever-increasing population. While, cost of mineral nitrogen fertilizer cover for a major portion of the total cost of cultivation. More over if we apply more amount of nitrogenous fertilizer then there will be soil pollution. Therefore, there is a need to reduce nitrogen loss, input cost and need to maximize output. So all these thing can be achieved through improving NUE. There is considerable genetic variability for NUE which provide opportunity for its genetic improvement. Moreover several candidate genes responsible for NUE have been identified in several crops like Arabidopsis, Rice and maize etc. By hybridization programme, it is possible to transfer these identified NUE related QTL to the elite genotype having good agronomic background. Incorporation of NUE trait in a genotype will increase the ultimate grain yield which will contribute to our national economy.

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MANAGEMENT OF COW AROUND PARTURITION

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The success of a dairy farm largely depends upon the care and management of the dairy animals. All the operations of the farm should be planned and performed with great caution. The care of an animal should start from its embryonic stage if you want more production from it at adult life. So the management of a pregnant animal must be done with special attention before, during and after parturition. Any small mistake during this time can cost large economic loss for the farmer or producer. In this article, we will discuss the management steps that should be followed at the time of parturition of dairy cattle.

Before parturition

- ❖ Firstly, the most important thing is to know the probable date of parturition of the cow. The average gestation period of a cow is 282 days. But it may vary from 270 to 290 days. The farmer can easily calculate the day of parturition from the day of artificial insemination or natural mating. Proper care and management planning should also start accordingly.
- ❖ The nutrient requirement of the animal changes with the progression of pregnancy. Vitamins, minerals and other nutrients should be provided in optimum quantity. It is better to consult with a veterinary doctor to formulate the ration of the animal in different stages. Very often, deficiency of calcium leads to milk fever after parturition.

- ❖ It is very essential to protect the cow from wound or injury. They should be kept away from bulls or mounting cows. It is better to keep them isolated from the whole herd.
- ❖ When the gestation period is near to be completed, the cow should be examined regularly for the symptoms of calving. It includes swelling of the vulva, dropping away ligaments around the tail, swelling of the udder, thick mucus discharge from vulva and uneasiness of the animal.
- ❖ When the symptoms are prominent the cow should be shifted immediately to the calving pen. The calving pen should be cleaned with disinfectant, well ventilated and well bedded.

During parturition

- ❖ Normally the parturition process takes around 2 to 3 hours. In the case of primiparous animals, it may take 4 to 5 hours or more. During parturition, the animal should not be disturbed but should be observed from a distance.
- ❖ Generally, domestic animals do not need any assistance from a human. But it is also advisable that someone should be present all the time if any emergency situation arises. If the condition goes beyond the control of the farmer, veterinary doctors must be consulted immediately. Sometimes, the calf is presented in an abnormal condition which is termed as dystocia. In this condition, veterinary help is very much essential.

After parturition

- ❖ After parturition, the genitalia and tail should be washed with warm water containing some crystals of potassium permanganate or Neem leaves boiled in water. This antiseptic wash is very much essential to avoid contamination of pathogens. Just after parturition, the immunity of the animal goes very down and the animal becomes very much susceptible to diseases.
- ❖ The animals should be kept warm. It is advisable to provide some warm water mixed with molasses to the animal.
- ❖ The udder is swollen before calving. It should be protected from injury. The animal should be milked after parturition.

- ❖ The placenta generally expels within 2 to 4 hours. Beyond 8 to 12 hours, the veterinary doctor should be consulted. Care should be taken to avoid ingestion of the placenta by the animal. It can result in excess protein intake that can cause a decrease in milk yield.
- ❖ The diet should be formulated carefully after parturition. After parturition, the cow starts milk production and there is a huge physiological change in the body of the animal. So, the feed provided to the animals should fulfill all the need of the animal. It should also be remembered that the calf is totally dependent on its mother at this time. Care should be taken if we want the calf to be a productive animal in later life.

Conclusion

It is very much clear that taking care of the cow around parturition is important not only for the animal itself but also for the future generation. Necessary managerial steps should be taken to protect the animal from stressful conditions and diseases in this critical period. It will ensure a good productive performance from the animal and strengthen the economy of the farmer.

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APPLICATION OF BIOTECHNOLOGY IN AQUACULTURE

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World fish production comprises both catches of wild fish and production through aquaculture. In recent years, fish production has steadily increased to approximately 120 million tons. Behind this success, aquaculture biotechnology has a prominent role. It is the process in which biological systems or living organisms and technological aspects are combined. It is a branch, where the production process is enriched through the proper utilization of biological systems or living organisms. Proper utilization of biotechnology has a wide range of useful applications in the fisheries and aquaculture sector. The biotechnological tools have the great potentiality to increase aquacultural and agricultural production to improve the health and livestock, prevent pollution, provide protection to the environment. In this article, we will discuss briefly the application of biotechnology in aquaculture.

Application in aquaculture

Provide an alternative protein source for fish

Fish meal is the most common protein source for fish. It is high-quality by-product of fish processing with high protein content. But the use of fish meal as a protein source for fish has several drawbacks. First of all, fish meal is very much expensive, so there is a need for a cheap alternative for fish meal. Secondly, because of the declining phase of wild fish stock, the supply of fish meal sometimes become irregular, as we know that fish meal is a by-product of wild fish. Last of all, the use of fishmeal for aquaculture purposes, is not environmentally friendly, because it can cause several environmental problems. The main reason for that, it contains a high level of phosphorus. When this excess phosphorus mixed up

with water, causes excess algal growth, otherwise known as eutrophication. So, the replacement of fish meal with any alternative plant-based protein source can be the best option to solve this problem. Through the use of plant-based protein source, we can minimize the problem of phosphorus accumulation. But plant-proteins contain anti-nutritional compounds which must be destroyed during processing or otherwise alter the feed utilization ability of the fish. Biotechnological tools are used to treat those anti-nutritional factors during the processing of these plant proteins. Researchers are trying to encounter these anti-nutritional factors through the production of some feed enzymes. Phytase is one example.

Bio-remediation

Unlike, terrestrial animals, aquatic animals are more sensitive to their surrounding environmental changes. The immediate environment of the aquatic animals, i.e., water, act as a carrier of their waste products and pollutants from nearby environment. The disease-causing mechanisms of aquatic organisms are more strongly connected to environmental conditions than terrestrial animals, like cattle. So, biotechnological tools are developed in aquaculture, is bio-remediation to solve this circumstance. Bio-remediation is a breakdown process through which environmental pollutants are consumed by micro-organisms to produce a cleaner environment. In the aqua cultural field, this indicates the use of “friendly bacteria” for the treatment of water/feeds by natural processes and discourages the development of “unfriendly bacteria” that have the capacity to cause disease.

Development of transgenic fish

Transgenic fish is one species that contain genes from other species. Main purposes of the development of transgenic fishes are to enhance fish quality, growth, resistance and productivity. So, we can say that transgenic fish is an improved variety of fish consists of one or more foreign gene which are desirable to solve these purposes for that species. These fishes are genetically modified fish. Various types of biotechnological tools are incorporated into those transgenic techniques.

Genetic biotechnology on fish health

Genetic biotechnology have a greate role on improvement of fish health and their treatment. These biotechnological tools help scientists to select disease-resistant strains. DNA-based technologies are being used for these purposes. Molecular investigations on

genetic characterization of pathogens provide information about their origin. They meet the purpose of detection of viral diseases of marine shrimp as well as bacterial and fungal pathogens in fishes. Rapid, reliable and highly sensitive diagnostic tests are required for effective control and treatment of aquatic animal diseases. Because of cost-involvements, time-taking nature and unavailability of suitable cell-line for shrimps /crustaceans for the virus, a direct method of pathogen culture is not available. Most of the time, immunoassay methods, DNA-based diagnostic methods and PCR techniques are used to overcome these problems.

Vaccines

Biotechnological tools have great contributions to the development of vaccines and immune stimulants for aqua cultural species. Vaccines and immune stimulants have a great role either in immunity enhancement or disease prevention. Many commercially available vaccines are there, e.g. furunculosis. Many more are under processing e.g., viral hemorrhagic septicemia(VHS). Apart from their role in the reducing of the severity of the diseases they also serve many other purposes, like reduce the importance of antibiotics and do not induce antibiotic resistance. These vaccines and immune stimulants are incorporated in fish via feeding additives, immersion or in case of larger animals, via injection. Recently, genetically engineered vaccines are being applied for the purpose of protection against pathogens.

Challenges

- Transgenic techniques offer the way of producing large scale changes in growth rate in comparison to other approaches. The exploitation of transgenic techniques most of the times causes environmental damages, which can result in the development of some reversible sterile fishes. These fishes could be made fertile by simple treatment like hormonal injections.
- Another important concern is that the unpredictable consequences of these transgenic fishes because of unknown genetic modifications, make their uses undesirable.
- Careful planning, field trials and cost-evaluations are also necessary before the development of vaccines and their applications which demand considerable research upon target pathogens, as well as resultant diseases.

- Above all, the use of vaccines is very much difficult or some times, too costly for developing countries, which creates major obstructions in the path of adoption of biotechnology in aquaculture.
- Intellectual property and accessibility are the two most important limiting factors, that limit the application of biotechnology in aquaculture.

Conclusion

The applications of biotechnology in aquaculture have significant contributions. It is considered as one of the most promising areas to enhance fish production. The increased application of biotechnology in aquaculture not only revolutionizes the aqua cultural sector but also increases the foreign earnings of the country in a strategic way. But due to several negative environmental impacts, the excessive use of biotechnology in aquaculture is not recommended. So, it should not be used as the substitutes of traditional technologies. We can conclude that the application of biotechnology in aquaculture should be need-driven instead of technology-driven.

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QTL MAPPING

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For most of the period up to 1980, the study of quantitative traits has involved statistical techniques based on means, variances and covariances of relatives. These studies provided a conceptual base for partitioning the total phenotypic variance into genetic and environmental variances, and further analysing the genetic variance in terms of additive, dominance and epistatic effects. From this information, it became feasible to estimate the heritability of the trait and predict the response of the trait to selection. It was also possible to estimate the minimum number of genes that controlled the trait of interest. However, little was known about what these genes were, where they are located, and how they controlled the trait(s), apart from the fact that for any given trait, there were several such genes segregating in a Mendelian fashion in any given population, and in most cases their effects were approximately additive (Kearsey and Pooni, 1996). These genes were termed ‘polygenes’ by Mather (1949). Sax’s (1923) experiment with beans demonstrated that the effect of an individual locus affecting a quantitative trait could be isolated through a series of crosses resulting in randomization of the genetic background with respect to all genes not linked to the genetic markers under observation. Even though all of the markers used by Sax were morphological seed markers with complete dominance, he was able to show a significant effect on seed weight associated with some of his markers.

It was realized that most of the commercially important traits in crop plants are quantitative in nature. Each of these quantitative traits is controlled by many genes which were termed as polygenes by Mather (1949). With the aid of molecular markers and appropriate statistical tools one can identify chromosome loci each carrying one or more genes controlling quantitative or complex trait. Each such identified locus is described as quantitative trait loci (QTL). A QTL is defined as “a region of the genome that is associated with an effect of a quantitative trait.” So a QTL can be a single gene, or it may be a cluster of

linked genes that affect the traits. QTL mapping studies have reported in most of the crop plants for diverse traits like yield, quality disease and insect pest resistance, abiotic stress tolerance and environmental adaptation.

Principles of QTL Mapping

Identifying a gene or QTL within a plant genome is like finding the needle in a haystack. QTL analysis is based on the principle of detecting an association between phenotype and the genotype of markers. The markers are used to partition the mapping population into different genotypic classes based on genotypes at the marker locus, and apply the correlative statistics to determine whether the individuals of one genotype differ significantly with the individuals of other genotype with respect to the trait under study. A significant difference between phenotypic means of the two / more groups depending on the marker system and type of population indicates that the marker locus being used to partition the mapping population is linked to a QTL controlling the trait. A significant P value obtained for the differences between the marker and QTL is due to recombination. The closer a marker is from a QTL, the lower the chance of recombination occurring between marker and QTL. Therefore, the QTL and marker will be usually be inherited together in the progeny, and the mean of the group with the tightly-linked marker will be significantly different ($P < 0.05$) to the mean of the group without the marker. When a marker is loosely-linked or unlinked to a QTL, there is independent segregation of the marker and QTL. In this situation, there will be no significant difference between means of the genotype groups based on the presence or absence of the loosely linked marker. Unlinked markers located far apart or on different chromosomes to the QTL are randomly inherited with the QTL; therefore, no significant differences between means of the genotype groups will be detected.

Steps in QTL Mapping

The various steps in the identification and characterization of quantitative trait loci (QTL) for use in marker assisted selection are presented in figure 2. The process of QTL mapping involves the four major steps, which were discussed below under following subheadings.

Developing of mapping population: A suitable mapping population generated from phenotypically contrasting parents is prerequisite for QTL mapping (E.g.: highly resistant and

susceptible lines). The parental lines used in development of mapping population should be genetically diverse, which enhance the possibility of identifying a large set of polymorphic markers that are well distributed across the genome. Several different populations may be utilized for mapping within given plants species. With each population type possessing advantages and disadvantages. The mapping population could vary based on the objective of study, the time frame line and resources available for undertaking QTL mapping. The ability to detect QTL in F2 or F2 derived populations and RILs are relatively higher than other mapping population. The F2:3 families have the advantage that it is possible to measure the effects of additive and dominant gene actions at specific loci. The RILs are essentially homozygous and only additive gene action can be measured, the advantage with RILs is that the experiments can be performed at several locations in multiple years. The size of the mapping population for QTL analysis depends on several factors viz., type of mapping population used for QTL analysis, genetic nature of the target trait, objective of the study, and resources available for handling a sizable mapping population in terms of phenotyping and genotyping. From the practical point of view the purpose of QTL mapping is to detect the QTL, with major effects, and it is possible only when large number of individuals say 500 or more being used for QTL analysis. So in general size of the mapping population is around 200-300 individuals.

Generating saturated linkage map: Mapping means placing the markers in order, indicating the relative genetic distance between them and assaying them to their linkage groups on the basis of recombination values from all pair wise combination between the markers. Linkage map indicates the position and relative genetic distance between markers along chromosomes. We can analyse the segregation patterns for each of the markers by screening the mapping population using polymorphic molecular markers, which is referred as genotyping. A variety of molecular markers viz., RFLPs, RAPD, SSRs, AFLP, and SNPs etc have been used to identify individual QTLs and to find out effects and position of these QTLs.

Phenotyping of mapping population: The target quantitative traits have to be measured as precisely as possible. Strictly speaking there should not be any missing data, but limited amounts of missing data can be tolerated. The missing data in the population causes the effective in the sample size and intern affect the power of QTL mapping. The data is pooled over location and replication to obtain a single quantitative value for the line. It is also

necessary to measure the target traits in experiments conducted in multiple location to have better understanding of the QTL x Environment interaction.

QTL detection using statistical tools: The basic purpose of QTL mapping is to detect QTL, while minimizing the occurrence of false positive (Type I Error) i.e. declaring an association between a marker and QTL when in fact it does not exist. The tests for QTL or trait association are often performed by the following approaches:

- A) Single marker approach, B) Simple interval mapping, C) Composite interval mapping, D) Multiple interval mapping.

QTL Application

The introgression of QTLs into elite lines / germplasm, and marker-aided selection (MAS) for QTLs in crop improvement has to be undertaken in some of the crop like Maize (Li et al., 2008), Tomato (Stevens et al., 2007) and Wheat (Naz et al., 2008). The plant breeders may need not to know the precise location of QTL as the QTL has large effect and can be introgressed using marker assisted back crossing (MABB). In Maize the QTLs with major effects which conferring resistance to downy mildew has been identified and transferred into CM139 elite but downy mildew- susceptible inbred line (George et al., 2003; Nair et al., 2005). QTLs so identified for diverse traits in different crops have been met in crop improvement especially to enhance the yield and to develop disease resistance elite lines.

Utility and Prospects

QTL mapping plays significant roles to identify genetic regions responsible to important phenotype variation. One of the common strategies of QTL mapping uses a large number of RILs, which are established for at least several generations of inbreeding (typically up to F₆ or F₇). QTL Information Despite lack of precise information about the molecular nature of the QTL, introgression of QTLs into elite lines or germplasm, and marker-assisted selection (MAS) for QTLs inbreeding could be undertaken in some crop plants such as maize, tomato and rice, with reasonable success. Plant breeders may not need to know the precise locations of the QTL, so long as the QTL has large effect, and can be introgressed using marker-assisted backcrossing. The methods available will enable them to pick such useful QTL, which could well have been missed by conventional phenotypic selection. Also,

another important advantage of the markers is in the reduction of linkage drag during the introgression of QTL by backcrossing. At IARI, we have mapped and validated QTLs conferring resistance to downy mildews of maize (George et al., 2003; Nair et al., 2005) and have recently transferred two major QTLs for downy mildew resistance into CM139, an elite but downy mildew-susceptible inbred line.

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EFFECT OF NUTRITION ON FERTILITY IN CATTLE – AN OVERVIEW

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There is a strong relationship between nutrition and fertility and is a topic of increasing importance and great concern among dairy producers, feed dealers, extension workers, veterinarian and animal nutritionists. The financial viability of cow-calf enterprises is highly affected by nutrition. Nutritional status can affect animal's fertility at different stages of reproductive cycle. It also affects the endocrine system. It plays a vital role in the development of reproductive function after calving in cattle. Scientists have long been recognised the contribution of nutrition in achieving reproductive success in livestock. Differences in nutrition account for the variation in the reproductive performance among animals.

Over or under nutrition, both are equally detrimental to the reproductive functions in cattle. Under-nutrition results in loss of body condition, delay in onset of puberty, increase in calving to conception interval, increasing infertility and reduction in milk yield. A more complete understanding of role of nutrition in reproduction can provide an alternative approach in managing reproduction in commercial farms without the use of exogenous hormones.

Effect of nutrition on different reproductive performance of animals

1. Effect of energy

a. Effect of energy on age of puberty

There is a close relationship between energy intake and onset of puberty in males and females. Body condition and weight are the main stimulus rather than the age for the puberty to be achieved. Age of puberty decreases with the increase in feed intake. Low feed intake results delay in puberty, reduced follicular development, delay in onset of estrus, infantile ovaries, under-developed udders and silent ovulations. Energy deficiency also impairs the function of endocrine system.

b. Relationship between nutrient energy and post-partum reproductive health

During early lactation, the peak milk yield overtakes the peak feed intake. Milk production reaches its peak 6 weeks post-partum whereas feed intake reaches its peak 10 weeks after parturition. In this 10 week period, the net nutrient requirement exceeds the net nutrient intake, so animal uses its energy stores like glycogen, protein and triglycerides to meet the deficit results into negative energy balance (NEB). NEB causes inhibition of GnRH secretion from hypothalamus, absence of LH pulses which is required for ovulation. When the cows are in negative energy balance, the blood concentration of Non-Esterified Fatty Acids (NEFA) increases whereas, the concentration of glucose, insulin, Insulin like Growth Factor-1(IGF-1) decreases which ultimately leads to impaired follicular growth, formation of ovarian cysts, non- functional corpora lutea. The interval of first ovulation after calving is also prolonged which impairs the fertility. Improvement in cow's energy balance is an important signal to the ovaries for the resumption of estrous cycle.

c. Negative effect of Overfeeding on reproduction

Overfeeding is dangerous for heifers as well as for post-partum dairy cows. In over-conditioned dairy cows, appetite is decreased which results into severe NEB. When the heifers are given overnutrition before puberty, they store excess amount of fat in developing udder which leads to decrease in the number of milk producing tissues. In overfed cows after calving, the interval from calving to first ovulation increases which impairs fertility. Overfed heifers show weak estrus behaviour with reduced conception rate.

2. Effect of protein on reproductive function in cattle

In most of the third world countries, animals thrive on nutrient deficient poor quality roughage and crop residues. The main constraint is very low amount of digestible crude protein in roughages. Protein plays an important role in proper growth of fetus and function of reproductive organs. Protein deficiency results in delayed onset of puberty, reduced survivability of embryo, impaired development of embryos in cows and sheep, increased incidences of silent heats and lowered conception rates and cessation of estrous cycle. Protein deficiency in lactating cows leads to emaciation and reduction in milk production. In bulls, protein deficiency causes reduction in sperm concentration in semen.

Overfeeding of protein leads to impairment of hormonal balance and high blood urea levels which has a toxic effect on sperm, ova and developing embryo. High levels of ammonia or urea impair oocyte maturation and subsequent fertilization and embryo development. When cows consume excess protein, they require more services per conception and there is prolonged calving interval.

3. Role of minerals on reproduction

Minerals have a great impact on reproductive function of animals and its alteration causes various problems which leads to lowered reproductive efficiency and resultant economic loss to the dairy industry. As most of the roughages, greens, concentrates and even most of commercial feeds available in Indian market are deficient in important minerals, so adequate mineral supplementation is required.

i. Macro-minerals

a. Calcium

One of the most important functions of Ca is to allow the muscles to contract. Ca deficiency reduces the muscle contraction, affecting rumen function. Reduced rumen functions affect the dry matter intake and thus severe NEB in animals. As a result, fat mobilization increases which results in ketosis and fatty liver kidney syndrome. Ca deficiency also prevents insulin production which leads to reduction in milk yield and impaired fertility. Ca deficiency also affects uterus tonicity and thus cows may experience prolonged calving and retention of fetal membranes. Involution of uterus can be impaired which will lead to fertility problems. The ration containing 0.75 to 0.8 % Ca on dry matter (DM) basis should be provided to the high yielding dairy cows.

b. Phosphorus

Low intake of phosphorus leads to delayed sexual maturity, inactive ovaries, low conception rates, decreased fertility rate and irregular estrous cycle. Increased occurrence of cystic ovaries, decreased milk production, decreased ovarian activity also occur at low phosphorus intake. Plasma phosphorus concentration consistently below 4.5 mg/dL indicates the deficiency. Bone phosphorus is more sensitive indicator of phosphorus status in the body. Total dietary levels of 0.75% Ca and 0.45% P and 1.5: 1 Ca:P ratio should be maintained in the diet of lactating cow. Phosphorus deficiency decreases total feed intake which causes a lower energy supply and lower weight gain in heifers, so it is a risk factor in poor fertility. Dietary requirement of phosphorus for high producing cows is 0.45 to 0.5 % on DM basis.

ii. Micro-minerals**a. Zinc (Zn)**

Zn is an essential component of more than 200 enzymes which help in carbohydrate and protein metabolism, nucleic acid metabolism, vitamin A and E transport and utilization etc. Zn is essential for proper sexual maturity, reproductive capacity, onset of estrus etc. Zn has an important role in repair and maintenance of uterine epithelium after parturition. Zn deficiency is associated with prolonged labour, lower birth weight, abortion and fetal mummification. Zn deficiency leads to delayed puberty, failure of implantation, lower conception rates and reduced litter size.

In male, Zn deficiency also leads to atrophy of seminiferous tubules, reduced testicular size, lack of libido and may also adversely affect spermatogenesis. Animal should be given 23 to 63 mg/kg Zn on DM basis for proper reproductive function.

b. Selenium(Se)

Selenium is a powerful anti-oxidant and protects the cells from oxidative stress. Severe Se deficiency causes retention of fetal membranes, abortion, irregular estrous cycles, still birth, early embryonic mortality, mastitis, metritis and ovarian cysts. Sub-clinical Se deficiency leads to reduced reproductive performance with increased number of services per conception, poor uterine involution, weak or silent heats, abortion and birth of weak calves which is unable to stand or suckle. In male animals, Se deficiency causes low sperm production and poor sperm quality. Se supplementation improves sperm motility. Diets should contain at least 0.1 ppm Se for proper reproductive performance.

c. Copper (Cu)

Cu acts as co-factor of different vital enzymes which helps in energy metabolism, iron transport, elimination of free radicals etc. Cu deficiency leads to early embryonic death, necrosis of placenta, retention of placenta and resorption of embryos. The main important sign of Cu deficiency is decreased fertility. In Cu deficiency, estrus is weak and silent. There is also increase in days open due to inactive ovaries. Cu should be present in diet as 10 – 15 mg/kg on DM basis for proper reproduction.

d. Iodine (I)

Iodine is required for thyroid hormones. Signs of I deficiency are delayed puberty, cessation of estrus and anovulatory estrus periods. Iodine deficiency, during pregnancy leads to birth of weak or dead or hairless calves. Diet of lactating cow should contain at least 0.5 ppm Iodine on DM basis.

e. Manganese (Mn)

Mn deficiency is rare in ruminants. The main disorder in Mn deficiency is infertility, poor growth rate in calves and congenital limb deformities. Mn deficient cows are likely to have poorly developed follicles, silent heat, delayed ovulation, reduced conception rate and cows may abort or give birth to weak calves. In males, Mn deficiency leads to absence of libido, reduced number of sperm in ejaculate and reduced sperm motility. Diet should contain 15-25 mg/kg Mn on DM basis.

f. Cobalt (Co)

Co is an important element of vit B₁₂. It is required for DNA synthesis. Signs of Co deficiency include irregular estrous cycles, delay in uterine involution and reduced conception rate. For lactating cows, dietary requirement of Co is 0.1 ppm on DM basis.

4. Relation between Vitamins and reproductive function of cattle**a. Vitamin-A**

It is a fat-soluble vitamin. It maintains the healthy tissue in reproductive tract. Vitamin A directly affects the structure and function of the uterus, gonads and pituitary gland. Its deficiency leads to delay in sexual maturity, low conception rate, abortion, birth of dead weak calves, metritis, retained placenta and suppressed libido in males. Deficiency also causes

delay in ovulation, uterine ovulation, first estrus after calving and increased chance of cystic ovaries. Fresh green roughages contain high concentration of vitamin A. Supplementation of vitamin A before and after calving increases conception rates. Dietary requirement of vitamin A is 4400 IU/kg body weight on dry matter basis.

b. Vitamin E

Vitamin E acts as intra-cellular antioxidant to protect the cells from free radicals. In absence of vitamin E, these free radicals damage cell membranes, impair the synthesis of steroids, prostaglandins, sperm motility and development of embryo. Vitamin E has influence on embryonic and early fetal development. Vitamin E deficiency leads to decreased ovulation rate, conception rate, milk production, uterine motility, sperm motility and transport. There is placental retention, low sperm count, high incidence of cytoplasmic droplet. The dietary requirement of vit E is 90 IU/kg on dry matter basis.

Conclusion

It is clear that nutrition plays instrumental role in reproduction. Nutrition either deficient amount or in excess can impair the proper reproductive function in animals. At present, the best recommendation is to provide the dairy cows a diet which is balanced in all nutrients and meets all the nutrient requirements.

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DAESI: AN INITIATIVE OF MANAGE TO STRENGTHEN EXTENSION SYSTEM IN INDIA

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Agriculture is a very dynamic field of science with innovations every day. Farmers are the most important seekers of information. Agricultural extension functionaries are the key information disseminators but often there is an acute deficiency of these workforce. So, farmers often look for an alternative source of information. In India, there are about 2.82 lakh practicing agri-input dealers, who are the prime source of farm information to the farming community. The first contact point for majority of farmers is the agri-input dealer. Considering the two facts viz. lack of sufficient number of extensionists and deep reliability of the agri-input dealers by the farmers, MANAGE (National Institute of Agricultural Extension Management) developed DAESI (Diploma in Agricultural Extension Services for Input dealers) for the agri-input dealers to develop them as para-extension professionals. DAESI imparts locality based agricultural knowledge. It is launched as a Central Sector Plan scheme. MANAGE had launched DAESI program in the year 2003 and so far covered the practicing input dealers of Andhra Pradesh, Telangana, Tamil Nadu, Maharashtra, Orissa, Jharkhand, and West Bengal.

Classes

This course is developed in such way that it do not hamper daily lifestyle of these input dealers. Classroom courses and work related field visits are organised either on Sunday and/or market closure days at the district level. The course contains 48 classes including 40 classroom lectures and 8 regional visits. The candidates are taken to the different institutes of agriculture, laboratories, demonstration units and fields of innovative farmers as part of practical classes.

Eligibility and fee

MANAGE is the national level working agency whereas at state level, there are nodal agencies that look after programmes of the SAMETI. Interested candidates have to register themselves either at District Agriculture department or Project Director, ATMA at district level for taking admission in the course. Every batch has 40 applicants. All applicants who possess a minimum of 10th pass standard of educational qualification and has obtained a license of atleast any one agricultural input can avail the 50 per cent sub sidised fee of Rs. 10000 for the course. Applicants willing to be an agri-input dealer can also get admission in the course by depositing the total course fee of Rs. 20000. One can avail sponsorship from Rashtriya Krishi Vikas Yojana (RKVY) and agri-business companies also.

Course Structure

Duration: The program is spread over a period of 48 weeks with 40 classroom sessions and 08 field visits.

Module-wise Coverage of Theory and Practical Sessions.

I. Theory (classroom sessions)

1. Agro Ecological Situations.
2. Soil Health Management.
3. Rainfed Farming.
4. Seed & Seed Production.
5. Irrigation Techniques and their Management.
6. Weed Management.
7. Farm Implements and Machinery.
8. Pest and disease Control in Agriculture.
9. Crop Production Technology of major local crops.
10. Acts, Rules and Regulations related to Agricultural Inputs.
11. Schemes related to Agricultural Sector.
12. Extension Approaches and Methods.
13. Other Optional Areas based on requirement.

II. Proposed Practical Sessions / field visits against each module

1. Agro-Ecological Situations and its acquaint with relevance to Agricultural Production Systems.
2. Soil Health Management.
3. Rainfed Farming.
4. Seeds & Seed Production.
5. Irrigation Techniques and their Management.
6. Weeds & weed Management.
7. Farm Implements and equipments.
8. Integrated Pest & Disease Management (IPDM).
9. Package of Practices on predominant crops of the district.
10. Acts, Rules and Regulations related to Agricultural Inputs.
11. Extension Approaches and Methods.

70 percent of the course material contains basic agricultural knowledge and is prepared with the help of ICAR and its agricultural institutes and 30 percent content is derived from the problems of the locality. The entire course material is composed in regional languages.

First-hand experience in taking of soil samples, methods of seed sowing, seed germination testing and identification of nutrient deficiency syndrome and insect, pest and diseases is imparted. Trainees make several records in which they note the things encountered during field visits and later they discuss on these notes in the class. They also prepare the pictorial records of damages due to insects, pests, diseases and nutrient deficiencies. They maintain a problem-solution register in which they make entries of farmers' problems and suggestions obtained during their field visits and later on discuss them in the class. Every applicant has to present their assignment of field visit in an order to enhance their communication skills.

Instructor and Examiner

An agriculture graduate having experience of 5 – 20 years in SAUs, KVKs or other ICAR institutes is made to act as facilitator. He appointed on contract basis for one year which can be renewed based on the performance. He organises this programme and looks

after the examination, evaluation, results, etc. Since the input dealers are different from each other in respect of age, experience, business, income, etc. they are provided with uniforms to bring uniformity in the batch.

Examination and Certification

Only those applicants who attain atleast 64 classes out of 80 classes and atleast 6 out of 8 field visits are eligible to appear in the final examinations. Applicants are evaluated on the basis of bimonthly quizzes, midterm, final and practical examinations. Practical examinations, viva-voce and spotting are conducted by the external examiners. DAESI certificate is awarded to all those applicants who secure 40 percent or more marks in the examination. These certificate holders can take 3 days revision course organised after three years for them.

Strengthening professionalism

With the aim of developing input dealers as para-extension professionals, MANAGE encourages every input dealers to make an “Extension Corner” in their shops where newsletters, pamphlets, leaflets, books, etc. published on the major crops of that region are placed. Further the technological information and information on government schemes published in regional languages are also kept here in order to strengthen the extension system. Now the input dealers first demonstrate the seed germination before selling quality seeds to the farmers. After being trained under DAESI programme, the input dealers now first ask for the soil health card before handing over the chemical fertilizers to the farmers. They now also teach the farmers about the different levels of toxicity symbols printed on the packages of chemical pesticides, brief about the different types of nozzles for spray, proper spraying methods and precautions during sprays.

MANAGE has developed trimonthly e-bulletins, web pages and Facebook page to inform about the different events and programmes of DAESI. Also the trained input dealers have made WhatsApp group to share their experiences.

Status of DAESI

1. A total of 380 batches of DAESI have been completed covering 14,715 candidates since inception.

2. Currently, 309 batches of DAESI programs are in progress with 12360 enrolled candidates.

(Source-e bulletin Oct-Dec 2018)

Conclusion

MANAGE is the apex institution for agricultural extension in India. Through DAESI programme it has achieved success in developing agri-input sellers as para-extension professionals and further strengthening the extension system in the country. Though at present input dealers of only few states are being benefited by this programme but sooner it will be adopted and implemented by all the states which will ultimately be fruitful for the end users i.e. farmers.

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www.manage.gov.in/daesi

<https://www.youtube.com/watch?v=1EI1kCq9A6A>

HIGH THROUGHPUT PHENOTYPING IN PLANTS

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Global food demand is increasing rapidly. Several studies have shown that global crop production needs to double by 2050 to meet the projected demands from rising population. However, achieving this goal will be a significant challenge for plant breeders because crop yields would have to increase at a rate of 2.4% per year, yet the average rate of increase is only 1.3%. Development of improved varieties relies on both molecular approach (DNA sequencing or genotyping) and accurate quantification of plant traits (phenotyping) to identify useful genes/QTLs. Despite recent advances in genomics a lack of suitable phenotypic data has led to poor results in gene/ QTLs discovery, ultimately limiting the progress of genomic assisted crop improvement. Therefore, acquisition of high throughput, effective and comprehensive trait data needed to understand the genetic contribution to phenotypic variation has become an acute need.

High-throughput image-based plant phenotyping facilitates the computation of phenotypes by analyzing a large number of plants in short time interval with precision, nullifying the need for time-consuming physical human labour. The process is generally non-destructive. It allows the same traits to be quantified repeatedly at multiple times and scales during a plant's life cycle. It is an interdisciplinary research field involving computer science, biology, remote sensing, statistics, and genomics in the effort to link intricate plant phenotypes to genetic expression in order to ensure future food security under dwindling natural resources and projected climate variability and change.

In recent years, there has been increased interest in high-throughput phenotyping platforms (HTPPs). Most HTPPs are operated by the big transnational seed companies and the most advanced public plant research institutions around the world, such as the Australian Plant Phenomics Facility, the European Plant Phenotyping Network and the USDA. They have fully automated facilities in greenhouses or growth chambers with robotics, precise

environmental control, and remote sensing techniques to assess plant growth and performance. However, low-cost HTPP approaches are now starting to be developed.

High throughput phenotyping can be divided into three different approach

- i) Technology to collect imaging or other remote sensing data
- ii) Computational data approach to convert the image data into numerical phenotypes
- iii) Use of numerical phenotypes to map genes or QTL to built genomic prediction model and to integrate them in breeding program

Environmental monitoring

Earlier HTPP initiatives have largely focused on phenotyping and little emphasis has been placed on environmental monitoring and reducing error variances. The environment plays a crucial role in plant phenomics since most of the important traits in plants are quantitative in nature and highly influenced by environmental factors. Further, plant breeders aim to develop crop varieties with good buffering and stability that perform well under different environmental conditions. Therefore, appropriate documentation of the experimental environmental conditions (e.g. rainfall, temperature, photoperiod and soil characteristics) is essential for any crop phenomics strategy. Even under controlled environment phenotyping, detailed environmental metadata is preferred. New technologies allow the systematic collection and integration of meteorological data at different spatio-temporal scales. Moreover, the low cost of these sensors permits the deployment of many of them in the field, enabling detailed characterization of the effects of fluctuations in the environment. Certainly controlled environments (including growth chambers, walk-in rooms, and research greenhouses) can provide high quality and highly reproducible data. Plant breeders and agronomists usually prefer field phenotyping especially for complex traits like yield and drought tolerance. On the other hand, phenotyping under controlled conditions can provide a better understanding of trait response to stress factors that cannot be reliably controlled or are difficult to measure in the field.

Plant phenotyping platforms

The area of plant phenotyping is continuously progressing, with invasive, low throughput phenotyping methods being replaced by high-throughput, non-destructive methods. Rapid developments in non-destructive inexpensive sensors and imaging techniques

over the last decade have revolutionized crop phenomics. Current implementations of non-destructive high-throughput phenotyping platforms include the use of sophisticated technologies such as: i) infrared thermography and imagery to scan temperature profiles/transpiration; ii) fluorescent microscopy/spectroscopy to assess photosynthetic rates; iii) 3D reconstruction to assess plant growth rate and structure; iv) light detection and ranging (LIDAR) to measure growth rates; v) magnetic resonance imaging and positron emission tomography to measure growth patterns, root/leaf physiology, water relations, and/or assimilate translocation properties; vi) canopy spectral reflectance for monitoring dynamic complex traits; vii) nuclear magnetic resonance for monitoring the structure of tissues, mapping water movements, and monitoring sucrose allocation; and viii) digital RGB imaging for recording data on various attributes of roots, shoots, leaves, seeds, and grains.

A variety of high-throughput phenotyping platforms exist and are currently used to phenotype different traits in almost all crop species. Some examples of these software /platforms include the Microsoft Excel-based macro, a tool called “LEAF-E” developed for analysing leaf growth parameters, “Zeppelin NT aircraft” as an experimental sensor platform used for remote aerial phenotyping “Phenovator” and “GROWSCREEN FLUORO” for phenotyping large samples for photosynthesis and growth, and “TRiP (Tracking Rhythms in Plants)” for determining circadian period.

Traits for phenotyping

The variety of high-throughput phenomics methods/platforms that have been developed over the past decade (some discussed above) have been used for phenotyping of a variety of plant traits including growth, phenology, physiology, disease incidence, insect damage, drought tolerance and for recording data on different plant organs such as roots, seeds and shoots. For example using different phenotyping platforms, data has been recorded in high-throughput and automated manner for plant height, leaf growth parameters including leaf area, area of canopies, photosynthesis, photosynthesis efficiency, chlorophyll content, leaf nitrogen content and canopy height in different plant species including wheat, maize, barley, rice, pea, Arabidopsis, potato, canola, and soybean among others.. Similarly, phenological traits like flowering (spikelet anthesis) in rice that is considered one of the most important but difficult to capture phenotypic characteristics and circadian period could be also estimated using high-throughput phenotyping platforms.

High-throughput methods have been also used to study plant responses to various types of abiotic stresses (drought, heat, cold tolerance, salinity, Nitrogen limitation, and UV light). Drought tolerance is considered one of the most important complex quantitative traits and many phenomics approaches have been used to understand the nature of drought tolerance. Different high throughput techniques have been successfully used for drought tolerance. These methods are based on imaging, robotics and computers which allow for automatic measurement of phenotypic traits for thousands of plants in a day in non-destructive manner. For biotic stress like insect pests, phenomics platform based on automated video tracking has been developed such as quantifying aphid feeding behaviour on leaf discs to assess the level of plant resistance. Such automated video tracking platforms can be used to screen large plant populations for resistance to aphids and other piercing-sucking insects in plants, as has been already tested on *Arabidopsis* and lettuce. Phenotyping for disease resistance in plants by visual assessment and rating is often time consuming and expensive. Therefore high-throughput platforms /methods developed like hyperspectral imaging (HSI) are considered promising non-invasive sensor techniques in order to accelerate and to automate classical phenotyping methods. The use of hyperspectral microscopy to determine spectral changes on the leaf and cellular level in plants during resistance reactions has been used in barley (*Hordeumvulgare*)-powdery mildew interaction studies.

Several high-throughput platforms and computer software programs are available and being used for collecting and analysing root images. Typically, root phenotyping platforms are divided into two main groups: ex situ where samples or the entire root system are evaluated outside of the growth environment, and in situ also called non-invasive evaluation of the entire root system is done non-destructively under the natural growth environment.

Field-based phenotypingsystems

The most successful traits for evaluation integrate in time (throughout the crop cycle) and space (at the canopy level) the performance of the crop in terms of capturing resources (e.g., radiation, water, and nutrients) and how efficiently these resources are used. Different methodological approaches have been proposed to evaluate these traits in the field (Figure 1). Using the criteria proposed in [20] they can be summarized into three categories: (i) proximal (remote) sensing and imaging, (ii) laboratory analyses of samples, and (iii) near-infrared reflectance spectroscopy (NIRS) analysis in the harvestable part of the crop. Besides the choice of the most appropriate traits, it is also crucial to determine the key time for their

evaluation. Measuring these traits at more or less frequent intervals during the crop cycle together with the measurements of the harvestable components would be unfeasible (or at least impractical) and may even be negative in terms of the impact of the trait for breeding.

Proximal (remote) sensing

Remote sensing phenotyping methods are non-destructive, non-invasive approaches based mostly on the information provided by visible/near-infrared (VIS-NIR) radiation reflected (or transmitted) and far-infrared (thermal) radiation emitted by the crop. These methods are termed proximal in the sense that information is gathered ‘near’ the crop. Remote sensing techniques may be deployed in in situ screening for a wide range of breeding objectives, including yield potential, adaptation to abiotic (water stress, extreme temperatures, salinity) and biotic (susceptibility to pests and diseases) limiting conditions, and even quality traits. Many categories of traits may be measured under different environmental conditions using remote sensing approaches, ranging, for example, from green biomass through to photosynthetic transpirative gas exchange and on to quality traits or even to predict grain yield. Proximal (remote) sensing and imaging techniques include different approaches. The approaches that are most implemented (feasible) for field phenotyping can be grouped into three different categories: (i) VIS-NIR spectroradiometry (ii) infrared thermometry and thermal imaging, and (iii) conventional digital photography (RGB colour cameras). There are several software programs available to process information to extract phenotype data from images.

Cameras for crop monitoring

Different categories of imaging systems used for remote sensing evaluation of vegetation are RGB/CIR cameras, Multispectral cameras, Hyper spectral visible and near-infrared imager, Long-wave infrared cameras or thermal imaging cameras and Conventional digital cameras (NDVI type work).

Integrating high-throughput trait phenotyping with genomics for genetic dissection of traits

To understand the genetic makeup of a complex character, we need both genotypic and phenotypic data of that character. The effectiveness of genetic dissection and reliability of marker-trait associations identified largely depends on the accuracy of trait data. The evolution of high-throughput phenomics platforms during the last decade has revolutionized

trait phenotyping by helping in recording data effectively and cost-efficiently. The data generated was used in trait dissection using a variety of approaches like QTL interval mapping, association mapping, candidate gene association studies, genome-wide association studies, QTLseq. and genomic selection leading to discovery of genes/QTLs for important targeted traits. The rice automatic phenotyping platform (RAP) was used for high-throughput screening of recombinant inbred line (RIL) mapping population combined with genome-wide association studies (GWAS) that led to the identification of 141 associated loci, 25 of which were previously known genes such as the Green Revolution semi-dwarf gene, SD1. Thus high-throughput phenotyping has the potential to replace traditional phenotyping techniques and can provide valuable for gene identification.

Conclusion

Phenomics is a field of science at the junction of biology and informatics which solves the problems of rapid, accurate estimation of the plant phenotype. At present, plant phenomics is rapidly developing. It is characterized by wide approbation of new phenotyping methods for the solution of diverse problems and involvement of the newest computer and engineering technologies in the creation of these methods. Field phenotyping of the appropriate traits, using low cost, easy-to-handle tools, should become an integral and key component in the breeding pipeline. Efficient integration of all the components of the system is needed to pave the way for the adoption of field HTPPs in the near future. This includes more user-friendly data management combined with data gathering and processing. The successful development of the methods of automation and computerization will open lot of new things in our understanding of the functioning of the genome and its interrelation with the phenotype and environment.

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