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RESEARCH ARTICLE

IOT BASED MOLECULAR MARKERS FOR DISEASE RESISTANCE STUDIES IN RICE - STRATEGY AND CHALLENGES

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Abstract

Rice production is constrained by diseases of fungal, bacterial and viral origin. The Internet of Things (IoT) – network of interconnected devices - is an application for disease related uses, collection of data, processing for testing and monitoring. This review article aims about how IoT can track and allows disease resistance studies in in Oryza species. Among them Xanthomonas oryzae, Magnaporthe grisea, RYMV (Rice yellow mottle virus), and brown planthopper causes the high yield losses. Disease resistance genes are identified and they are screened by the SSR (simple sequence repeats), RAPD (Randomly Amplified Polymorphic DNA) and RFLP (restriction fragment length polymorphisms) analysis.

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Introduction:-

With the increasing growth of IT-based technology such as IoT and cloud computing, low-cost health facilities and their support, centralized management can be efficiently managed and public health monitoring can be achieved [1]. All over the world, rice cultivation has been used as the main staple grain crop, nearly 90% of the world food crops are grown and consumed especially in Asia [2]. Rice is the important staple food in Asia to provide the nutritional requirements and the economy of India depends mainly on the agricultural products which is the major producer as well as the exporter of rice [3]. Rice is primarily cultivated by farmers as a cash crop and also it provides an opportunity for agricultural workers across the globe [4]. China occupies first place in rice production with total area harvested rice of 154 million hectares and India is the second largest producer of rice while for export, Thailand and Vietnam occupies first and second places and the third place occupied by India [5].

Wearable Sensor

Wearable sensor technologies produce large scale, multi-dimensional datasets that can be used to classify environmental and drought risk factors of adverse diseases in plants [6]. Here we are providing a solution that combines web app and CC3200 techniques in a wireless sensor network to monitor the disease condition of crop. A

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farmer who stays nearby can examine and observe the health condition of the crop and can react with effective services to save the crop. The sensors incorporated measures the nutrients, water content, air quality which is transferred to micro controller CC3200, which has an inbuilt WIFI and ADC module, so that the crop health condition can be monitored by the farmers from anywhere at any part of time with the help of IP address link generated by the cloud data. At any point of emergency an alarm will be generated both to the farmer and the technician relation who can react and help to save the crop [7].

Crop improvement strategies

Pesticide use is both expensive and harmful to the environment. As a result, there is a huge need to create approaches that provide long-lasting resistance and protection over a wide geographic area [8]. Plant breeders at IRRI (International Rice Research Institute) in Philippines, attempting progressive research activity to achieve more yield and disease resistant varieties that balance the world's rice demand and increase the farmer incomes. Rice was recognized as a genetic model for genetics and molecular biology research for understanding mechanisms for growth, development, stress tolerance and disease resistance because it has a small genome. Rice as a model crop is a fortuitous situation since it is also a crop of world significance [9].

Molecular markers

The considerable progress made in the development of the molecular markers, starting from protein-based isoenzymes to the RFLPs (restriction fragment length polymorphisms) and other DNA-based markers. Among DNA-based markers, simple sequence repeat (SSR) markers are widely used in plants because of their suitability, abundance, hyper-variability, and for highly specific analysis. Microsatellites / Simple Sequence Repeats (SSR) had become major molecular markers for a wide range of research in plants and animals after its emergence as a Polymerase Chain Reaction (PCR)-based genetic marker. SSR has been widely used in various plants and in rice alone it has been used to fingerprint accessions, analyze diversity, and identify introgressions in inter specific crosses, trace pedigrees, locate genes and quantitative trait loci on rice chromosomes and in marker assisted selection [10].

Bacterial infections

Xanthomonas oryzae causes the Bacterial leaf blight (BLB) that affects the rice crops. The rice yield losses of up to 10– 20% were recorded under moderate infection while they were as high as 50% in fields severely affected by bacterial blight [11]. Bacterial blast was first noticed by the farmers of Japan in 1884, subsequently its existence has been reported from different parts of Asia, Africa, northern Australia, and USA. This disease reduces grain productivity in different levels; mainly depends on the stage of the crop, the environmental conduciveness. The pathogen is yellow colored motile gram-negative rod with a polar flagellum. And it enters the host through wounds or natural openings. It reaches particularly the xylem, where it multiplies and spreads throughout the plant. *Burkholderia glumae* and *gladioli* associated with the hot and dry weather, causes bacterial panicle blight, important seed-borne diseases of rice in the South [12]. Late Rice plantation in the season and the land that fertilized with relatively high N amounts tends to have more disease. Losses include poor milling with loss ranging from a 0-70 %. At flowering stage, this population affects grain and resulting grain abortion during grain filling. Over time, diseased grains become gray to black or pink because of growth of secondary fungi. Disease resistance varieties should be chosen because no chemical control measures are recommended [13].

Fungal infections

Magnaporthe grisea is rice blast fungus, one of the most serious diseases of rice worldwide. It causes dangerous threat to world's food production [14]. Many studies have been concerned with resistance mechanisms of rice to the blast fungus, and, thus, several antifungal substances have been isolated from rice leaves. The plants have evolved an array of defense strategies to resist against plant pathogens. The rice blast defense response at molecular level remains poorly understood. It is hoped that the manipulation of these genes may lead to the generation of broad-spectrum resistant rice plants to rice pathogens. In addition to the genetic approach, a direct assessment of the biochemical and physiological changes during disease infection has been used to identify genes involved in defense pathways in many plants. Using both cDNA differential screening and SSH methods, identified 56 defense genes that were responsive to blast infection and to treatment with benzothiazole and jasmonic acid. Among the 56 defense genes, some were differentially expressed their function in susceptible plants after pathogenic infection. The rapid changes that occur in the virulence characteristics of population's raises a continuous threat to the effectiveness of existing blast resistant varieties. Although major genes have often been cited as the underlying cause of resistance instability. Strategies for developing durable resistance mediated by major these have been proposed. Mapping blast

resistance genes and locating closely linked markers has made it possible to confirm the presence of given gene in a variety with multiple genes. In this study presented here fine-mapped resistance alleles of three major genes for blast resistance. Pi1, Piz-5 and Pita on chromosomes 11, 6 and 12 respectively. Identifying flanking DNA markers located within 5–10 cM from a gene of interest has yielded high level of selection accuracy for resistance. It was possible to combine the genes using molecular markers to attain a wide spectrum of resistance. Here, using closely linked restriction fragment length polymorphism (RFLP) and polymerase chain reaction (PCR)-based markers we combined blast resistance genes in a CO39 background [15]. Using For the parental polymorphism survey, 30 RFLP markers each were used for Pi1 and Pita on chromosome 11 and 12, and another set of 12 markers were used for Piz-5 on chromosome 6. The polymorphic markers were subsequently identified and used to probe the segregating populations to identify any additional closely linked markers. The closely linked markers identified were then used to select the plants that contained the two and three genes in the homozygous state.

Pyricularia grisea the fungus causes blast disease which initially Leaf spots start as a small white, blue or gray-tinged [16]. Blast occurs between the seedling and late tillering stages. Under moist conditions they enlarge quickly to narrow brown borders. Leaves and whole plants are often killed under severe conditions. The tissue turns brown to chocolate brown and shrivels, causing the stem to snap and lodge. Panicle branches and stems of florets also have grey-brown lesions shown in Figure1. Scouting for blast should begin early in the season during the vegetative phase and continue through to heading. Leaf blast will usually appear in high areas of the field here the flood has been lost or is shallow. Fungicidal applications are advisable to reduce the infections.



Figure.1:- Leaf blast showing grey-brown lesions on leaf of oryza caused by *Pyricularia grisea*.

Viral infections

Insect pests and diseases are the major constraints limiting rice production in Africa and Asia [17]. The Rice yellow mottle virus (RYMV) was first reported at Kenya in 1966. The RYMV has by far been reported in many countries in East and West Africa including Cameroon, where in some cases whole field have been devastated [18]. Unfortunately, 2002 - 2004, two sampling methods were combined to assess the population of insect's vectors of rice yellow mottle virus (RYMV) in the three major irrigated rice ecosystems in northern Cameroon, and in low land rice fields. The sampling was conducted using sweep net and D-Vac in low land rice fields, while in the irrigated fields, samplings occurred. From samples obtained at different sites: (i) the dominant structure of the RYMV insect vectors was analyzed according to the rice phenology and (ii) the diversity and the occurrence of potential major groups of predators and parasitoids were assessed [19-22]. The potential should develop to manage viral infections that causes yield losses. Pathogen Related proteins have been well studied as a major defense response in several dicot plants, both in R gene-mediated resistance and in SAR. The roles of PR genes in disease resistance have been suggested by the tight correlation between expression levels of PR genes and disease resistance and by the observation of enhanced disease resistance in the transgenic plants over expressing certain PR genes. Several defense-related PR-like genes have been cloned from rice [23].

Conclusion:-

Digitization of data, known as the Internet of Things-IoT in agriculture has been rising increasingly worldwide. The study article offers an overview of the worldwide emergence of IoT is becoming a major part of almost every industry and it's no exception to agriculture sector. Different rice infections are monitored and regulated by the application of the molecular markers, and the disease resistance genes for the different infections are identified and tagged with the markers, and insertion to rice species finally observed disease resistance to the specific pathogen. Molecular markers help in effective identification of pathological symptoms expressed in different parts of the plant body, which in turn provides control measures by causing inactivation of disease inducing characteristics.

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