Proceedings

Brain Storming

Asian Rice Gall Midge - Present Status & Way Forward

BACKGROUND

Asian Rice gall midge (*Orseolia oryzae*) is an endemic pest and reported from nearly 12 Indian states. However, in recent years, there is a change in the time and intensity of incidence. In many of the traditional endemic areas the infestation is occurring late in the season and is continuing beyond the vegetative phase ensuring insect survival. For the past few years, there is an upsurge of this early stage pest in mega varieties grown in large tracts of Tungabhadra, Cauvery basin and Telangana regions. This is one of the pests where we do have extensive knowledge on the mechanisms of host plant resistance and genes conferring resistance vis-a-vis insect virulence. At the moment very few insecticides are available for its control. In this context, this brain storming session is organised to have a relook at the available options and come up with a road map for timely and critical management of this early-stage pest.

JULY 4TH 2023 (TUESDAY)
10.00 AM – 01.00 PM (Hybrid Mode)
ICAR-Indian Institute of Rice Research
https://us06web.zoom.us/j/81209171095?pwd=OUxlbi9mU3hGVGpyK09JSmlaV1R
ZOOM Meeting ID: 812 0917 1095 Passcode: 997152

ICAR-Indian Institute of Rice Research
भारतीय चावल अनुसंधान संस्थान
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Proceedings of the Brain storming session on

Asian Rice Gall midge- Present status and way forward

A brain storming session on "**Asian Rice Gall midge-Present status and way forward**" was held on July 4, 2023 in hybrid mode at ICAR-IIRR, Hyderabad under the Chairmanship of Dr. R.M. Sundaram, Director, ICAR-IIRR. Eminent scientists Dr JS Bentur, PS. Scientist (Retd), ICAR- IIRR, Dr Suresh Nair, Arturo Falaschi Emeritus Scientist (AFES), ICGEB, Dr Arvind Kumar, DDG, ICRISAT, Dr Ch V Durga Rani, Prof &Univ, Head , PJTSAU; Dr Shamkuwar, ADR, ZARS, Sindewahi, Maharashtra and Dr Dr Vikas Singh, IRRI South Asia Lead served as panellists. In all, 90 participants - 75 participants comprising of Head of Departments of IIRR, Entomologists and Plant breeders from 12 states which are endemic to gall midge, members of SARR participated in online mode and 15 scientists in the offline and deliberated at length on the various factors which could be looked into for the management of this pest. Dr. V.Jhansi Lakshmi, PS & Head, Entomology, ICAR-IIRR welcomed all the dignitaries and participants and made the introductory remarks about the importance of Asian rice gall midge and its virulence pattern. Dr. R.M. Sundaram, Director, ICAR-IIRR welcomed the scientific fraternity and invited them for detailed deliberations for management of rice gall midge with its increased incidence in some of the endemic areas where susceptible cultivars are grown.

Dr. A P Padmakumari, PS Entomology, ICAR- IIRR made a detailed presentation about the "**Asian Rice Gall midge- Present status and way forward".** The presentation included a briefing on the losses due to gall midge (GM), and its occurrence in different regions of the country, life cycle and the favourable conditions for incidence of gall midge based on the information collected through survey questionnaire answered by entomologists from 18 endemic locations. It was observed that direct seeded rice has less incidence of gall midge and emphasized on the role of weeds as alternate hosts and off season survival of the pest. The current management practices through chemicals, bio control methods and management options were discussed. Dr. A P Padmakumari briefed about the available the genetic resources, genes deployed, virulence pattern in endemic locations - and the various options available for its management. Till date 12 gall midge resistant genes were identified of which three genes (*Gm4* and *Gm 8* and *gm3*) were cloned and seven insect biotypes were reported in India based on their reaction to a set of host plant differentials. Although gall midge is considered as an early duration pest, incidence at reproductive stage at few locations where the tillers are affected with galls was observed. Among the 11120 breeding lines (NSN1 and NSN2 from 2012 to 2022) screened at multi-locations under AICRP on rice, only 0.15% lines were identified to be resistant to either one or two populations as they were not specifically bred for GM resistance. It was also mentioned that some of the donors, though PCR positive for the gene specific markers, they were not phenotypically resistant indicating the recombination between the marker and phenotype. The scope of utilization of available resistant sources including INRC 3021, Aganni, INRC 17470, ARC 6605, ARC 5984 and varieties chosen for introgression was discussed. She emphasized on understanding the behaviour of the pest with reference to crop stage, sharing and evaluation of landraces / wild accessions, Sensitizing the farmers in endemic areas to go in for granular application at the right time; to differentiate an active gall from an emerged gall and parasitized gall; to identify the parasites and predators which build- up late in the season. She also suggested for utilization of the 3k panel to identify the lines with promising genes to dissect the mechanism of resistance for appropriate breeding strategies; Studying the effect of background on expression of resistance/ tolerance; the compatibility of a specific type of plant resistance with other pest management methods will vary and these variations need to be assessed; exploring the possibility of using sex pheromones for gall midge management.

Dr. Y. Sridhar, PS Entomologist, IIRR introduced all the panelists for their expertise and contributions in the field of rice research especially in gall midge. Dr JS Bentur PS (Retd), ICAR-IIRR, Hyderabad suggested genome editing for susceptibility genes of Rice as well as Genome editing for gene drives. He also suggested that application of ds RNA (Double Strand RNA) for Asian Rice Gall midge control. He opined that pyrimiding resistance genes would increase the durability, but the combination needs to be decided based on the virulence studies. *Gm8* is the best resistance gene for Gene pyramiding for breeding programme and gm3 and *Gm4* may have additional protection for rice gall midge.

Dr Suresh Nair, insisted on maintenance of biotypes in the glasshouses and collection of insect populations from field for further in-depth studies to study the change in virulence pattern.

Dr Shamkuwar ADR, ZARS, Sindewahi, Maharashtra highlighted the severity of the gall- midge in the Vidarbha, Maharashtra. He also emphasized on the development of marker assisted breeding lines with *Gm8* and *Gm1* resistant genes. He emphasized that as gall midge was high in late planting of rice he suggested to go in for 15 days early panting for reduction of the pest incidence in rice. He also suggested that biological control of gall midge can be given due importance.

Dr Ch. V Durga Rani, Prof & Univ, Head, PJTSAU presented an overview of gall-midge research done in the combined state of Andhra Pradesh with Warangal centre for development of many resistant varieties in collaborations with other institutions. Among the seven distinct biotypes, three differentials based on resistant *gm3*, *Gm4* and *Gm8* were targeted in the Telangana regions. RARS WGL rice varieties conferring resistance to GMB 1, 4, 5 and 3 available.

She also insisted that more studies are needed to identify new gall-midge biotypes as well as novel resistance genes in rice. She suggested that Markers assisted breeding is useful to track recessive genes *viz, xa13, xa5* with functional markers.

Dr Arvind Kumar DDG, ICRISAT suggested that all the future released varieties in endemic areas need to have inbuilt GM resistance. *Gm4* and *Gm8* resistant genes need to be used in breeding and also should go for multigene pyramiding. We also need to identify novel sources for resistant genes and test them with various gene combinations for enhanced resistance and suggested that research should be focused on how biotypes react to mutations. We need to employ genome-editing techniques to impart GM resistance and also need to focus on BPH together with GM.

Dr Vikas Kumar Singh, Coordinator, IRRI- South Asia Hub suggested the utilization of Gm4 and Gm8 in breeding programs special emphasized on direct seeded rice (DSR) as well as haplotype-based breeding for GM resistance. We need to identify novel resistance genes.

Dr Gururaj Katti Ex Principal Scientist & Head Entomology, ICAR-IIRR, Hyderabad suggested exploring the possibilities of chemical mediated seed priming to control the GM in early stages. The effect of climate changes on gall midge can be studied.

In the interactive session with all the participants discussion ensued on the use of light traps, pheromones and other prominent chemicals in controlling the GM at nursery stage. Each of the panelists expressed their views and suggestions on the topic and the summary of the deliberations which are worth adopting for advancement of science and benefit of the farmers are listed below.

1. Gall midge is typically a manageable pest with a buck and boost in the incidence with several options of management including early planting, chemical control and genetic improvement being the best approach.
2. The gene pyramided lines *viz.*, IBT WGL3, WGL 1119, WGL14 and ISM with *Gm4* and *Gm8* are promising across locations. The best gene combination to deploy includes *Gm8* in combination with *Gm4* or *Gm8* in combination with *Gm1* for deployment in different genetic backgrounds through MAS.
3. Studies on virulence of gall midge populations need to be strengthened.
4. The resistance gene *gm3*, which is recessive in nature, can be utilised in breeding programme for effective durable resistance.
5. Phenotyping to be supplemented with genotyping data in the coordination trials. Molecular profiling of identified donors from gall midge screening trials was suggested.
6. Recessive genes, which are mostly non-functional alleles, can be good target genes for gene editing studies.

7. Research focus on candidate genes governing gall midge resistance need to be carried out for advanced studies including gene editing to know precise gene function.
8. Cloning and characterization of the recessive genes (*gm3 and gm12*) for more understanding of the functional basis of tolerance.
9. Susceptibility of rice to gall midge is not a default phenomenon where several genes might be responsible for the survival of the pest and in the gall formation. Those genes can be targeted for gene editing.
10. Gene silencing is another strategy to understand the host and pest. Effector genes and salivary gland proteins of the gall midge can be targeted.
11. There is a need to maintain glasshouse cultures of the recognised biotypes of gall midge all around the year.
12. Emphasised regular screening of the germplasm, elite lines and breeding material which will enable identification new sources of resistance.
13. Regional stations endemic to gall midge should maintain the biotype population prevalent in their area.
14. Systematic studies on molecular biology of the insects to be initiated to understand the change in gall midge population structure to be initiated. Mitogenome markers specific to single insect are available. *O. oryzae* can be identified by two repeat elements in CO1 region.
15. It is important to rule out the cross talk and cross infestation with other biotic stresses to declare that a biotype has really emerged.
16. Gall midge has become a major problem in Vidharbha region of Maharashtra in kharif and summer rice, management practices and the new molecules to be identified and a complete package of practices for famers need to formulated and disseminated.
17. Wild rice is the major problem in Vidharbha region and eradication of wild rice could remove the alternate hosts for gall midge survival.
18. Increased incidence of GM could be due continuous rainfall, congenial micro- climate and overlapping generations. High tillering varieties are prone to GM.
19. Chemical interventions resulted in loss of natural enemies in the Telangana region.
20. Leaves of *Cleitanthus collinus* applied @1.5 t/ha control gall midge, stem borer and WBPH damage in rice.
21. A package of practices upto 20 DAT needs to be prepared and circulated among the farmers for effective early stage pest control. If necessary, prophylactic measure may also be taken up in endemic areas based on past history of incidence.
22. At the time of planting rice hybrids, 2-3 seedlings may be planted in the endemic areas.

23. First MAS derived variety for gall midge resistance, WGL 1119 (WGL32100xB95-1/Abhaya) conferring resistance against biotypes GMB 3& 4 available from PJTSAU.
24. Several gene pyramided lines: 9 IBTR lines with *xa13, Xa21, GM4& Pi54; 60 IBT GM/* IBT WGL lines: *xa13, Xa21, Gm4, gm3 & Gm8* were developed at PJTSAU, Telangana. However, some of these lines do not have yield advantage. The present lines with yield enhancing genes were developed possessing *xa13*, *Xa21*, *GM4*, *3 & 8*, *OsSPL 14*, *Gn1a* and three lines with tolerance to multiple biotypes. The donors for resistance sources include Abhaya, RMS GM3-GM8; RP 5923(*gm3*).
25. International Gall midge Nursery (IRGMN) from IRRI was the main resource for many of the genes and donor identified. So this needs to be given impetus.
26. Field screening to be complemented with greenhouse screening is recommended as it helps in the identification of novel sources of resistance and gives insights into the biotypes and genes involved.
27. Research work on rice GM on all aspects on bioytpes, gene identification, molecular analysis successfully led to development of varieties until 2010. Now the gall midge scenario is changing and hence **No variety should come without GM resistance for the rice areas where the GM threshold is high.**
28. Deployment of genes *Gm4+ Gm8* (Abhaya+ Aganni) has been carried out. It is understood that Abhaya is not very good combiner. To combine *Gm4+ Gm8* in breeding programmes, there is a need to introgress this gene into a line with **high combining ability.**
29. Instead of one gene combination (*Gm4+Gm8*), other alternative combinations to be looked at for deployment among the 12 identified genes. Research on the identification of new genes need to be strengthened.
30. Hybrids resistant to GM needs emphasis and presently *Gm4+Gm8* combination being used.
31. Studies to identify the damage caused by gall midge in the early stage even before the gall is formed need to framed from the current understanding of silver shoot damage which is late for management. Probability of identifying the damage in the initial stages through the use of AI tools maybe explored.
32. Studies related to understanding the possibility of anticipating the changes in the biotypes was suggested, so as to understand the pattern of biotype emergence and postulate the future emergent strategies.
33. We need to strengthen the research on gene cloning of the identified genes. Gene editing as tool can be utilized for further insights.
34. Haplotype breeding to identify the superior and best haplotypes of already known genes suggested.

35. New set of genes/or the important genes that are required for plant life cycle need to be identified and their associated traits need to combined. The marker trait associations need to be identified through network screening at hot spots.
36. Artificial intelligence can be deployed for novel trait discovery
37. The native landrace collections sequenced at IRRI can be explored for any novel haplotypes conferring gall midge resistance based on gene based information available.
38. Chemical control –preventive application at nursery level. Suggested to study the effect of seed treatment in the control of GM
39. Studies on the impact of climate change on GM need to be initiated.

The panel discussion was followed by Q & A moderated by Dr CN Neeraja, PS & Incharge Biotechnology, IIRR .

1. Any information about seed treatment?
    A. Studies on seed treatment with thiamethoxam and Fipronil across 13 locations and are already working in this direction and the results are encouraging
2. Gall midge is attracted towards light during early stage. Whether light traps can help in control?
    A. We need to identify the *Orseolia* species that is bein g attracted towards light. We need to identify which species of *Orseolia* is in the light trap- is it from weeds or from rice plant. Light traps can be used only to monitor the GM species but not for management but for assessment it is fine. Deployment of sex pheromones is another strategy to be explored.
3. Can we collect gall midge populations form different areas/centres and mitochondrial bar coding can be done
    A. Yes, different insect populations need to be maintained on susceptible genotypes and marker specific biotype identification is possible based on ribosomal genes.
4. How to identify the gall biotypes.? which biotype is prevalent.?

A. SN: We do have markers now which can differentiate biotype 4 and 4M.

5. GM is increasing year on year. Is there any management practice in addition to seed treatment. During the nursery as pocket application

A: Fipronil can be applied.

5. In field screening: 10 percent damage;; whether the qualitative infestation is shifting to quantitative?

A: JS: GMresistance is qualitative. However if it is 10% it is needed to ascertain what are these 10% damaged in respect to insect or seed mixture. If % is <20% infestation, we need to investigate whether it is due to segregation, seed mixture or some other reason to arrive at the conclusion.

6. GM species are attracted to flowers.

A: we need to explore.

7. How to identify the gall biotypes? Which biotype is prevalent?

A .We can identify the population through the available set of host plant differentials or single insect based markers are available.

8. GM is increasing year on year.... is there any management practice in addition to seed treatment during the nursery as pocket application

Ans: Fipronil can be applied

Dr RM Sundaram Director, ICAR- IIRR in his concluding remarks gave the following suggestions for taking the research forward:

* Utilization of the 3k panel lines to identify the donors

* Phenotyping and genotyping of landrace collections for identification of the new donors. Locations / hot spots may be identified for screening during next kharif season.

*Land race collections can be subjected to association panel. AUS and BAAP population can be screened.

*Development of two genes pyramids with HR+ and/ or HR- mechanism needs a rethinking for their strategic deployment. We need to know the functionality of gene being deployed.

* Need to move from PCR based markers to SNP markers. A panel to be made for GM specific markers, and routine genotyping to be carried out with InterteK at least for the three-cloned gene based markers. Dr. Vikas Singh may help us with the genotyping.

*GM gene responsible for virulence like OODAD and cell elongation genes could be ideal candidate genes. They might be housekeeping genes. Gene silencing could to a promising approach.-an opportunity to apply gene silencing of GM virulence.

*Culture maintenance: At IIRR, currently we are maintaining only one biotype- GMB1. He had suggested making efforts to collect other biotypes and maintain them.

* *Gm4/ Gm8* may be targeted to either overexpress or gene knockout to prove their functionality.

* With the climate change imminent, whole country is moving towards direct seeded rice or wet direct seeding. Simultaneously we can expect more GM incidence. Hence, we need to gear up management strategies like exploitation of botanicals, sex pheromones and develop slow release formulations to improve the efficacy.

* Emphasized the preservation and utilization of promising donors/ breeding lines through joint registration by breeders and entomologists.

* Breeding approach: we should move through forward breeding –pedigree breeding for better products and backcross breeding for development of NILs.

* As a community approach we should select good background genotypes in order to develop NILs for all the gene differentials.

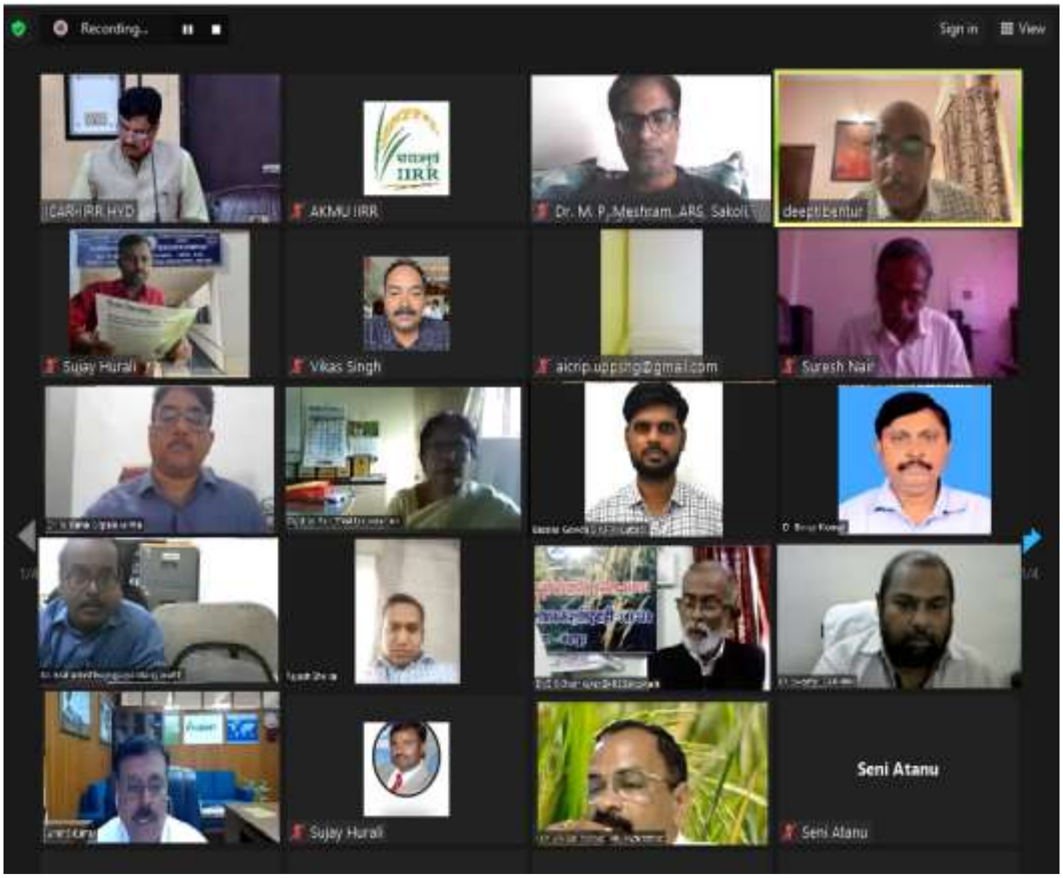
* Field *vs* glass house screening – For consistent pheonoytping we need to consolidate the locations and strengthen them.

* Tools like AI for precision phenotyping may be explored.

*For association mapping a set of 3k, BAAP and landrace;-phenotyping and for marker trait association.

* To assess the impact of climate change on GM we need to analyse past 10 year data and can look for consistent signals and should initiate some studies so as to come up with suitable forecasting models.

Dr K.Suneetha, SS, ICAR-IIRR, Dr Chinna Babu Naik and Dr V. Papa Rao served as Rapporteurs for the session. Dr B. Sailaja, PS and Inchare AKMU, and her team Ms S Gayatri and Ms M Shalini coordinated the live streaming of the session. Meeting ended with vote of thanks proposed by Dr Y Sreedhar, PS. ICAR-IIRR.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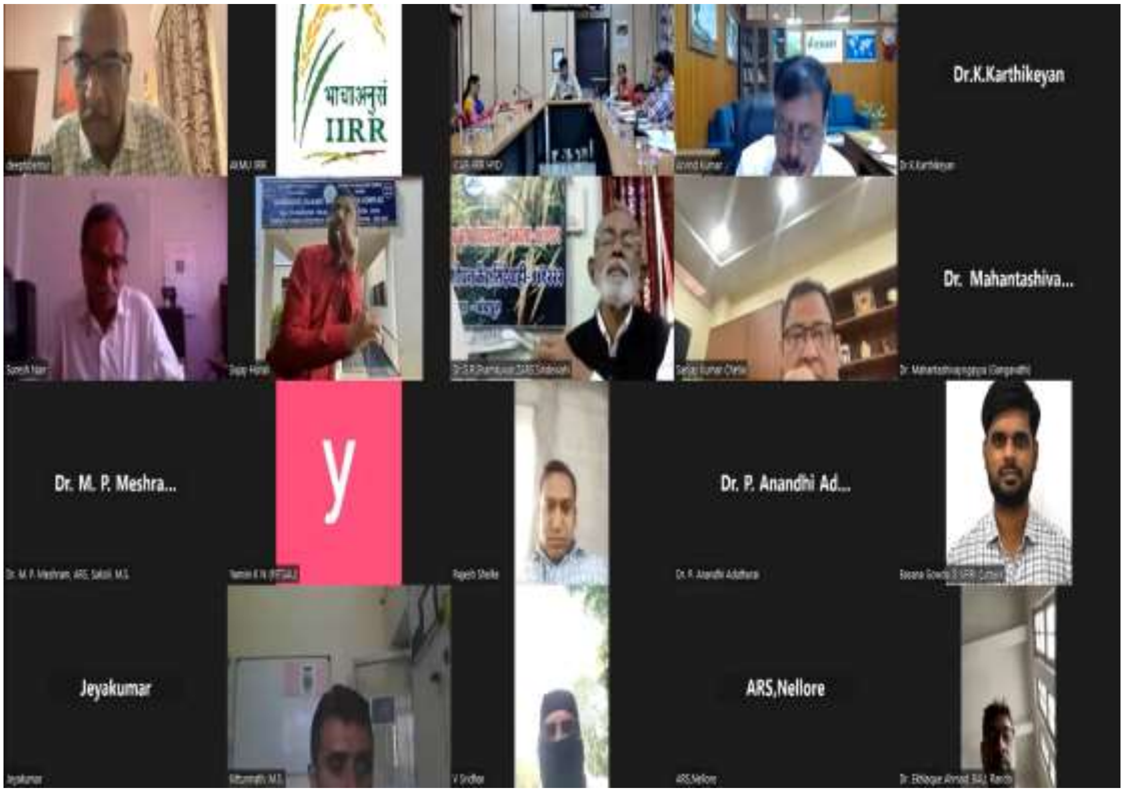
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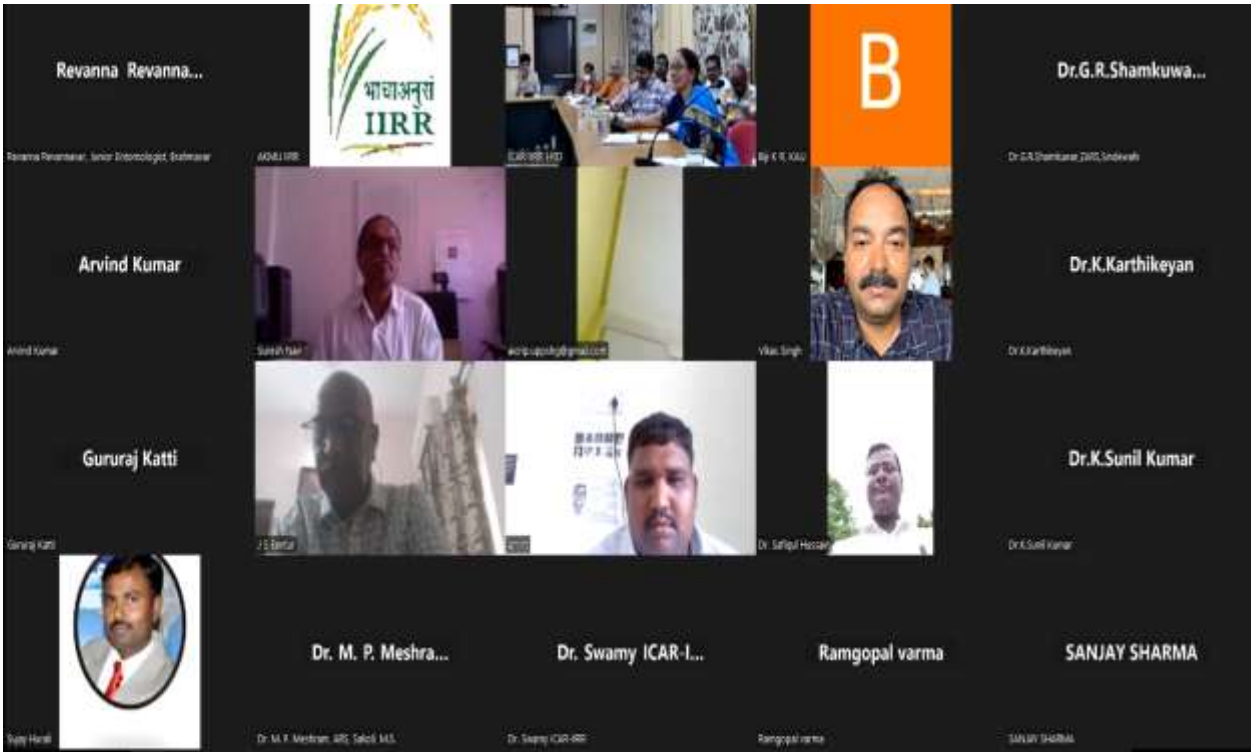
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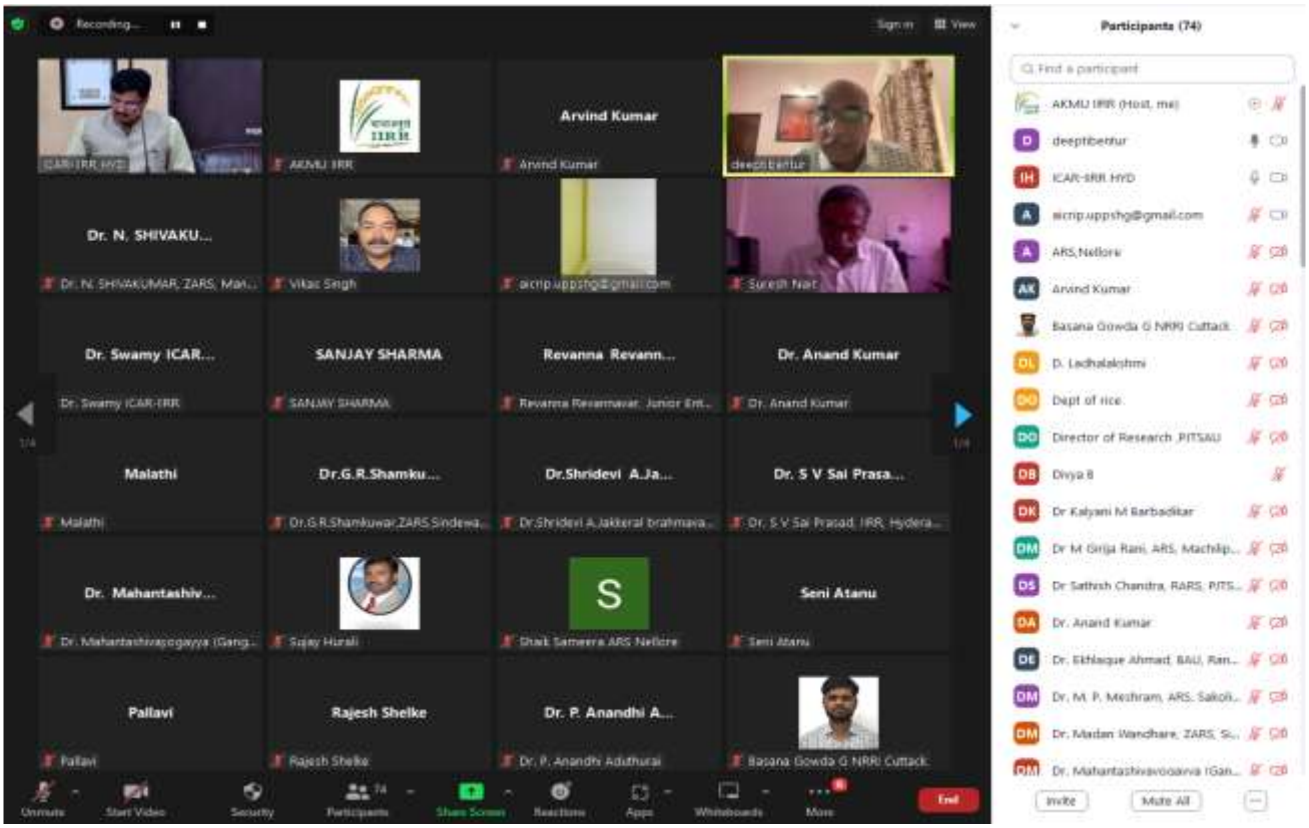
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