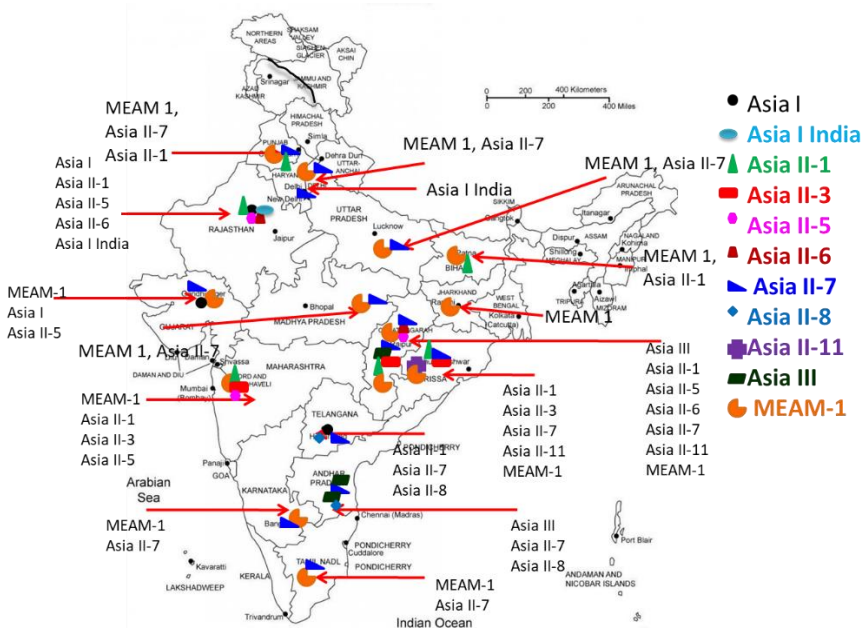
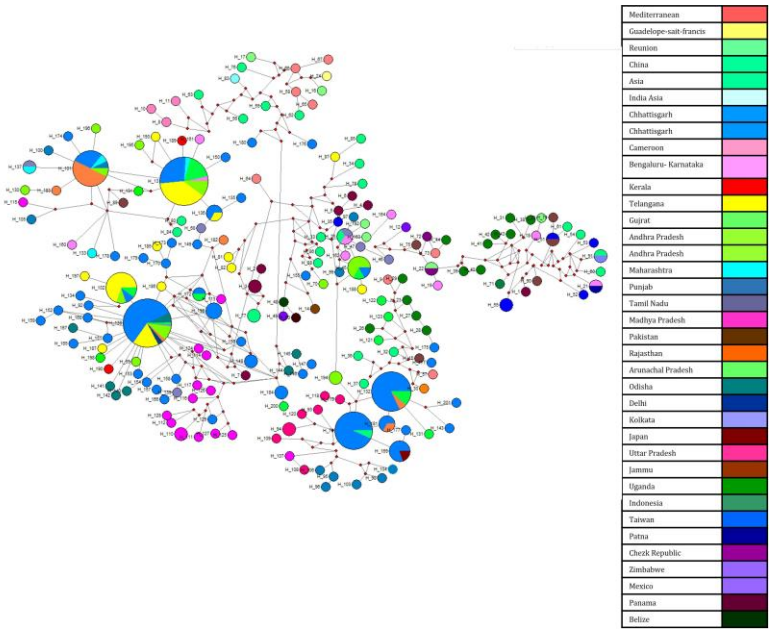
1. Mapping of genetic groups of *Bemisia tabaci* and their transmission efficiency

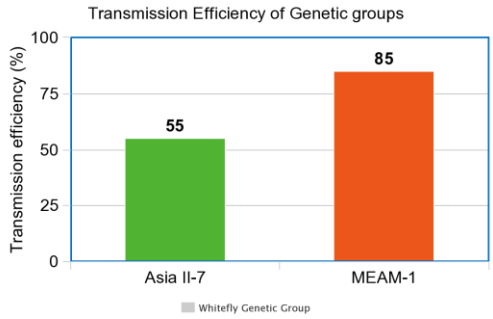
Salient Acievements

- Collected/procured 1225 *B tabaci* samples from 20 states of India. Isolated and amplified mitochondrial DNA from individual whiteflies and identified eleven distinct genetic groups of *Bemisia tabaci*, Asia 1, Asia I India, Asia II-1, Asia II-3, Asia II-5, Asia II-6, Asia II-7, Asia II-8, Asia II-11, Asia III, MEAM-1 of which Asia II-3, Asia II-6 & Asia III new to India and reported for the first time.
- The begomovirus transmission efficiency was determined to be 50-55% for genetic group, Asia II-7 and 80-85% for MEAM-1 in tomato. It is clear that MEAM-1 having very high transmission efficiencies with respect to begomovirus transmission. However, Asia II-7 also transmit begomovirus upto 50-55%.





Haplotype networking of *Bemisia tabaci* across locations in India



Begomovirus transmission efficiencies of Asia II-7 and MEAM-1

2. Pest dynamics and their management under conservation agriculture production system

Unusual infestation of Bihar hairy caterpillar

Monitoring of biotic stresses in longterm conservation agricultural Maize-mustard production systems. In Greengram, the first appearance of the BHC was recorded on the 35 DAS (days after sowing) with an initial mean population of 0.77 larvae/plant and reached a peak mean larval population of more than 18 larvae/plant at 52 DAS. Additionally, the pest was observed in greengram crop without residue with a mean larval population of 6.60 larvae/plant at 52 DAS. There was a gradual decrease in the incidence of Bihar hairy caterpillar after the application of Imidacloprid insecticide, and the population suddenly declined to 1.17 larvae/plant after the 59 DAS. The young larvae feed gregariously mostly on the undersurface of the leaves, causing the leaves to appear brownish yellow in colour.

a) Severe Bihar hairy caterpillar population on greengram leaves.

b) Skeletonized greengram crop.

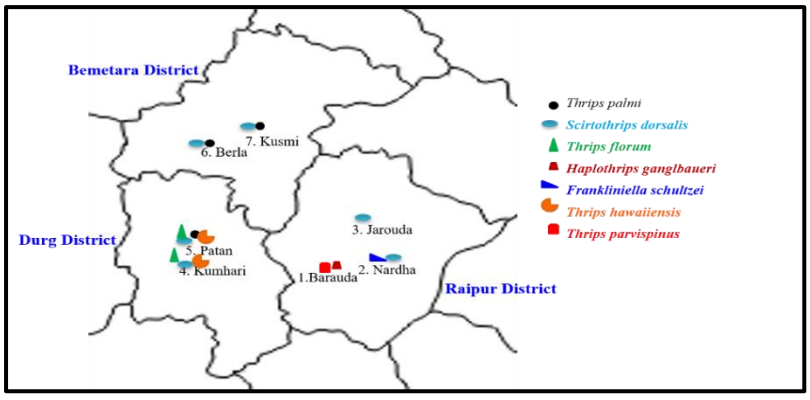
c) Larval scrabbing

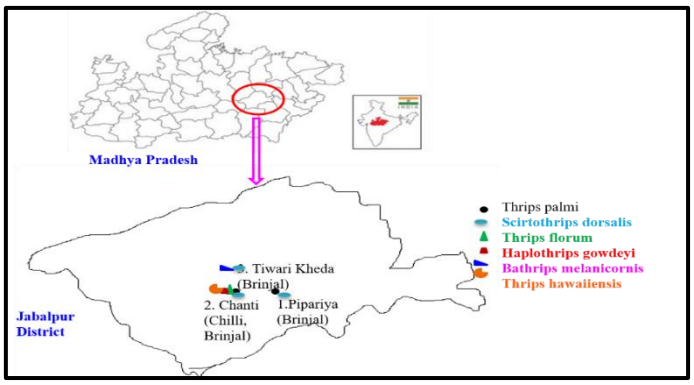
d) Infestation of Bihar hairy caterpillar on greengram crop.

3. Status of thrips species occurring on vegetable crops in Chhattisgarh and Madhya Pradesh

Collected thrips from vegetable crops (flowering and fruiting stage) 10 different locations covering four districts in Chhattisgarh and Madhya Pradesh and same were characterised using COI based makers.

1. A total of nine distinct species of thrips namely, *Thrips palmi*, *Scirtothrips dorsalis*, *Thrips florum*, *Haplothrips gowdeyi*, *Bathrips melanocrnis*, *Haplothrips gangldaueri*, *Francliniella schultzi*, *Thrips parvipsinus*. and *Thrips hawaiiensis* (Morgan) among various vegetable crops in these states.
2. Thrips species *Scirtothrips dorsalis*, *Thrips hawaeiinsis*, *Thrips parvispinus*, *Thrips palmi* and *Bathrips melanicornis* have been recorded on vegetables in Chhattisgarh. Cryptic species such as Thrips palmi and *Thrips hawaiiensis* were recorded in this study. *Haplothrips ganglbaueri* and *Thrips parvispinus* were reported first time from Chhattisgarh state while six species (*Thrips palmi*, *Scirtothrips dorsalis*, *Thrips florum*, *Haplothrips gowdeyi*, *Bathrips melanicornis* and *Thrips hawaiiensis*) were recorded on brinjal, chilli in Madhya Pradesh.

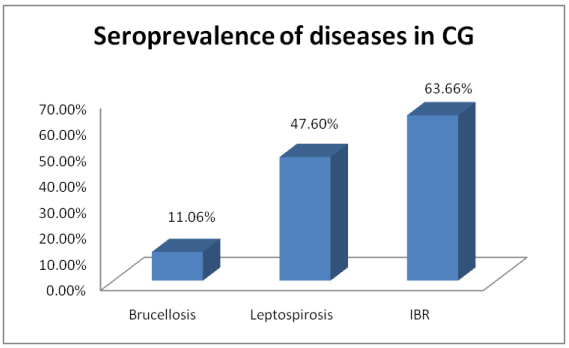


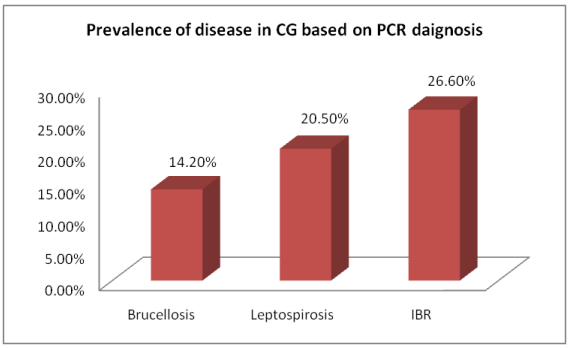


4. Studies on Microbes associated with Reproductive Biotic Stresses of Bovine

Salient Achievements:

- A total of 642, 464 and 432 serum samples of cattle and buffaloes from different districts of Chhattisgarh were tested by i-ELISA for presence of antibodies for brucellosis, leptospirosis and IBR respectively. The overall seroprevalence for brucellosis, leptospirosis and IBR was found to 11.06%, 47.6% and 63.66% respectively in bovine of Chhattisgarh.
- Out of 458 blood samples, 65(14.2%), 94(20.5%) and 122 (26.6%) were positive for brucellosis, leptospirosis and IBR using gene specific PCR.
- Attempted for isolation of *Brucella* spp. from 135 blood samples (stored at -80°C) and 16 clinical samples (10 vaginal swab and 6 aborted placenta): A total of 4 isolates of *Brucella abortus* were isolated from 2 blood, one vaginal swab and one aborted placenta. Isolates were confirmed by *bcsp31* gene PCR.

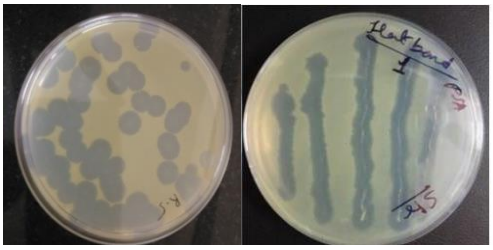




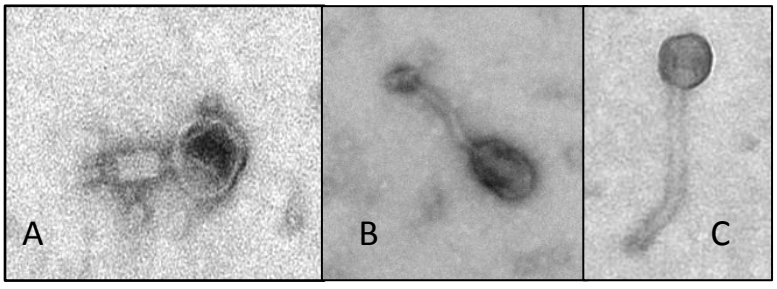
5. Identification and characterization of bacteriophages against rice bacterial leaf blight pathogen *Xanthomonas oryzae pv. oryzae*

Salient Achievements:

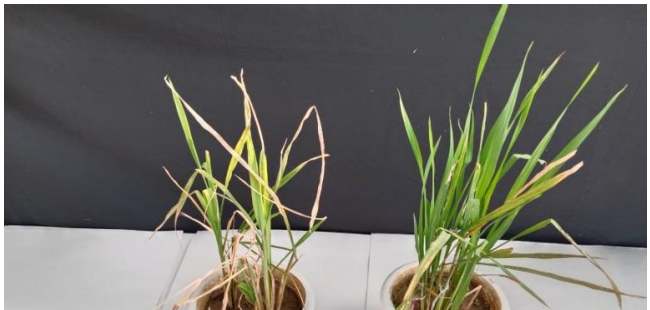
- A total of 146 rice field water and soil samples were collected from 26 districts of Chhattisgarh the adjoining seven states, out of which a Total of 19 bacteriophages (14 from Chhattisgarh, one Madhya Pradesh and one from Telangana state) were isolated against *Xoo* from rice field water and soil samples of 26 districts of Chhattisgarh the adjoining seven states.
- On Transmission Electron Microscopy, all phages were found to belong in order *Caudovirales* (having head and tail), and families *Myoviridae* (5), *Siphoviridae* (12), *Podoviridae* (1) and Unclassified (1). The length of head and tail varies from 60 to 75 nm and 135 to 265 nm, respectively.
- All the 19 phages were found to have ds-DNA as genetic material. Sixteen phages were whole genome sequenced using illumina based sequencing approach. The genome size range from 43.6 kbp to 203 kbp, GC content ranging between 46 to 67 % and having predicted number of genes ranging from 56 to 418.
- *In-vitro* efficacy studies in liquid culture medium shows up to 99.99% bactericidal activity for the host bacteria.
- Efficacy against BLB in rice pots: Rice plants were infected with *Xanthomonas oryzae* pv. *oryzae* pathogen at concentration of 2 x 10^8 cfu/ml. After 72 hours of BLB infection, plants were treated with selected bacteriophages at concentration of 2 x 10^7 pfu/ml using spray method. Preliminary protective efficacy of phage against BLB infection in rice pots shows significant reduction in symptoms of BLB in phage treated plants compared to untreated control plants.
- The field evaluation conducted during Kharif 2023 in small plots in rice cultivar TN-1showed high efficacy when Phage NR 08 alone or with skimmed milk (SM) was sprayed and observation recorded after 21 days of inoculation. The lesion length was reduced more than 70% when phage preparation used alone and with skimmed milk, the reduction was about 60%. The reduction in the infected leaf area due to bacterial blight was more than 77% and 67% respectively.



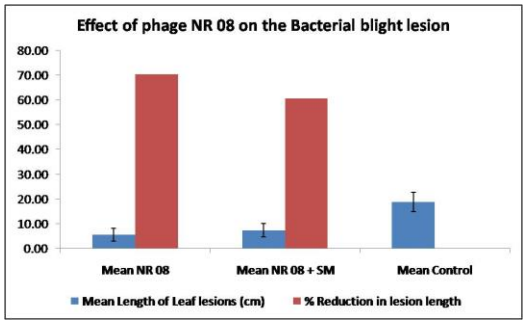
Plaques on overlay agar Clear zone around streaked lines

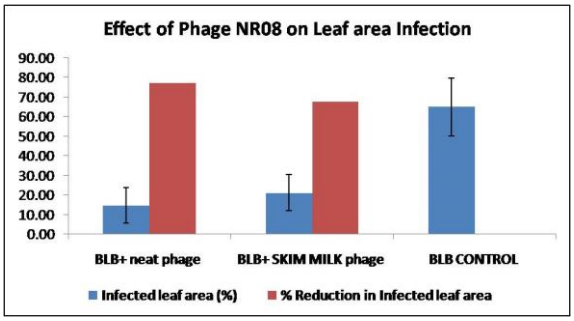


Electron micrograph of Bacteriophages: *Myoviridae* (A), *Siphoviridae* (B, C)



Significant reduction of BLB symptoms in phage treated rice plants and its leaves as compared to untreated control plants





6. Exploring rhizospheric microbiome diversity under emerging production systems in agriculture

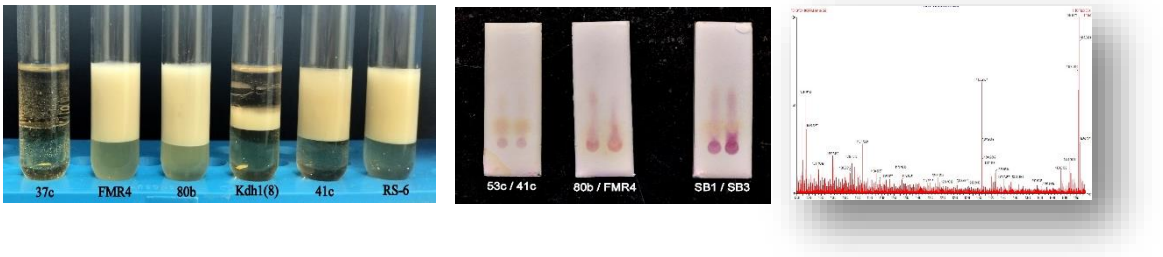
Salient Achievements:

- Collected rhizospheric soil and root samples from conservation agriculture fields of ICAR-DWR, Jabalpur from Kharif (From rice and maize based CA field), Rabi (from wheat and chickpea) and summer crop (from green gram) and from IARI, New Delhi Kharif Crop (Cotton).
- For culturable microbes: Isolated more than 300 bacterial isolates from rhizospheric soil of all the three season from Jabalpur and about 50 isolates from IARI. Isolates were screened on basis of colony morphology, KOH string test, catalase and oxidase test and stored as slant and glycerol stock.
- DNA samples from kharif crop of DWR, Further, for unculturable microbes identification through metagenomics approach, the rhizospheric soil and root tissues of maize crop from CA field of DWR were processed for full-length (V1-V9 region) 16s RNA amplicon sequencing using PacBio sequencing approach. Samples were processed for total genomic DNA extraction, quality check of DNA, amplicon and library preparation and amplicon sequencing.

7. Developing Antimicrobial Biosurfactant Producing-Bacterial Resources from Chhattisgarh State for Control of Phytopathogens Causing Diseases in Chickpea

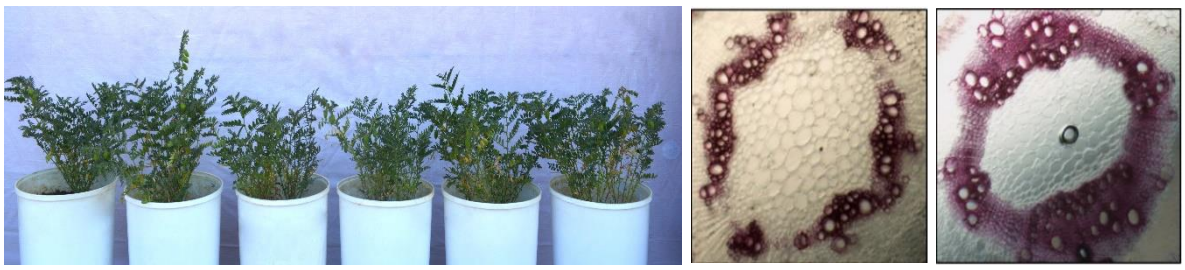
Achievements

- Out of 166 bacterial isolates recovered from different crop niches, more than 30 isolates have been found antagonistic to *Fusarium oxysporum* f.sp. *ciceris*, *Macrophomina phaseolina* and *Sclerotium rolfsii*.
- Off these antagonistic bacteria, 16, 25, 21,19 isolates have displayed oil spreading activity, parafilm test, emulsification assay and drop collapse, respectively, as tests for biosurfactant.
- Crude biosurfactant of 8 bacteria have inhibited growth of soil-borne pathogens and the biosurfactant was identified as lipopeptide by TLC and surfactin and fyngicin were found in crude lipopeptids as detected by UPLC-ESI-MS.
- Two potential isolates 80b and FMR 4 have been identified as *Bacillus amyloliquefaciens* spp *plantarum* by MALDI-TOF.



Confirmation of biosurfactant as a lipopetide. (left: Oil emulsion index test; Middle: TLC test ; Right: peaks of surfactin)

- Two strains of *Bacillus cabrialesii* IS-10 and *B. cabrialesii* BATS-13 isolated from chickpea rhizosphere soil of Chhattisgarh state have shown many plant growth promoting and biocontrol traits including lipopeptide production.
- Inoculation of *B. cabrialesii* IS-10 in two varieties of chickpea (Vaibhav, moderately resistant and JG-62, susceptible) improved growth and yield by controlling wilt diseases by around 50 % by inducing enhancing defence enzymes activities along with other PGP traits

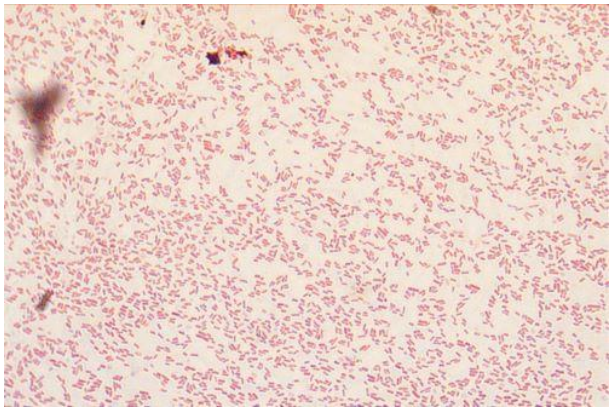


Influence of inoculation on plant growth and xylem lignification of chickpea cv JG-62. (Left: plant growth; Right: xylem lignification)

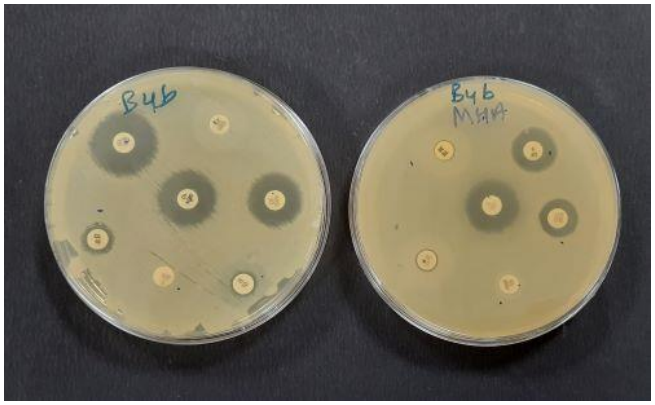
8. Prevalence and antimicrobial resistance profile of bacterial pathogens isolated from mastitis affected cattle in Chhattisgarh

Bovine mastitis, characterized by udder inflammation, is one the most prevalent diseases of dairy animals to spread antimicrobial resistant bacteria to human through contaminated milk. Therefore, isolate and characterize the pathogens associated with mastitis and to detect newly emerged antimicrobial resistant genes New Delhi metallo-β-lactamase (NDM1) and β-lactamases (bla_{TEM}) in the prevalent isolates was planned. Milk samples (n=84) were collected from three different districts in Chhattisgarh viz. Raipur, Durg and Bilaspur. The prevalence of clinical and subclinical mastitis was 15.5% and 38%, respectively. A total of 136 bacterial species were isolated with the majority being Bacillus spp. (16.9%), Staphylococcus spp. (14.7%), Micrococcus spp. (14%), Streptococcus spp. (11.8%) and Escherichia coli (11.7%) on preliminary observations through Gram staining and biochemical tests. The antibiotic sensitivity tests were carried out against 11 commonly used antibiotics belonging 4 antibiotic classes. These isolates showed high resistance rate to Beta Lactam Penicillin and Cephalosporin (74%) followed by Aminoglycosides (55.3%), Tetracycline (44.6%) and while the least resistance was detected for Sulfonamide (38.3%) group of antibiotics. The presence of antimicrobial resistant genes viz. NDM1 and bla_{TEM} were screened through PCR on 11 bacterial isolates. A total of 10 isolates (91%) showed resistance to bla_{TEM} while 4 isolates (36%) showed resistance to NDM1 antimicrobial gene.

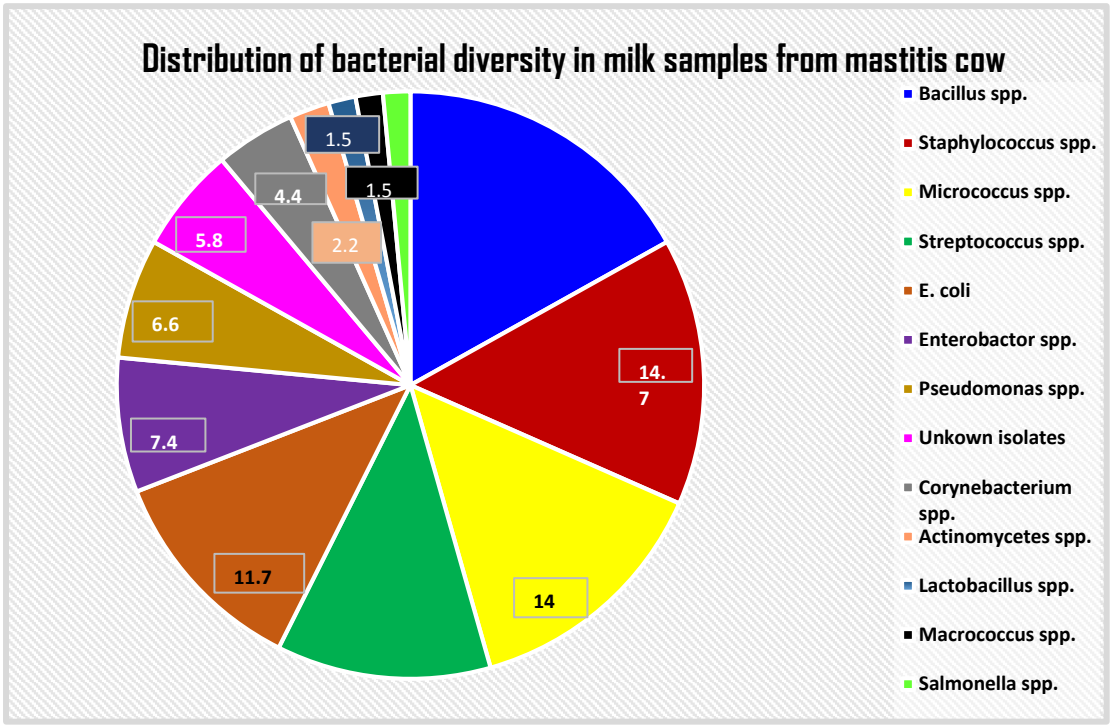
Pure culture of B4b isolate



Gram staining of B4b isolate



Antimicrobial susceptibility testing of B4b bacterial isolate



Distribution of bacterial diversity in milk samples from mastitis cow.