

## Emerging Insights into Staphylococcal Food Poisoning and MRSA: A Call for Enhanced Surveillance and Research

Staphylococcal food poisoning (SFP) is a prevalent foodborne illness globally, with around several million cases reported annually. As per a report, in India, over 100 people fell ill from SFP, wherein microbiological tests detected Staphylococcal enterotoxins. The potential impact of research on SFP is significant, particularly in the case of *S. aureus*, which is shown to transition from a harmless commensal to a harmful pathogen, posing a critical clinical threat with its antimicrobial resistance, rapid transmission, and severe infections.

Over the years, numerous studies have attempted to delineate the molecular mechanisms behind staphylococci's adaptability, making it one of the most extensively researched pathogens. While the bacterium continues to cause food poisoning, its increasing antibiotic resistance makes it even harder to control. In this regard, DBT-funded research at @icar-cift highlights the aspects of aquaculture-associated public health concerns.

Thus, methicillin-resistant *Staphylococcus aureus* (MRSA) clones, once thought to be region-specific, are now spreading globally, with strains found in both clinical and non-clinical settings showing genetic similarities and raising concerns about their widespread adaptability. Addressing this, researchers at - @ICAR-CIFT studied the whole-genome complexities of MRSA and MRSH strains isolated from commercial fish outlets, underlining the peculiarities attributed to their virulence, antimicrobial resistance, and epidemiological factors at the molecular level.

The study becomes the first one to confirm the occurrence of ST88 and ST672 MRSA strains in non-clinic settings. Genomic portraits described the presence of genes for heat-resistant staphylococcal toxins, increasing the risk of MRSA as food-borne pathogens. Evolutionary insights were sought through a comparative analysis of genomes from clinical and non-clinical settings, suggesting emergence from a common ancestor and indicating transboundary spread. Findings emphasize the critical need for comprehensive monitoring across humans, animals, food, and water sources to prevent them from becoming key hubs for the spread of AMR, as well as the broader environment, to better control the spread of MRSA.