

Breakthrough in Jute Retting by ICAR – CRIJAF through Genome Sequencing of Microbes of Microbial Retting Consortium

India is the largest producer of raw jute and jute goods in the world, contributing about 60% of the global production and providing livelihood support to about 5 million people in farming, trade and industry. Although, the domestic market continues to be the mainstay for jute sector, of late, our export market share is also showing an increasing trend. India today earns about Rs 2200 crores per annum through jute goods export because of bio-degradability and ecofriendly nature of this versatile natural fibre. However, to be suitable for high valued diversified products, the quality of fibre needs further improvement through evolving better varieties and efficient retting process. Research has been initiated by ICAR – Central Research Institute for Jute and Allied Fibres, Barrackpore under the visionary leadership of Dr. Trilochan Mahapatra, Honourable Secretary, DARE and Director General, ICAR; Dr. Tilak Raj Sharma, Deputy Director General, Crop Sciences, ICAR; Dr. R. K. Singh, Assistant Director General, Commercial Crops, ICAR to improve fibre quality and to make the jute fibre internationally competitive through retting with free flowing water, *in situ* retting tank based farming with a microbial consortium 'CRIJAF SONA'. Application of "CRIJAF SONA" microbial consortium during retting improved fibre quality by 1-2 grades, reduced duration of retting by 7 days and also reduced retting water requirement by 75%. Owing to its popularity, in last three years alone, 1428 MT of CRIJAF SONA worth Rs.7.85 crore was sold to 3.6 lakh farmers covering more than 50,000 ha area in different jute growing states of the country.

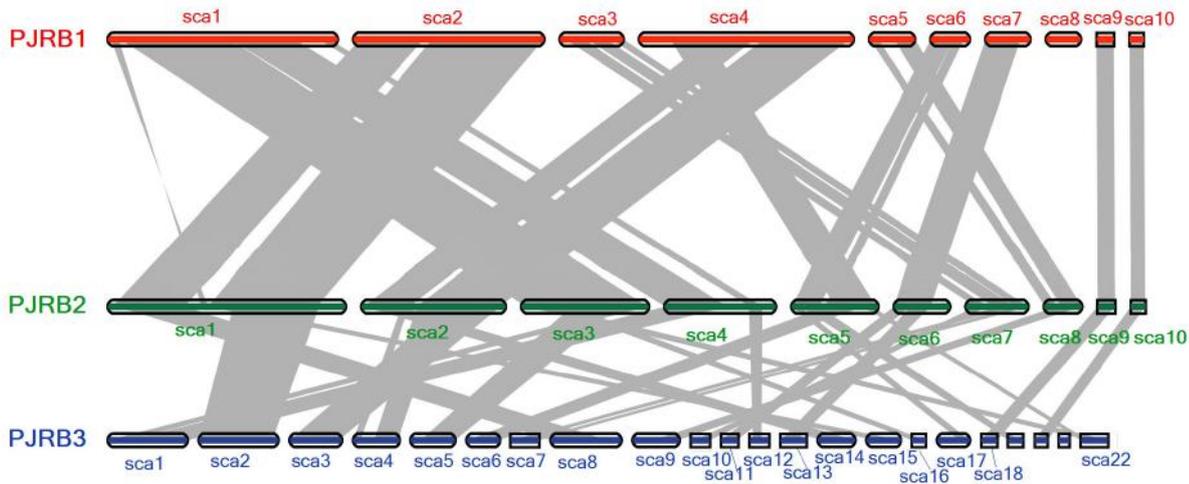


Packets containing Microbial Retting Consortium 'CRIJAF SONA'



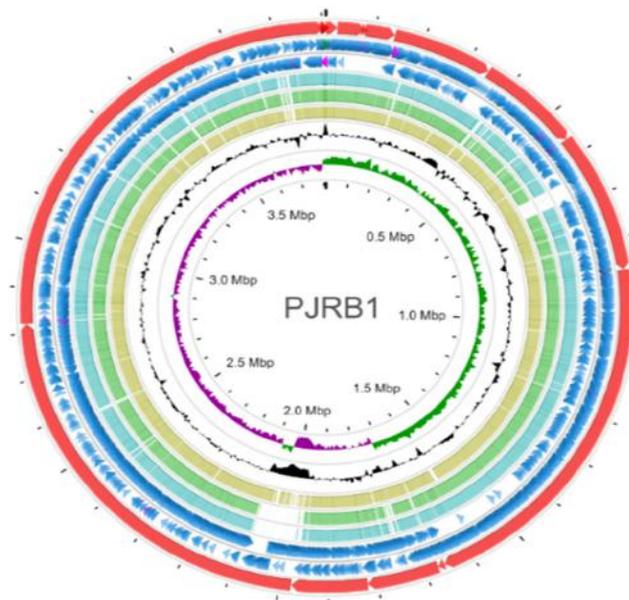
Application of CRIJAF SONA during jute retting

Dr. Gouranga Kar, Director of ICAR-CRIJAF, Barrackpore mentioned that recently a breakthrough in jute retting has been achieved by scientists of ICAR – CRIJAF who have decoded the genome sequences of jute retting microbes by high throughput genome sequencing. The in-depth genomic analysis significantly revealed three different species of *Bacillus* constitute the consortium strains. The genome sizes of these strains are ~3.8 Mb with 3729 to 4002 protein-coding genes. The sequence data has been submitted to the National Centre for Biotechnology Information (NCBI) database of NIH, USA. Genome sequencing also confirms that retting bacteria degrades pectin, hemicellulose and other non-cellulosic materials, non-harmful for fibre. The bacterial strains are also non-toxic and thus the retting water with microbial strains can successfully be used for irrigation purpose.



Investigators of the findings opined that these breakthrough findings will help to further the knowledge on the unique microbial retting process in jute and will accentuate the improvement in this microbial formulation. For example, the genes for degrading pectin, hemicellulose and other non-cellulosic materials can be altered for enhanced retting efficiency and shortening the retting duration with minimal water usage.

It is believed that this will also open up an avenue to characterize the enormous diversity of retting microbial population at the metagenome scale and incorporate other strains to complement the consortium. This will not only facilitate IPR protection of the indigenous microbiome but will also establish a correlation between the microbial diversities and regional differences in fibre.



The findings of the genome sequence research is recently published in high impact factor journal Scientific Reports (NAAS: 10.01) from Nature Publishing Group (Ref. Datta, S., Saha, D., Chattopadhyay, L. and Majumdar, B. (2020). *Genome Comparison Identifies Different Bacillus Species in a Bast Fibre-Retting Bacterial Consortium and Provides Insights into Pectin Degrading Genes.* **Sci Rep** 10, 8169. <https://doi.org/10.1038/s41598-020-65228-1>.)