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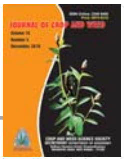

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Critical review on microbial perspective of jute retting

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ABSTRACT

Jute is considered as "cash crop" because of its economic importance which chiefly depends on the fiber quality. Amongst several factors, retting is considered to be the most important to obtain high quality fiber. Retting is the result of combined action of aquatic microorganisms and water on jute stem. During this process, enzymatic activities of aquatic microorganisms lead to degradation of "cementing materials" pectin substances between the cells and help to separate the fiber from stem. During retting, microbial status of retting water as well as biological property of water is changed. Literature study reveals the microorganisms having high pectinolytic activity coupled with xylanase activity is essential for effective jute retting while cellulosic activity of microorganisms degrade the fibers itself quality. Microbial jute retting has immense potential under the changed climatic situation due to global warming under water scarcity condition. Keeping view on the interdependent role of both of water and microorganisms, here an attempt has been taken to summarize the retting microorganisms with special reference to their role during retting.

Keywords: Enzyme, jute, microorganisms, retting

Jute, the fiber crop is considered as second cheapest natural fiber in the globe (Ray *et al.*, 2015), holds a significant position in fiber industry by providing nearly 15% of total industrial fibers (Haque *et al.*, 2001). Jute fiber is eco-friendly, recyclable in nature and most suitable for packaging of agricultural goods (Ahamed and Nizam, 2008). Fibers are also traditionally used to prepare mats, wires, carpets, bags etc (Jahan *et al.*, 2011). Beside jute improves the fertility of soil, preserve the ozone layer by absorbing and releasing CO_2 and O_2 respectively. Uses of jute stick for cooking in rural area reduces wood dependency which indirectly reduces deforestation rate (Islam and Ahamed, 2012). In India, jute based and associated industries are income generation source for nearly 4 million families (http://ministryoftextiles.gov.in/pdf/ar03_c11.pdf). Though there are several advantages, but low production of fiber as well as use of substitute (synthetic supplements/ plastic) make this industry vulnerable today in terms of its socioeconomic importance (Rahman et al., 2017). So there is need to improve the fiber quality with most updated technologies or diversifying the use of jute fiber to regain its value in international market. Ghosh et al. (2014) reported that jute varieties are significantly diversified on their fiber quality in terms of luster, length and rigidity of the fiber. Though fiber quality is influenced by several factors like variety, sowing time, agricultural practices but most important one is the retting (Islam and Rahman, 2013). Retting is carried out by aquatic microorganisms results separation of fiber from the stem. Since retting is major quality determining factor of jute fiber, here an attempt has been taken to review the microbial perspective of jute retting with special reference to its status, role and impact during retting.

Retting: Jute fibers are ligno-cellulosic due to presence of cellulose (mainly), hemicellulose and lignin on it (Duan *et al.*, 2017). Each fiber consists of large number of cells joined together by cementing materials such as pectin and hemicellulose (Deb, 1954; Mian *et al.*, 1996; Ray *et al.*, 2016). During retting, these fibers are isolated from the stem due to combined action of water and aquatic microorganisms (Ali *et al*, 2015). The effective retting showed superior quality fiber having high market value while improper retting leads to inferior quality of fiber. Retting time varies according to thickness and maturity of stem (Banerjee, 1955). So retting is not only related to fiber extraction but also quality determining factor of fiber i.e. market value of jute fiber (Jahan et al., 2016).

Retting may be either water or dew based retting (Tamburini et al., 2003) but till date most of jute retting based experiment is restricted to water retting due its simplicity. Though there are several problems such as more time consuming, improper retted fiber and more laborious (Chapke and Borkar, 2011) but till now, most of the jute growers are depending on the conventional method of retting over other improved methods of retting (chemical, microbial and mechano-microbial retting).

Conventional Jute Retting: During conventional retting, jute bundles are traditionally immersed in open water reservoir like rivers, canals and ponds with the help of jak materials (Majumdar *et al*., 2008). Thereafter mud and banana stems are used to put over the jak material for complete immersion of bundles of jute in water. Retting under water stress condition promotes low quality fiber in terms of its color and physiochemical parameters (Banik, 2016). At least 1:20 ratio for plant

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to water is suitable for jute retting under stagnant water (Jahan *et al*., 2016). Besides selection of covering material and deepness of layers of jute bundles are considered to be critical factor to get quality fiber (Kundu, 1956). During retting, the cementing materials i.e. pectins, hemicelluloses and proteins of stem are consumed by the aquatic microoagnism (Banik and Ghosh, 2008). Thereafter, these bundles are taken out from the water to extract the fiber manually from the retted stem (Sarkar and Sengupta, 2015). But this method is time consuming and responsible for water pollution due to biomass deposition within water reservoir.

This problem could be overcome by using the ribbon retting suggested by several authors. In this method, bark is detached from stem prior to transfer into water. Due to this invention, retting microorganism gets more surface area of inner side of the bark with respect to conventional method (Banik *et al*., 2007). Though ribbon retting is more advantageous over the traditional method in terms of retting duration, water content and environmental pollution (Banik *et al*., 2003) but more laborious in nature.

Jute retting: Microbial perspective

***Status of retting microorganisms during retting*:** After immediately transfer of plants into water during conventional retting, water uptake by plants results swelling and rupturing the plant surfaces leads to release of the organic compounds (soluble carbohydrates, proteins and various organic compounds) from the plant body into water (Ahmed and Akhter, 2001). These soluble components are utilized as energy source by retting microorganisms to enhance the microbial population in water reservoir (Ali *et al*., 1976; Das et al., 2014). At this stage, due to fermentation of the organic compounds, pH and oxygen content of water reservoir is reduced. As a result, anaerobic (especially microaerophilic) microorganisms are found more prevalent during the later stage of retting while aerobic microorganisms are active on initial stage of retting (Islam and Rahman, 2013).

Micro-aerophillic/anerobic bacteria is entered into the tissues to decompose the cementing materials (mostly pectin) connecting the fiber strands with release of galacturonic acid and sugar in retting water (Basak *et al*., 1998; Banik and Ghosh, 2008). The greater part of decomposition during retting was performed by anaerobic microorganisms. At this stage, the pH value is again increased because of the formation of buffering organic compound and the retting of the plant is completed (Ali and Alam, 1973; Islam and Rahaman, 2013).

Release of organic compounds and its products in stagnant water during retting interfere with the microbial growth and their activity. Hence retting under slow moving water is found better for good quality fiber (Kundu *et al*., 1952; Ray *et al*., 2015a).

Biochemical basis of microbial jute retting: Bast fiber is multicellular in nature and the aggregate of cells are joined together by pectin (Paridah *et al*., 2011). Pectic substances i.e. acidic polysaccharides are present in form of calcium and magnesium pectate in middle lamella of cell (Jayani *et al*., 2005; Murad and Azzaz 2011; Chiliveri *et al*., 2016). Pectins are composed of multiple units of galacturonic acid which are connected through á-1,4 glycosidic bond, with a side chain of simple monosaccharides (Gummadi and Kumar, 2006). Traditionally retting is performed by pectinolytic enzymes secreted by microorganisms (Tamburini et al., 2003). Quality of fiber depends on nature of retting. Over retting by microorganisms degrades the fibers (cellulose) while incomplete removal of fiber from stem due to under retting produces low quality fiber (Banik *et al*., 2003).

Pectinases are mainly consists three enzymes viz. polymethylesterase, polygalacturonase and pectate lyase (Jayani *et al*., 2005, Abbasi and Fazaelipoor, 2010, Prathyusha and Suneetha, 2011). Though according to Das *et al*. (2012), four enzyme *i.e*. polymethylesterase, polygalacturonase, pectate lyase and pectin lyase are belonging to group "Pectinase". Methylesterases converts the pectin substrate to pectate by eliminating the methoxyl group from pectin (Kohli *et al*., 2015) while degradation of á (1-4)–glycoscidic linkage between the galacturonic acid molecules is carried out by polygalacturonse (Prathyusha and Suneetha, 2011). Pectate lyase degrades pectin by removing oligosaccharides of á (1-4) linked galacturonic acid molecules. Various literature suggested that polygalacturonase (Chesson, 1978; Akin *et al*., 1998; Zhang *et al*., 2000; Tamburini *et al*., 2003) and pectin lyase (Soriano *et al*., 2005; Das *et al*., 2012; Das *et al*., 2015) are the primary retting agent. During retting, pectic components are changed into soluble pectin followed by pectic acid in presence of pectisinase and pectase respectively (Bhuiyan et al., 1979; Haq *et al*., 2001a). The pectic are converted to glutamate in presence of pectinase. In addition to pectinolytic activity, xylanase activity of retting microorganisms is improved the fiber quality (Gomes *et al*., 1992). Improper removal of the non-fiber components like hemicelluloses converts the jute fiber considerably softer for finer spinning (Ray *et al*., 2015). Hence microorganism having high pectinolytic and xylanase activity along with low/least cellulase activity can be considered as efficient retting microbes to get good quality fiber (Das *et al*., 2018).

Microorganisms in Jute retting:

Study on the role of microorganisms related to jute retting started at early nineteenth century. Prior to 1950s, jute retting based experiments were focused on influence of isolated aerobic microorganisms involved on retting of jute stem by conventional culture based approaches. During this phase, Debsharma (1946) reported several notable bacterial strains like *Bacillus subtilis*, *Bacillus* *mescentrichus* and *Bacillus macreans* for effective jute retting. Barinova (1946) sketched some quantitative assay about pectin fermentation by *Clostridium felsineum* and *Bacillus acetoethylicus*. Whereas Potter and McCoy (1952, 1955) checked the retting ability of *Clostridium felsineum* and *Bacillus polymyxa*. Ali (1958) isolated a spore forming rod shaped bacteria and reported as *Bacillus polymyxa*, and got retted jute stem within 10 days in laboratory condition. Betrabet and Bhat (1958) tried to explore retting efficiency of the microbes of the genera *Pseudomonas*, *Bacillus*, *Aerobacter* and *Flavobacterium* for jute under retting tank condition. Chakravarty et al. (1962) clearly reported and identified some fastidious fungal species which grown repeatedly in usual fungal medium from retting water were *Aspergillus terrreus*, *Pacilomyces varioti, Penicillium citrinium*. Whereas Ahmed (1963) reported some fungi of phylum Ascomycota *i.e. Penicillium* sp., *Aspergilus niger*, *Macrophomina phaseolina*, *Chaetomium* sp., *Phoma* sp. and *Mucor* sp. of phylum Zygomycota for efficient retting. Alam (1970) isolated some anaerobes from retting water and reported those species as *Clostridiumtertium aurantibutyricum*, *C. felsineum*. Haque *et al.* (2002) investigated the community structure of microbes of different stages of jute retting period. Munsi and Chatto (2008) analyzed the bacterial diversity of jute retting ponds located at southern region of West Bengal using metagenomic approaches and found seven groups of bacterial species like proteobacteria (41%), Fermicutes (12%), *Cytophaga–Flexibacter–Bacteroidetes* (7%), *Verrucomicrobia* (5%), *Acidobacteria* (5%), *Chlorobiales* (5%), *and Actinobacteria* (2%). On the other side Akhtar and Mandal (1996) elaborated the population structure of rhizosphere and retting ponds of jute and other fibrous plants and they concluded that fungal diversity was dominant on post retting water. Das *et al.* (2012) studied in details the diversity of pectinolytic bacteria from jute retting ponds and they found the variation in concentration for polygalactouronase, pectin lyase, as well as xylanase. Quantitative analyses of microbial jute retting enzymes were also studied by Ray *et al.* (2015). Keeping view in role of microorganisms in retting, scientists are engaged to identify effective retting microorganisms though reports are very less. Most of effective retting microorganisms identified till date either based on Bergey's Manual or Biolog analysis or 16S rDNA sequencing (Table 1). It is very much important to know the kinetics study of those enzymes and from that knowledge the optimum time period, temperature, pH can be standardized. This type of experiments was done different natural fibre crops like kenaf, hemp, mestha but in case of jute these types of research reports were very few (Basu *et al*., 2009; Juarez *et al*., 2009; Yu and Yu, 2007 and Zhang *et al*., 2000). Chiliveri et al (2016) reported an UV mutant *Bacillus tequilensis* strain SV-11-UV-37 which has highly efficient polygaclactouronase, pectin lyase and xylanase producing organisms and developed a solid state fermentation technique to produce high quality of jute fiber in cost-effective way. In another report, Nath et al. (2017) showed that three effective polygalactouronase and pectin lyase secreting microbes solely as well as in combination developed the overall retting process and produced a goodqualty of fibre. Das et al. (2018) used various microbial consortium and clearly showed high quality of fibre production with better strength and fineness using dry retting technique. Whereas Vijayraghaban and Stephen (2012) experimentally construct sequencing batch reactor which using aerobic microbial jute retting. In this method retting period was characterized based on tenacity and modulus, after 25 days of retting the quality of fiber is the best. After retting the liquor of retting was characterized and the structure of microbes was identified which showed species of *Bacillus*, *Clostridium*, *Aspergillus* and *Mucor* was predominant.

The glories of jute based industry declined due its low quality fiber and increase the use of synthetic fibers. So there is need to improve the fiber quality with most updated techniques. Retting is the quality determining factor of jute. Currently most problematic issue of jute retting is scarcity of water. In spite of high pectinolytic activity, improper retting leads to low quality jute under low water content. So dew retting or ribbon retting is going to be an alternative of conventional retting in upcoming time. There need to do multilocational trial of effective pectinolytic microorganisms to justify the activity against the biotic and abiotic factors. Till date the research on microbial jute retting is restricted to single microorganisms, need to explore the combined effect of retting microorganisms. Bioreactor based retting is also found most cost effective and profitable in comparison to others techniques.

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