Biodegradation of polyurethane

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Abstract: The worldwide occurrence of synthetic polymers are increases dynamically and their resistance against degradation creating various environmental concerns. These polymers linger on the environment for a long time period. In current scenario, researcher focus on the production and recycling processes of synthetic polymers. Polyurethane is one the representative member of this polymers group, it serve as manmade polymer and uses in sever sectors i.e. Industrial, medical etc. Polyurethane polymers form by the condensation process of polyalcohols and polyisocyanates. Such polymers having valuable importance due to their biodegradation susceptibility. Physical and chemical properties of polyurethane alter the degradation ability of microorganisms and hydrolyzing enzymes. Esterase reported as an effective enzyme for hydrolyzing of ester linkage and polyurethane degradation.
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1. Introduction

Incredible production and uses of synthetic polymer lead to several environmental threats. These polymers showing resistance against degradation which increases their persistence throughout the world. Polyurethanes uses in several areas due to their physical and chemical feasibility and rapidly replacing the preexisting polymer material such as latex rubber [Ulrich, 1983]. Industrial and medical sector one of biggest market of polyurethanes polymer. It employed in adhesives, elastomers, elastomers, synthetic skins and paints.

Polyurethanes serve with extensive properties such as tensile strength and melting points that provided abrasion resistance, weather resistance, oils and solvents resistance. These properties increase their valuable importance that make it suitable alternative of plastic [Howard G. T., 2002]. Polyurethanes also known as mixed polymer. It derived from poly addition of polyisocyanate, during their production initial hydroxyl groups of polyols reacting with precursors of isocyanate and form polyurethanes [Howard G. T., 2011]. These polymers consists ester, urethane linkages that make it susceptible to microbial degradation. Microorganisms contain extracellular or membrane bounded esterase and plays key role in breakdown the backbone of polyurethane [Howard G. T., 2002].

Biodegradation serving as eco-friendly approach to remediate polymer contamination. It effective against different type polymer and depends on their chemical constituents and physical properties. Numerous microorganisms were reported for polyurethane utilization as sole carbon source. In this study discuss the subset of microorganisms that associated with polyurethane degradation.

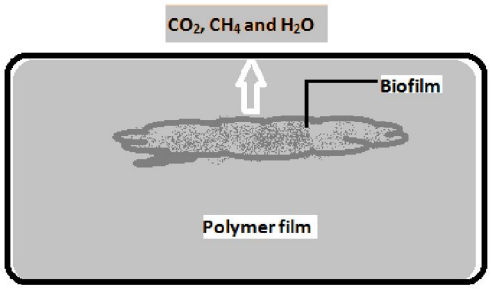

Fig. Biodegradation of polymer film

2. Biodegradation of polyurethane:

Polyurethane (PUR) contains urethane bond in between polyaddition of diisocynate and form high molecular weight polymer i.e. ~200 as well as 6000. Although these synthetic polymers are high molecular weight, hitherto it shows the susceptible to biodegradation [Shimao M., 2001].

In addition to polyurethane one another type of polymer exist i.e. polyethylene adipate (PEA), it is pre-polymer form of polyurethane and also contains urethane bonding in their structure [Bhardwaj *et al.*, 2012]. Some polyurethane hydrolyzing enzymes reported previously as lipases ureases, esterases and proteases. These enzymes involve in the breakdown of ester linkage. *Chaetomium globosum* and *Aspergillus terreus* were reported for urethane and esterase production, while *Trichoderma* sp. producing ureases and to utilized the polyurethane [Bhardwaj *et al.*, 2012; Howard G.T., 2012].

Candida ethanolica and *Fusarium solani* were associated with polyurethane substrate [Schink *et al.*, 1992; Zafar *et al.*, 2013]. But *Curvularia senegalensis*

was identified as most prominent polyurethane degrader microorganism [Howard G. T., 2002]. Howard G.T. (2012) observed the extracellular membrane bound enzymes play significant role in polyurethane degradation and they also reported polyurethane serves as nitrogen and sole carbon source for *C. acidovorans*. Bhardwaj *et al.* (2012) mention in their research article *Pestalotiopsis microspora* for the synthesis of serine hydrolase and utilize the polyurethane as carbon source. In previous, Loredo-Trevino *et al.* (2011) conducted the studied on 22 fungal strains and they found that 95% strains showing urease activity, 86% strains showing protease activity, 50% strains showing esterase activity and 36% strains showing laccase activity, all four enzymes comprises hydrolyzing properties.

Bhardwaj *et al.*, (2012) reported urease and papain as proteolytic enzymes for the biodegradation of polyester (polyurethane polymers) that uses medical sectors. Similarly Chandra and Rustgi (1998) observed polyurethane biodegrading ability with subtilisin as found in papain. Polyurethane utilized as substrate by *Comamonas acidovorans* TB-35 strain and diethylene glycol and adipic acid were identified as their microbial degraded products. *C. acidovorans* contains cell bounded enzymes and accountable for hydrolysis of polyurethane polymer. Genes that are responsible for synthesis of these enzyme are encoded the 548 amino acid sequence protein with different type domains i.e. hydrophobic domains serving for polymer interaction and attachment, signal sequence, lipase box and catalytic domain. Several bacterial and fungal species were identified and reported for polyurethane degradation i.e. *Pseudomonas aeruginosa, Bacillus, Comamonas, Aspergillus niger, Arthrographis kalrae, Aspergillus funeigatus, Fusarium solanii*, *Emericella*, *Thermomyces*, *Emericella*, *Corynebacterium* sp., *Alternaria*, *Plectosphaerella, Phoma, Nectria, Neonectria* [Shimao M., 2001; Chandra and Rustgi, 1998; Flavel *et al.,* 2006; Zafar U., 2013; Akutsu *et al.,* 1998; Bhardwaj *et al.*, 2012]. *Acinetobacter gerneri* soil bacteria characterized by Howard *et al.* (2012) and reported for polyurethane degradation.

Bacillus sp. AF8, *Pseudomonas* sp. AF9, *Micrococcus* sp. 10, *Arthrobacter* sp. AF11, and *Corynebacterium* sp. AF12 soil bacteria were characterized by Shah *et al.* (2008) and identified as polyurethane degraders by means of utilization such polymers as carbon source. SEM, FT-IR, CO_2 estimation and esterase activity some of the analytical approach that determining and conform the polymer degradation. In addition to these approaches, tensile strength is also on key determinative factor that help to the examination of polyurethane degradation. Such type practices were employed by Upreti and Srivastava (2003) and they analyzed the polyurethane biodegradation with *A. foetidus* treatment. Ma and Wong (2013) working with another key factor i.e. esterase activity in *A. favus*, which mainly responsible for biodegradation process. They also employed recombinant DNA technology for mass production of esterase enzymes, esterase genes transfer from *A. favus* transfer to the *P. pastoris*.

Howard G.T. (2012) reviewed the several reports on polyurethane biodegradation and explains the gene silencing and cloning analysis were conducted with *P. chlororaphis* and *Escherichia coli*. And gene *pue*A, *pue*B were characterized as key enzyme polyurethane degradation, which are located along with seven open reading frames and cluster gene of ABC transporter [Howard G.T., 2012]. Gene *pue*A played important role to enhancing cellular density and degradation capability. Enzymes that involved polyurethane hydrolysis followed the Type I secretion system (employed glycine-rich RTX motifs and C-terminal hydrophobic secretion signal) and maintain Ca^{2+} roll structure that important for secretion and alignment of signal [Howard *et al.,* 2007; Howard G.T., 2012]. Researcher reported previously *pue*A cloned from the *P. chlororaphis* to *E. coli* and encoded the extracellular enzyme that showed similarity with the Group I lipases. In addition Group I lipases, serine hydrolases also identified as polyurethane hydrolyzing enzyme which form serine triad structure with histidine and aspartate /glutamate [Howard G.T., 2012].

Stern and Howard (2000) reported protein having molecular weight 65kDa that displayed the serine hydrolase characteristic when exploited with pT7-6 vector. Similarly Howard *et al.* (2012) characterized the 66 kDa enzymes that involved in polyurethane hydrolysis. Enzymatic activity is alter positively as well as negatively in presence of nitrophenylpropanate and ethylenediamine-tetra acetic acid respectively. Polyurethanase also the example of 48 kDa protein that successfully cloned and expressed in *E. coli*. Researcher doing much of practices on isolation and screening of new potential polyurethane degrading enzymes in addition to expoilation of advanced analytic approaches.

3. Conclusions:

The synthesis process of polymer in addition to their physical properties and chemical nature determined durability and resistance nature of the polymer. Crystalline and amorphous regions are exists in polyurethanes, amorphous structure of polyurethanes are more susceptible to microbial degradation in compare to crystalline structure. Ureases, esterases, proteases and lipases were reported for polyurethanes biodegradation and esterase one of

the best studied hydrolyzing enzyme that act on ester linkage in polyester part of polyurethanes. Soil occurring microorganisms widely reported for polyurethane degradation. *Bacillus*, *Pseudomonas*, *Micrococcus*, *Arthrobacter*, and *Corynebacterium* spp. are the bacterial genus and *Aspergillus, Emericella* and *Fusarium* fungal genus associated with polyurethane degradation. In current still the need the Present study suggested that still needs the investigation on screening the of indigenous new polyurethanes degradation microorganisms for polyurethanes waste management point of view.

List of abbreviations:

PUR: polyurethane; PEA: polyethylene adipate.

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Authors' contributions:

All authors have contributed regularly in the manuscript. Author Vinay Mohan Pathak has carried out the data study. Author Navneet has guided throughout the study. All authors have examine and permitted the final manuscript.

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