Abstract

Pectinases are pectin degrading enzymes and are naturally produced by plants, animals and microorganisms. Their major source of production at industrial scale is from microorganisms especially *Bacillus* sp, *Aspergillus* sp. and yeast sp. which are generally regarded as safe. *Aspergillus* sp. generally produce acidic pectinases which are used in the food and beverage industry for the extraction and clarification of fruit juices and maceration of vegetables for production of purees and pastes. *Bacillus* sp. are usually capable of producing alkaline pectinases which have diverse functions and are in use in many industrial processes, successfully substituting the use of harsh chemicals which not only causes the deterioration of product quality but also the deterioration of environment. Pectinases from *Bacillus* sp. are generally active at broad ranges of pH and temperature and due to this reason, they are multi-functional enzymes. Pectinases account for more than 10% of the industrial enzymes market and they constitute 25% of the global food enzymes market.

The present study was concerned with the search for a novel bacterial isolate for the lab scale production of pectinase (Polygalacturonase). Keeping in view the increasing demand of pectinase, specially its need in Faisalabad, a textile city of Pakistan, isolation of new hyper producer bacterial strains locally is an easy and cheap way of getting the desirable products at low cost. Therefore, isolation of new strains for industrial enzyme production has been, and will be, a part of research. This method alone can also provide raw material for further research such as enzyme engineering or molecular directed evolution.

Pectinase positive cultures were isolated using PSAM, the medium that is able to grow and differentiate pectin consuming bacteria from others. The pectinase producing bacteria form clear halos around their colonies while others do not form any clear zones. For the identification of hyper producer strains, colony PCR was done for 16S rRNA analysis. The reason to use the 16S rRNA gene for identification purposes is that there is a large database of DNA sequences available for the gene from the widest range of microbial species as compared with any other genetic target.