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RESEARCH ARTICLE

BACILLUS THURINGIENSIS AS BIO PESTICIDE IN INSECT OF TEAK

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ABSTRACT

Bacillus thuringiensis (Bt) was a positive bacteria ,It is forming spore,it was crystalline protein which was called cry protein. It was toxic against many types of teak insect, cotton insect. This bacterira was toxin against insect.It toxin was used in bioinsecticide.

INTRODUCTION

Bacillus thuringiensis (Bt) was a well recognized entomopathogenic bacterium used as a biopesticide for many years. It insecticidal properties of Bt was mainly due to cry toxins forming a proteins with the spore. After intake of susceptible insect larvae, protein induced favorable atmosphere for spore germination. The bacteria increased in the insect and make mutual behavior using. Signaling molecules were present for quorum sensing. Microorganisms and microbial product with potential insecticidal activity can play an important role in controlling diseases by interrupting transmission mechanism by killing insect vectors at community level (Patil *et al*., 2012). Worldwide efforts to screen effective entomopathogenic microorganisms for control of agriculturally and medically important insect pests have yielded many Bacillus thuringiensis (Bt) isolates with various insecticidal properties (Feitelson *et al*., 1992). The Gram-positive bacterium *Bacillus thuringiensis* is well known for its ability to form spores and crystal proteins with insecticidal activity against a wide variety of lepidopteran, coleopteran, and dipteran insects (Schnepf *et al*., 1998). Bacillus thuringiensis is a gram positive ,spore forming Bacteirum that produces parasopral inclusions during the sporulation phase, These inclusions are composed of proteins (Cry proteins)or endotoxins which are highly toxic to a wide vaiety of insect pests and some invertebrates (Chattopadhyay *et al*., 2004 and Vilas Boas, 2007).

MATERIALS AND MATERIALS

Bacillus thuringiensis from soil a total of 50 soil samples were collected from Bhopal different region Samples were collected from 2to 5 cm below the surface with a Shovel. Each soil sample was collected in autoclave plastic bag at ambient temperature Bacillus thuringiens is strain were isolated from soil samples using Luria broth and agar media (Travers, 1987).

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RESULTS

We have identified 50 bacterial strains from larvae of five families of Coleoptera that had been feeding on decaying wood in tropical wet forests of teak. 50 isolated from *Bacillus thuringiensis.* Cotton leaves had Lepidoptera. The genus *Bacillus thuringiensis* was the most abundant; it was the only one associated with all five families of Coleoptera and also present.

DISCUSSION

We collected larvae of five families of wood-feeding Coleoptera in teak forest. Prediction of availability of bt in insect. With the aim of estimating the species composition of cultivable fungi and bacteria inhabiting their guts and to identify microorganisms with relevant lignocellulolytic activities. The main limitation of this study is that the cultivation-dependent approach, based on artificial media, covers only a small proportion of the total microbial diversity present in this particular niche. The positive trade-off of this approach was the identification of several isolates with lignocellulose-degrading capabilities, which can be further used for the respective enzyme characterization, for direct degradation assays on residues from agriculture and forestry, for the treatment of industrial effluents, and for bioprospecting novel metabolites with other biotechnological applications. Despite the inherent bias of the isolation method, our results suggest that gut microbiota of wood-feeding tropical beetles presents a relatively high diversity in terms of microbial richness, phylogenetic composition, and lignocellulolytic activities. This white-rot fungus is a known model for studying degradation of lignin in free-living conditions and in this work reported in its association with the gut microbiota of wood-feeding insects (Borokhov, 2000 and Abadulla *et al*., 2000). It is difficult to know whether these fungal isolates are truly endosymbionts of the intestinal tracts of the coleopteran larvae or are transitory inhabitants associated with host feeding habits. Hence, it is also possible that some of these microorganisms could be commensals, parasites, and facultative endosymbionts. They might even be using the insect as a dispersal mechanism (Morales-Jiménez *et al*., 2012 and Dreaden *et al.,* 2014). It is clear, however, that the overall taxonomic composition of the gut-inhabiting microbes and the proportion of lignocellulolytic-positive fungi seem to be particular to the larval microenvironment. The structure of this endosymbiotic community is distinguished from the fungal composition observed in other wood-related microhabitats such as the fungal populations in living plant tissues. They are also dominated by members of Ascomycetes, but they present a different abundance distribution of fungal families (Suryanarayanan *et al*., 2002 and Arnold, 2007); decaying logs are dominated mainly by Basidiomycetes (Heilmann-Clausen, 2005 and Prewitt, 2014). The analysis of the taxonomic composition of the bacterial isolates showed the presence of seven major phylogenetic classes, codominated by γ-Proteobacteria and Firmicutes.

This finding is consistent with results obtained in similar studies (Morales-Jiménez *et al*., 2009; Schloss *et al*., 2006; Vasanthakumar *et al*., 2008; Geib *et al*., 2008 and Reid *et al*., 2011). Within the γ-Proteobacteria, the most abundant genera were Enterobacter, Serratia, Acinetobacter, and Pseudomonas. Interestingly, Serratia and Pseudomonas were isolated from all five coleopteran families studied; Enterobacter and Acinetobacter were present in four out of the five insect families, and they exhibited positive results in the lignocellulolytic assays, except for lignin degradation. Similar characteristics related to the degradation of lignocellulose and to fermentative metabolism were observed in Bacillus, the most abundant genus within Firmicutes (Egert *et al*., 2003 and Lee *et al*., 2008). Together, these results support the notion that some species of fungi and bacteria, such as Trichoderma, Serratia, Pseudomonas, and Bacillus, can be common gut inhabitants of wood-feeding larvae in tropical forests, suggesting that certain affinities might have developed between the beetle host and its microbiota (Vargas-Asensio *et at*., 2014, Rhoads *et al*., 1995, Nagy *et al*., 2002, Weslien *et al*., 2011 and Jones *et al.,2013*).When comparing the fungal and bacterial species composition among the beetle families, the plots of the Bray-Curtis distances and canonical correspondence analyses produced biologically meaningful clusters to group the environments that share similar microbial compositions. The first fungal cluster relates the microbiota associated with the guts of Cerambycidae, Passalidae, and Scarabaeidae. This is consistent with the observation of a high diversity of isolates from Cerambycidae that shared members of the fungal phyla Basidiomycota and Ascomycota with Passalidae and members of Zygomycota and Ascomycota with Scarabaeidae. The cluster formed by Tenebrionidae-Elateridae shared, in a lower proportion, members of the Basidiomycota and Ascomycota. The bacterial microbiota associated with Passalidae and Scarabaeidae also formed a cluster, sharing members of five major bacterial clades; microbiota of Cerambycidae, Elateridae, and Tenebrionidae shared members only of γ-Proteobacteria and Firmicutes. efficacy of Cry1Ab can depend on additional factors (Schnepf *et al*., 1998). The clustering analyses revealed that Cerambycidae presented a high diversity of fungi but not of bacteria, while Passalidae and Elateridae exhibited a high diversity of bacteria and moderate diversity of fungi. Scarabaeidae and Tenebrionidae contained a similar composition of both. These results suggest that the nature of the beetle host has an important effect on the phylogenetic diversity of its associated microbiota and that many factors can influence its configuration. These factors may include the biology of the host, the physical and chemical characteristics of the gut compartments, the feeding habits of the insects, and the microbial diversity associated with the environment in which the insect is living (Egert *et al*., 2005, Ceja-Navarro *et al*., 2014, Lemke *et al*., 2003 and Geib *et al*., 2009). Our results consistently showed that both the fungal and bacterial populations associated with the guts of beetle larvae are highly diverse in terms of the number of species obtained and in their phylogenetic composition. These microbial inhabitants could be forming complex consortia that would be acting synergistically to provide many of the nutritional needs of the beetle host. Some of these functions include the degradation and fermentation of lignocellulosic materials, as shown by the high percentage of fungal and bacterial genera that presented positive activities or by the production of proteins and other metabolites necessary for the development of the insect (Scott *et al*., 2008, Geib *et al*., 2008, Cazemier *et al*., 2003, Genta *et al*., 2006 and Oh *et al*., 2009). Certain affinities for substrates can be expected according to the nature of the gut inhabitant. Members of the Basidiomycota could possibly degrade larger polymeric molecules, the Ascomycota deplete diverse lignocellulosic constituents, bacteria was degrade and ferment the smaller monomeric and dimeric hexoses and pentoses produced by the fungal counterparts. The bacteria also likely use these sugars to produce other nutrients and metabolites. Concerning the existence of microbial consortia acting synergistically to give the nutritional needs of the hosts, the nature of the ecological and evolutionary processes it contribute to ensure the fitness of the insect, and the mechanisms that rule the interactions among the fungi, the bacteria, and the beetle host.

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