The collection of bacterial diseases of silkworm (Bombyx mori L.) were carried through 16 provinces (Amnat Charoen, Buri Ram, Chaiyaphum, Kalasin, Khon Kaen, Loei, Maha Sarakham, Mukdahan, Nakhon Ratchasima, Nong Khai, Roi Et, Sakon Nakhon, Si Sa Ket, Surin, Ubon Ratchathani and Udon Thani) in the northeast of Thailand. There were 397 bacterial isolates, assayed on 3rd instar larvae of silkworm (DOAE 7) at room temperature (27-33 °C, RH 62-86%). It was found that 123 isolates, which were proved to be the bacterial causal agent of silkworm. Morphological characterizations and biochemical properties were conducted for identification and revealed that these isolates were classified into 4 species from 3 genus of, Bacillus thuringiensis (51 isolates), Serratia marcescens (39 isolates), Staphylococcus aureus (19 isolates) and S. sciuri (14 isolates). In addition, the morphology of the B. thuringiensis parasporal crystal were studied. It was found that these could be grouped into 5 categories depended on crystal shapes: spherical group; large bipyramid group; small-and large bipyramid group; small-, large bipyramid and cuboidal group; and small bipyramid group. Characterization of randomized bacterial isolates of each pathogen were also undertaken using ARDRA technique with 7 restriction enzymes. The 2 isolates of each groups of B. thuringiensis based on crystal protein shape, 6 isolates of S. marcescens and 2 isolates of each S. aureus and S. sciuri were selected for the test. Seven restriction enzymes, Ava II, BspM II, FnuD II, Hae III, Hpa II, Mse I and Taq I were used to cut the PCR products (~1400 bp) obtained from 16S rDNA of bacterial isolates tested. This study shows that ARDRA technique cannot be used to identify into isolate within the species. However, using the DNAsstar program (magalign) to compare with an alignment of the partial length on 16S rDNA sequences of the representative isolates of B. thuringiensis (1 isolate/group) reveals the differences between those isolates, which paralleled with the shapes of crystal. That means, B. thuringiensis isolates with similar morphological characteristic relate geneticaly among the groups more than those with different morphological crystal. Interestingly, the isolates with spherical crystal are least correlation with other isolates.