Apis cerana and A. mellifera are economically important honeybees in Thailand. It is important to understand infection and pathogen distributions in these species. For A. cerana, 10 and 45 hives were collected from Samut songkram (the Central) and Chumphon (the South) provinces respectively. For A. mellifera, 50 hives were collected from Nan (the North) province. In addition, 16 hives of stingless bees (Tetragonula larviceps) were collected from Chantabuti (the East) province. In A. cerana only, Varroa mites were 5x more frequent on pupae than on larvae. For multiplex PCR, we focussed on bees without any disease symptoms. 16S rRNA of target organisms and pol of the Sac Brood Virus (SBV) were used for primer design. Bees in Samut songkram were infected with Nosema apis (30%), N. ceranae (80%), and Paenibacillus larvae (10%). Also, 16%, 2%, and 20% of bees from Chumphon were infected by P. larvae, N. apis, and Ascosphaera apis, respectively. For A. mellifera, no infection by N. apis was reported but 2.5% was infected by N. ceranae and 25% were infected by P. larvae. However, we found no evidence of infection in stingless bees. No SBV infection was found in any bee samples. Life stage was an important predictor of infection. By morphology observation, abnormal morphology (brown and black) were seen 8x more in larvae than in pupae. By multiplex PCR, in A. cerana only, it seemed that any life stages could be infected by P. larvae and N. ceranae. In contrast, N. apis was found in adults only. In addition, A. apis was found in larvae and pupae more than adults. In the future, outbreak prevention in the country should be concerned. Keywords: Apis, bee disease, bee stage, infection, multiplex PCR, Thailand