

Chapter V

Conclusion

A total of 558 microbial strains were isolated from 27 fecal samples of captive Asian elephants at Maesa Elephant Camp. This may be a result of the fact that Thailand is in the tropical zone, and the weather is suitable for bacterial growth. The elephant's gastrointestinal tract has numerous numbers of bacteria, and its semi-natural feeding style may allow the elephant to pick up some strains from nature. The elephants from which the feces were collected were varying in gender, weight and age. However, after tracing back the five isolates that showed cellulolytic probiotic properties (E1-E5), it was found that these isolates were from healthy elephants that had never suffered from digestive problems. The natural behavior of Elephants is to eat food on the ground and from natural sources. Furthermore, the coprophagy behavior in the elephant calf eating the mother's feces can facilitate the transfer of bacterial strains from the mother's feces. Thus, elephant calf will suffer by pathogen from mother's feces. On the other hand, if there is a useful probiotic, the calf will have a healthy digestive system.

From the limited amount of existing research on the elephant gastrointestinal tract, useful data is very difficult to find. Because of this lack of information, the elephant was compared to the horse (which has a similar digestive system) to make the study continue smoothly. The researchers hope this study will be useful in other elephant conservation studies in future.

Conclusion of isolation characterization and identification of probiotics in the elephant gastrointestinal tract

Among the total of 558 colonies isolated from 27 samples, 46 isolates had cellulolytic properties. Bile salt resistance was found in 330 isolates. Ninety-three isolates were viable in pH 2, 3, 4, 5, 6, 7, 8, and 9. Carbohydrate utilization properties were found in twelve isolates; thirteen isolates had lipid utilization properties, and protein utilization properties were found in six isolates.

Moreover, identification of strain resulting from API 50 CHL identification kit, and phylogenetic identification was performed by 16S rDNA sequence analysis. The five isolates (E1-E5) were determined to be *Weissella cibaria*: DH8 (2 strains);

Lactobacillus plantarum LP-01 (2 strains); and *Enterococcus* sp. SF-1(1 strain). Even though several strains of *Enterococcus* are pathogenic and cause infections, some strains of *Enterococcus* sp. are reported to have probiotic properties.



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