

CHAPTER VI

CONCLUSION

Polyphasic taxonomy was employed in the Identification of slow-growing soybean rhizobia obtained from the host trapping method using 5 soybean cultivars grown in soils from 16 subdistricts in Phitsanulok province, Thailand. A total of 340 isolates were purified and categorized into fast- and slow-growers based on their visible growth on yeast extract mannitol with $0.25 \mu\text{g.ml}^{-1}$ Congo red agar plates. Identical RAPD-PCR fingerprints revealed the 202 slow-growing isolates consisted of 121 strains. Authentication tests showed all the 138 fast-growers did not nodulate soybean roots. Thus, they were not fast-growing soybean rhizobia. On the contrary, all the 121 slow-growing strains were found to nodulate soybean roots. Therefore, they were slow-growing soybean rhizobia. Comparisons of 16S rDNA sequences of 20 slow-growing strains with corresponding sequences deposited with GenBank revealed the slow-growing soybean rhizobia consisted of *Bradyrhizobium japonicum* and *Bradyrhizobium elkanii* and *B. yuanmingense*. This research is the first report on the presence of *B. yuanmingense* in Thailand.