5.0 CONCLUSION

In conclusion the results of this study show that PCR optimizations of the variable regions, V2 and V6 were not specific for *S. typhi* due to the high sequence similarity among the 15 *Salmonella* serovars that were tested. PCR also yielded little if no polymorphism in both these variable regions for the 16 strains of *S. typhi* from different parts of the world. This supported other studies done by David *et al.* (1990) and Zuraina *et al.* (1992) who found little heterogeneity among the closely related species of the genus *Salmonella* in these two variable regions. In contrast to the studies demonstrated by Barry *et al.* (1990) who generated a species-specific probe for *Aeromonas* sp. based on the V6 region of 16S rRNA gene, it was difficult to obtain a *S. typhi*-specific product from these two variable regions.

However, the optimized PCR conditions when tested on DNA from serum samples gave positive results. Although the results were promising, a larger collection of serum samples have to be tested before its clinical significance could be attested. The PCR-amplified V2 region of *S. typhi* was also used as probe in a series of hybridization and the slot-blot hybridization employed under high stringency conditions was found to be more specific compared to the Southern hybridization.

PCR-amplified V2 regions of *S. typhi* and *S. typhimurium* were also sequenced using direct sequencing of PCR products and results showed a high degree of sequence similarity between the two species which was in accordance to

sequence results reported by Chang *et al.* (1997) and to the work of Subramaniam,G (unpublished data). The results of the study showed that due to the low heterogeneity in the variable regions of V2 and V6 in particular the V2 region of *Salmonella* species, it was difficult to generate a suitable probe for *S. typhi* .