CHAPTER 5

DISCUSSION AND CONCLUSION

For the effective management of waterborne diarrheal diseases there are amongst others two important considerations, being able to rapidly detect and characterise the causal agent, and to have an understanding of the survival and population genetics of these pathogens in their natural aquatic environments.

- It has been shown in the work presented here that a polymerase chain reaction based detection technique for *Vibrio cholerae* compares favourably to biochemical detection, with the PCR assay being at least as sensitive and slightly more accurate than the biochemical testing approaches initially used for the 251 samples.

- No *ctxA* genes were found upon screening environmental *Vibrio cholerae* populations in the Vaal Barrage, these strains thus lack the genetic potential to produce Cholera Enterotoxin and therefore the associated ability to cause epidemics.

- No strains were found to harbor the tcpA gene, which forms part of the larger TCP pathogenicity island coding for the toxin co-regulated pili. It is therefore unlikely that bacteriophage CTX , needing toxin co-regulted pili as a receptor, could donate the *ctx* genetic element to these environmental strains thereby presenting them with the genetic potential for epidemic disease.

- Data generated by Amplified Fingerprint Length Polymorphism fingerprinting suggests that environmental populations, at least as seen in the Vaal Barrage system, is genetically diverse. Single isolation sites contained heterogenous populations, with unrelated strains sharing the same immediate environment. Highly related strains were also found, but only within localized geographical areas and over short time frames.

- These findings may suggest that environmental *Vibrio cholerae* populations are dynamic and well established, with the ability to constantly adapt, by selection, to changing environmental factors. These populations may persist and act as pre-cursors for future epidemic strains, or at the very least serve as models for studying the survival and persistence of current enterotoxigenic *Vibrio cholerae* strains.