

CHAPTER 1

INTRODUCTION

Vibrio cholerae is the infective agent of cholera, a diarrheal disease that affects hundreds of thousands of people each year. Serious pandemics of cholera have occurred throughout the known history of humankind, with the current seventh pandemic originating in Indonesia in 1961 from where it has spread to Southern Asia, the Indian subcontinent, the Near East, Africa and South America (Cameron *et al.*, 1994; Coelho *et al.*, 1995; Sharma *et al.*, 1998; Tenover *et al.* 1995, and Wachsmuth *et al.*, 1993). South Africa has not escaped the cholera onslaught, with close to 130 000 cases of cholera and 396 associated deaths being reported in the epidemic raging from January 2000 to December 2003 (Department of Health, South Africa. 2004). The epidemiological pattern of cholera is so distinctive that its fundamental characteristics were clearly defined over a hundred years ago. In a memorandum of the Privy Council of Great Britain in 1871 Sir John Simon wrote: *“It is characteristic of cholera, not only of the disease in its developed and alarming form, but equally of the slightest diarrhea, that all matters which the patients discharge from their stomachs and bowels are infective. Even a single case of cholera, perhaps of the slightest degree, and perhaps quite unsuspected in the neighbourhood, may, if local conditions cooperate, exert a terribly infective power on considerable masses of the population”* (Mosley and Khan, 1979)

A better understanding of the epidemiological behaviour of the causal organism, *Vibrio cholerae*, could aid in the effective control and management of the disease, thereby

reducing cholera epidemics. Accurately identifying the source of infections and the survival and proliferation of reservoir populations is one of the main epidemiological considerations. With the advent of molecular techniques it has become possible to rapidly detect and characterize pathogens, these techniques also convey the ability to trace the origins of epidemics, not just on a small regional scale, but also on a global scale as done for the causal strains of the seventh pandemic (Lan and Reeves 2002). Various researchers have proposed environmental reservoirs of toxigenic *Vibrio cholerae*, and or that non-enterotoxigenic environmental *Vibrio cholerae* strains may serve as progenitors for future enterotoxin producing epidemic strains (Colwell and Huq, 1994; Beltran *et al.*, 1999; Singh *et al.*, 2002; Jiang *et al.*, 2000 b). Environmental *Vibrio cholerae* strains not producing enterotoxin have also been shown to be closely related to clinical strains by the same authors, and may serve as a model for studying cholera epidemiology. Insight into the population dynamics of environmental *Vibrio cholerae* might broaden our understanding of cholera epidemiology, and could aid in the implementation of effective control and management strategies so as to avoid or at least reduce cholera epidemics.

Aims

- Evaluating a PCR based *Vibrio cholerae* detection technique and comparing it against biochemical testing.
- Screening environmental *Vibrio cholerae* populations for the enterotoxin (*ctxA*) and toxin co-regulated pili (*tcp*) genes, so as to determine the epidemic potential of environmental strains.

- Ascertaining the genetic diversity of environmental *Vibrio cholerae* populations in the Vaal barrage system using Amplified Fragment Length Polymorphism fingerprinting so as to gain insight in *Vibrio cholerae* population dynamics.