

## CHAPTER 1

### Introduction

Hepatitis E virus (HEV), the etiological agent of hepatitis E, was first discovered in the late 1970's after it had become evident that there was a hepatitis virus other than hepatitis A virus and hepatitis B virus (Wong *et al.*, 1980). Hepatitis E virus was initially classified in the family *Caliciviridae*, but is currently recognised as the type species of the genus *Hepatitis E-like viruses* (Pringle, 1999; Berke and Matson, 2000).

Hepatitis E virus is transmitted via the faecal-oral route and is an important cause of acute epidemic viral hepatitis in some developing countries (Favorov *et al.*, 2000; Schlauder and Mushahwar, 2001; Van der Poel *et al.*, 2001). Outbreaks of hepatitis E are primarily associated with faecally contaminated drinking water (Favorov *et al.*, 2000; Schlauder and Mushahwar, 2001; Van der Poel *et al.*, 2001), and have been reported from countries in Asia, Africa and the Middle East (Byskov *et al.*, 1989; Mushahwar *et al.*, 1993; Swanepoel *et al.*, 1995; Hunter, 1997; Van der Poel *et al.*, 2001; Grabow, 2002).

Hepatitis E occurs predominantly in the young adult population, while it tends to be asymptomatic in the younger age groups (Van der Poel *et al.*, 2001). The onset of disease follows an incubation period of one to eight weeks (mean of 40 days) (Purcell, 1996; Van der Poel *et al.*, 2001). In areas where the disease is endemic, HEV is an important cause of death due to liver failure, especially in pregnant woman during the third trimester, with mortality rates of up to 25% (Grabow *et al.*, 1996; Van der Poel *et al.*, 2001). Chronic HEV infections have not been observed and the disease is usually mild and resolves within 2 weeks (Van der Poel *et al.*, 2001).

Hepatitis E virus may be endemic in certain areas of South Africa (Tucker and Kirsch, 1994; Tucker *et al.*, 1996; Grabow *et al.*, 1996). It was thought that clinical cases of hepatitis E in South Africa were limited to a small number of imported cases, but it would appear that there might be more local cases of clinical disease (Grabow *et al.*,

1994; Grabow, 1997; South African Virus Laboratories Surveillance Bulletin, 2003). The rare diagnosis of clinical cases of hepatitis E in South Africa is therefore surprising, since outbreaks have been recorded in the neighbouring countries Namibia and Botswana (Byskov *et al.*, 1989; Swanepoel *et al.*, 1995; South African Virus Laboratories Surveillance Bulletin, 2001).

Although a reservoir of HEV has not yet been established, indirect evidence has suggested that at least some strains of HEV may be zoonotic (Meng *et al.*, 1997; Hsieh *et al.*, 1999; Kabrane-Lazizi *et al.*, 1999; Tei *et al.*, 2003). An increase in HEV infection among persons with occupational exposure to swine has been reported (Meng *et al.*, 1999; Drobeniuc *et al.*, 2001). Recently a few cases of foodborne HEV have been reported after the consumption of raw pig liver and deer meat, which provides direct proof of zoonotic transmission of HEV (Matsuda *et al.*, 2003; Tei *et al.*, 2003; Yazaki *et al.*, 2003; ProMed, 2004).

Rare cases of hepatitis E without a travel history have been reported in non-endemic countries, in which case the transmission of the virus remains uncertain (Hsieh *et al.*, 1998; Erker *et al.*, 1999; Schlauder *et al.*, 1999; Zanetti *et al.*, 1999; Favorov *et al.*, 2000). It has been established, however, that the genomic sequences of the HEV strains detected in these patients were more related to the swine HEV strains prevalent in the swine population of the same area than to human HEV strains (Wu *et al.*, 2000). These swine HEV strains may undergo genetic reversion to HEV strains that cause clinical disease in humans similar to that in many parts of the world where hepatitis E has major public health implications (Meng *et al.*, 1998; Hsieh *et al.*, 1999).

The detection of anti-HEV IgG in swine populations from both developing and industrialised countries has been documented (Clayson *et al.*, 1995; Meng *et al.*, 1997; Chandler *et al.*, 1999; Hsieh *et al.*, 1999; Meng *et al.*, 1999; Pina *et al.*, 2000). It was found that swine herds from developing and industrialised countries contained many pigs that were seropositive for HEV, which suggests that HEV may be enzootic in swine regardless of whether HEV is endemic in the human population (Meng *et al.*, 1999).

Introduction

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Since the waterborne transmission of HEV is well established and animal strains of HEV are closely related to the human strains, it would appear to be possible that the virus may be transmitted from animals to humans via water sources polluted with animal wastes. It is, therefore, important to determine what the prevalence of HEV is in the swine population of South Africa as well as the role that swine may play in the transmission of the disease. The purpose of this study was to determine the seroprevalence of anti-HEV IgG in swine sera and to detect HEV strains in swine faecal specimens and domestic sewage samples. This could cast light on the prevalence of the virus in selected areas of South Africa, as well as the possible relationship of these viruses with known strains of HEV from other parts of the world.

The objectives of this study were to:

1. Validate and optimise an enzyme-linked immunosorbent assay (ELISA) for the detection of anti-HEV IgG in swine serum samples.
2. Assess the seroprevalence of anti-HEV IgG in swine from selected areas of the Gauteng and Limpopo Provinces of South Africa by means of the ELISA.
3. Validate and optimise a reverse transcriptase-polymerase chain reaction (RT-PCR) procedure for the detection of HEV RNA.
4. Attempt to detect HEV RNA in swine faecal specimens by means of the RT-PCR.
5. Analyse selected domestic sewage samples for the presence of HEV by means of the RT-PCR.
6. Determine the relationship of HEV viruses detected in swine excreta and sewage to those described in other parts of the world using nucleotide sequence analysis.

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Introduction

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Introduction

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