INTRODUCTION

*Cryptosporidium parvum* is an important cause of gastroenteritis in children worldwide, with prevalence rates varying from 1 to 4% in the developed world (Baxby and Hart, 1986) and 6 to 17% in the developing world (Salon *et al*, 1990; Enriquez *et al*, 1997). This coccidian protozoan usually causes a self-limiting watery diarrhea lasting 10 to 14 days in immunocompetent hosts. However, a protracted life-threatening illness can occur if the host is immunocompromised. Infection occurs following ingestion of oocysts, which are transmitted via the fecal-oral route and via contaminated water supplies. The source of infection is humans with animals such as cattle or domestic pets being possible sources (Juranek, 1995).

Kelantan is a predominantly rural state in the northeast of peninsular Malaysia. Lai (1992) reported that 11.4% of hospitalized children with diarrhea in Kota Bharu, the capital of Kelantan State, were positive for *C. parvum*. This is much higher compared with prevalence data from other parts of Malaysia: 4% in Penang (Mat Ludin *et al*, 1991) and 2% in Kuala Lumpur (Ng and Shekhar, 1993). *C. parvum* isolates can be characterized at the molecular level (Morgan *et al*, 1997) and given that the prevalence of *C. parvum* was reported to be relatively high in Kota Bharu, a molecular epidemiological study was planned to determine the extent and nature of genetic variation in *Cryptosporidium* isolates from north east Malaysia. The aim of the present study was to confirm the high prevalence of *C. parvum* in children and collect *C. parvum* samples for the molecular epidemiological study.

MATERIALS AND METHODS

This was a prospective study conducted...