LETTER TO EDITOR

Continuous Genotyping for Human Rotavirus Group A

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Dear Sir,

The human rotaviruses (RV) are responsible for nearly 450,000 deaths in infants and young children each year especially in the developing countries[1]. Several factors affect the magnitude of this problem. Hitherto the magnitude of RV disease has yet to be determined. In Malaysia, many studies were carried out to investigate acute gastroenteritis (AGE) caused by RV. In one such study, RV was reported in 38% of children of 6-17 months old in Hospital Kuala Lumpur and Hospital Umum Sarawak[2]. In another separate study, cumulative risk of hospitalization of 1 in 61 was recorded[3,4]. It was also noted that the peak incidence of admissions was between January to March, and September to October with 8.2% AGE[5]. However, no significant relationship was noted between the prevalence of the disease and quantity of rainfall[6].

Globally, the common RV types associated with diarrhoea have the genotype combinations of G1P[8], G2[P4], G4P[8], or G9P[8][1]. Our laboratory based surveillance which was carried out over three decades identified predominant strains as G4P[8] in 1977-1988[7] and 2000-2001[8]; G1P8] in 1996 and 2007[8], and G9P[8] in 2001-2002 and 2007[2,9]. Due to either genetic drift, reassortment or emergence of novel strains, some 9%-14% remained untypeable since their G/P types could not be assigned. Recently, identification of G3P[9] strain which causes severe diarrhoea and has close similarity to a strain from a raccoon dog continues to highlight the presence of rare strains here[10].

These results therefore highlighted the diversity of RV and this forms the baseline information in Malaysia which would be highly essential prior to RV vaccine introduction. Furthermore, new primers should be included to minimize the proportion of untypeables RVs for more effective surveillance and its importance as it is critical to also ascertain the frequency and virulence of other distinct G/P types like G5, G8, G10, G12, P[10] and P[11][11]. Recently, the large RV outbreak in Perak was able to be further genotyped using both stool or water samples since the virus can spread via hands, objects, food and water.

Currently, RV genotyping is not a routine test in any hospital laboratories and most information on RV were based on separate studies conducted in various research settings. Furthermore, at present Malaysia has no national surveillance program in place and no RV National Immunisation Program. Taking the Australian study into consideration, it was reported that differences in genotype distribution is dependent on the vaccine used[12]. Also it is noted that in areas with high prevalence and strain diversity, vaccines could result in selection of genotypes for which the vaccines have limited efficacy[13]. When Rotarix vaccine were used, G2P[4] emerged, while G3P[8] strains were common in locations using RotaTeq[12]. In conclusion, given the unparalleled opportunity to control RV with existing RV vaccines present in the market, pre genotyping information is a definite need and after RV vaccine is introduced in the country, post surveillance is again needed to monitor changes in the ecology of rotavirus infections.

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