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Specific HCV antibodies, RNA, and genotypes detection correlated to the age of pregnant women in Iraq

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Background: Hepatitis C virus (HCV) is age dependent disease, affecting more than 170 millions worldwide. The six genotype of HCV that recognized in different prevalence and geographic distribution have been shown to be associated with age and mode of transmission. Little is known, about this issue among pregnant women.

Objectives: To determine the correlation of HCV markers (Abs, RNA and genotypes) with maternal age.

Methods: Multi-central cross-sectional study. Sample of 3491 pregnant women, during their third trimester. HCV-antibodies of 3491 maternal sera were investigated, using third generation; enzyme immunoassay (EIA-3) and immunoblot assay (Lia Tek-III) subsequently, as screening test and confirmatory tests respectively. In addition molecular analysis carried-out on 94 maternal sera (at laboratories of Sorin BioMedica – Italy) for detecting HCV RNA and genotypes. Using RT-PCR & DNA Enzyme immunoassay (DEIA) method.

Results: Seropositive prevalence of; HCV Abs ,HCV-RNA were 3.21%., 62.7% respectively. Pregnant women with positive HCV Abs and RNA sera, were significantly older (30.3+7.8, 30.7+7.7 years respectively) than those with negative HCV Abs, HCV-RNA (27.15+7.26, 26.6+6.66 years**,** P=0.0001, P=0.01). Interestingly, pregnant women with age ≥30 years considered as a high risk mothers for acquiring HCV infection, ORs and (95% C.I.) were 1.72 (1.17-2.5) and 3.51 (1.96-6.18) for age 30-39, ≥40 years. Significant direct Positive linear correlation for HCV Abs, HCV-RNA seropositive rate with increased maternal age were detected. Moreover, by multivariate regression analysis, age of the mother was found independently as unconfounding risk factor for contracting HCV infection (adjusted OR=1.06, 95% C.I.=1.03-1.09).

Although no significant relationship between maternal age and various HCV genotypes/subtypes. However, our study found that women infected with HCV-1b were significantly older than those infected with HCV non 1b (33.9+5.4 versus 27.9+9.5 years, respectively), P=0.05.

Conclusion: Prevalence of HCV infection significantly increases with increased maternal age, woman at age ≥30 year are considered as a risk group for HCV infection. Pregnant women infected with HCV-b were significantly older than those infected with HCV other than 1b. Therefore, HCV screening for every pregnant woman and further studies to identify other risk factors are recommended.

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Possible reassortment of rotaviruses in communities where humans and domestic animals live closely together in Accra, Ghana

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Background: Rotaviruses are the most common cause of severe diarrheal disease in infants and young children worldwide. In 2004, rotavirus infections were estimated to cause approximately 527 000 deaths, predominantly in developing countries including Ghana. This high morbidity and mortality associated with this disease has necessitated urgent development and introduction of rotavirus vaccine, whose efficacy will be affected by many factors including the emergence of recombinant strains of rotavirus from communities where humans and animals live in close associations. The objective of this study was to identify circulating rotavirus strains in Accra communities where humans and domestic animals live closely together.

Methods: A total of 215 stool samples were collected from both children less than five years and domestic animals living together in households from parts of Accra, Ghana. Rotavirus RNA was detected using Polyacrylamide Gel Electrophoresis (PAGE). VP4 and VP7 genotyping were performed using RT-PCR.

Results: Using PAGE analysis, three positives were detected in the samples from pigs. These samples exhibited a 4-2-3-2 migration pattern and were assigned rotavirus group A. These were all P-genotyped by RT-PCR as genotype P[6]. None of these could however be assigned a G-genotype. Thirty-five human samples were then randomly selected for RT-PCR. Out of which 16 (45.7%) were positive for rotavirus RNA. The positive human samples were typed by RT-PCR. After VP7 genotyping, 3 (19.7%) were genotypes G1, G8 and G4/G12/G9 whereas 13 (81.3%) were non-typables. During VP4 typing, 13 were typed P[4] (18.8%), P[6] (6.3%) and P[8] (25%) and 3 were P-non-typables). There were also mixed infections such as P[4/8] (18.8%), P[6/8] (6.3%) and P[4/6/8] (6.3%).

Conclusion: The identification of relatively high numbers of possible reassortant and non-typable rotavirus strains could influence the introduction of rotavirus vaccines which currently have undergone trials in Ghana and are awaiting their administration to children. There is therefore the need for further community based surveillance in addition to ongoing nationwide surveillance for rotavirus genotypes.

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