Genotyping of Nigerian *Helicobacter pylori* isolates by pulsed-field gel electrophoresis

*Helicobacter pylori* is the causative agent of chronic gastritis and peptic ulcer and is a risk factor in the development of gastric cancer (Blaser, 1987; Parsonnet et al., 1991). *H. pylori* infects up to 50% of the human population worldwide. Tremendous genetic diversity has been reported for *H. pylori* and Taylor et al. (1992) reported that this bacterium possesses a great deal of diversity in genomic DNA restriction profiles when analysed by pulsed-field gel electrophoresis (PFGE); the molecular and epidemiological bases for this phenomenon are not understood.

The aim of the study was to compare DNA profiles of *H. pylori* strains isolated from Lagos and Ile, Nigeria and also to determine if the isolates obtained from the antrum and corpus of the same patient were genotypically similar.

Genomic DNA of 41 *H. pylori* strains isolated from 38 patients was prepared for PFGE, as described previously (Taylor et al., 1992). Six of the 41 isolates were from three patients, from whom biopsies were taken from both the antrum and the corpus. The remaining isolates were obtained from the antrum. DNA plugs were digested with the restriction enzymes NotI/NruI and DNA fragments were separated using the contour-clamped homogeneous electric-field electrophoresis system of PFGE. DNA patterns were visualized by staining with ethidium bromide and photographing under a UV light source.

DNA from 15 of the 41 *H. pylori* strains could not be digested with the restriction endonuclease NotI, while DNA from 25 of the 41 *H. pylori* strains could not be digested with the restriction endonuclease NruI. Nine of the 15 *H. pylori* strains that were not digested with NotI were isolates from Lagos; 15 of the 25 *H. pylori* isolates not digested with NruI were isolates also from Lagos. In some cases, the isolates (seven isolates) overlapped in that they were not digested with either restriction enzyme. Amongst the isolates from Ile, only three isolates overlapped in their inability to be digested with both restriction enzymes. There was no change in the restriction profile of the isolates, even after several (four) passages of these isolates on culture medium. Therefore, the possibility exists that this restriction profile could be region-specific, as an earlier report by Takahami et al. (1993) from Japan showed that 12 of 24 isolates were not digested by the restriction enzyme NotI.

The DNA digested from different patients in different geographical regions showed different patterns, while the six strains isolated from the three patients at different sites (antrum and corpus) showed identical genomic DNA restriction profiles from each site when the DNA was analysed by PFGE. An exception is that the *H. pylori* DNA isolated from the corpus and antrum from one patient had different band patterns. A similar report was given by Smith et al. (2002) on these same isolates using PCR. Other workers have also corroborated this view, in that some patients are infected by a single and individual strain of uniform genotype (Salama et al., 1995; Han et al., 2000).

In conclusion, PFGE was found useful in typing some of our isolates from Nigeria, although its main disadvantage is the non-digestion of some *H. pylori* DNA by the restriction endonucleases NotI/NruI.

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