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Project: The identification and characterization of clarithromycin resistant strains of *H. pylori* isolates in Spain in several years 1999 and 2008. I developed three different projects in my period in New York School of Medicine, New York.

The goal of the first project was the prevalence of clarithromycin resistance in Spanish patients and association with *H. pylori* genotypes in year 2008. We determined clarithromycin susceptibility and determine risk factors associated with resistance.

We studied *H. pylori* strains isolated from patients of whom 76.3% were born in Spain, 52.7% were children, 20.3% have been treated previously and 66.1% were female. Clarithromycin resistance determined by E-test, strains was defined if MIC<sub>≥</sub>1 mg/L. DNA extraction was carried out by the NucliSens easyMAG platform (bioMérieux). Sequences of clarithromycin-resistant and sensitive strains were analyzed for mutations in the 23 sRNA gene. *VacA* genotype and *CagA* status were determined by PCR. The identification of the number and type of *CagA* EPIYA motifs was based on sequencing analyses. Our results were that 42 of 118 (35.6%) strains were resistant to clarithromycin by E-test. E-test results were confirmed for the presence of point mutation in 34 (88.1%) of these strains. However, 8 *H. pylori* strains were resistant to clarithromycin by E-test but without point mutation in the 23 rRNA gene. Mutation A2143G was found in 85.3% of the strains, follows by A2142G (8.8%) and T2182C in 5.9% of the strains. Clarithromycin-resistant *H. pylori* strains were strongly associated with paediatric patients, with patients born in Spain and with patients previously treated. In addition *H. pylori* resistant to clarithromycin were more frequently *vacA* genotype s2/m2 and *cagA* negative than the susceptible strains. Strains with more than three EPIYA motifs were more often recovered from adults than from children. We found the EPIYA-ABD in patients from no East Asian countries.

Our results suggested that in Madrid, Spain, patients colonized with clarithromycin-resistant *H. pylori* are children, born in Spain, that have been treated and they are infected with a less virulent *H. pylori* strain.

The goal of my second project was the characterization of *H. pylori* strains obtained from different parts of Spain in 1999. This was extremely relevant because we found a big difference between different parts of Spain, in the virulence factors and clarithromycin resistance. We determine how much that resistance has changed in 10 years.

The third and final project was related to efficacy of commercial molecular methods using gastric biopsies positive for *H. pylori* and involve the study of clarithromycin resistance.

In the three projects, we characterize all the rare strains by Multi Locus Sequence Typing (MLST). MLST is a nucleotide sequence based approach for the unambiguous characterisation of isolates of bacteria and other organisms via the internet. We introduce our new isolates into this base data.