sified according age. The highest rate of infection was observed in 50-60 years old patients.

Conclusion: Since HP is related to dangerous disease, therefore diagnosis and treatment of infected people's especially symptomatic cases is significant. UBT make possible more recognition of infected people (in previous study the rate of infected people was 62.56% in patients with digestive complaints by direct stain, urease and culture method).

PP-055 Detecting the genotypes of Helicobacter pylori in the development of gastric carcinoma subjects in Andhra Pradesh population

G. Manoj*, Tiwari Santosh, G. Sivaram, R. Saikant, Bardia Avinash, Habeeb Aejaz, Khan Aleem, C.M. Habibullah. *Center for Liver Research and Diagnostics*

Background and Aim: *Helicobacter pylori* has been a key determinant causing gastric adenocarcinoma. Not much is known of the genotypes of *H. pylori* infection among the gastric cancer subjects. Therefore the present study was designed to ascertain the genotypes of *H. pylori* in gastric cancer subjects.

Methods: 72 patients grouped on their endoscopic findings. Gastric biopsies were obtained for culture and DNA isolation.

Results: Genotypic analysis showed *cag*T+ve/*cag*A+ve/*cag*E+ve/ *vac*As1+ve genotype to be highly prevalent in 81.2% cases. This genotype was predominant among the Group-I subject those with gastric adenocarcinoma. Intestinal type adenocarcinoma subjects 91.4% harbored the remaining genotypes.

Conclusion: Certain genotypes of *H. pylori* in this study had higher predictive values for the development of intestinal type carcinoma at an early age. Further this study also showed genotyping *H. pylori* could well be used as an ideal tool for screening subjects at an increased risk of developing malignancy.

PP-056 Status of hepatitis A surveillance in China

Fuqiang Cui*. Chinese Center for Disease Control and Prevention

Background: To better define the current epidemiology of hepatitis A and status of surveillance in China, in anticipation of introduction of universal hepA vaccination of young children in 2008.

Methods: Data from national notifiable disease reporting system from 1990 to 2007 was reviewed and epidemiology characteristics analyzed. Hepatitis A vaccine distribution was also reviewed.

Result: Incidence of hepatitis A has declined by 90% since 1990; declines in age specific incidences were seen in all age groups, but most dramatically among children less than 10 years. Disease incidence still varies substantially, with poorer Western provinces having highest incidence since 2000. In the high incidence provinces, young children less than 10 years continue to have high disease incidence. Over 135 million doses of hepatitis A vaccine have been distributed since 1992, with increasing use since 2003.

Conclusion: Although incidence of hepatitis A has decreased in all age groups, high risks remain among Western populations with transmission predominantly among children. The epidemiology of hepA transmission is not well defined, and only 50% of cases are laboratory confirmed. Improved surveillance with more laboratory confirmation is needed to monitor impact of universal hepatitis A vaccination.

ntostinal motanlasia

S65

PP-057 Risk of glandular atrophy, intestinal metaplasia and dysplasia in subjects with vacA positive and complete or disrupted cagE, cagT *Helicobacter pylori* infection

Tiwari Santosh^{*,1,2}, G. Manoj^{1,2}, G. Sivaram^{1,2}, R. Saikant^{1,2}, Bardia Avinash^{1,2}, Habeeb Aejaz^{1,2}, Khan Aleem^{1,2}, C.M. Habibullah^{1,2}. ¹Deccan College of Medical Sciences; ²Center for Liver Research and Diagnostics

Introduction: Glandular atrophy, Intestinal metaplasia and dysplasia are pre-neoplastic lesions common in patients with chronic gastritis as in those with *Hp* infection. Therefore the present study was to investigate the association among *Hp* infection with *cagE*, *cagT* and *vacA* genes and the risk of precancerous lesions. **Methods:** 120 patients were divided into different groups.

Results: Genotypic data revealed 42.5% strains with cagE+/cagT+/vacAs1+, and 7.5% strains with partially deleted cagE, cagT & vacAs2. With respect to the clinical status, 67.5% subjects with overt diseases were infected with cagE+/cagT+/vacAs1+ genotype whereas 22.5% NUD subjects harbored strains with partial deletions and s2 allele of vacA (p<0.01). Histology revealed atrophy, IM and dysplasia to be more prominent among subjects harboring above genotype compared to those with partially deleted genes (p<0.05).

Conclusion: Results demonstrates that the risk of overt gastric diseases was progressively higher as the number of virulence genes possessed by *Hp* increased.

PP-058 Helicobacter pylori genotypes in different ethnic groups resident in Tehran, Iran

Hossein Dabiri^{*,1,2}, Akbar Mirsalehian¹, Yoshio Yamaoka³, Fereshteh Jafari², Kaveh Baghai², Leila Shokrzadeh², Maryam Rezadehbashi², Mahsa Molaei², Homayoun Zojaji², Mohammad Reza Zali². ¹Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran; ²Research Center for Gastroenterology and Liver Diseases in Shaheed Beheshti University, M.C., Tehran, Iran; ³Department of Medicine-Gastroenterology, Michael E. DeBakey Veterans Affairs Medical Center and Baylor College of Medicine, Houston, Texas, USA

Objectives: There is a geographic variation in *Helicobacter pylori* genotypes. *cagA* and *cagE*, *oipA* and *vacA* genotypes of *H*. *pylori* are associated with peptic ulcer disease (PUD). This study compared the distribution of these genotypes in major ethnic groups residing in Tehran, Iran and their association with clinical outcomes.

Methods: *H. pylori* infected patients proven by culture were recruited prospectively. DNA was extracted from isolated *H. pylori* and PCR was carried out to determine the *cagA*, *cagE* and *oipA* status and *vacA* alleles.

Results: A total of 124 patients living in Tehran were enrolled in this study. The ethnic distribution was 74 Persian, 33 Turkish and other ethnics including 7 Kurdish, 5 Lurs, 3 Afghani and 2 Arab patients. The predominant *vacA* signal region genotype was s1 among isolates from all ethnics. The *vacA* middle region genotypem2 was predominant in Persian and Turks. Of the Persian, Turkish and other ethnic isolates, 64.9%, 72.7% and 70.5%, respectively, were *cagA* positive, and 47%, 30% and 76.5%, respectively, were *cagE* positive. The *oipA* gene was present in 51.4% of Persian, 33.3% of Turks and 70.5 of others ethnics isolates.

Conclusion: There is difference in the *H. pylori* strains among the ethnic groups in Iran. However, there was no significant association between *cagA*, *cagE* and *oipA* status or *vacA* genotypes and clinical outcomes in Iranian patients irrespective of ethnic groups. None of these markers were helpful in predicting the clinical presentation of a *H. pylori* infection in Iran.