P.1.10.2.005 (A)
Occurrence of Giardia duodenalis genotypes in sheep and goats in Tehran, Iran

E. Razmjou[1], A. R. Meamar[1], A. Tavakolikareshk[1], L. Akhlaghi[1], M. Moradi-Lakeh[2] and H. Oormazdi[1]

[1]*Department of Medical Parasitology and Mycology, School of Medicine, Tehran University of Medical Sciences, Tehran, Tehran, Iran;* [2]*Department of Community Medicine, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran*

INTRODUCTION Giardia duodenalis is one of the most common and important gastrointestinal protozoan parasites in humans and animals, especially in developing countries. Based on genetic differences, *G. duodenalis* isolates classified into several genotypes, host-specific and potentially zoonotic genotypes. This study was performed to determine the occurrence of Giardia genotypes in sheep and goats in Tehran slaughterhouses.
MATERIAL AND METHODS Two hundred forty faecal samples were collected from the rectum of sheep and goats in Tehran slaughterhouses, during April to November 2011. The presence of *G. duodenalis* cysts were microscopically examined after sucrose gradient purification. For the molecular identification of Giardia, a semi-nested PCR protocol was used to amplify a 432 bp fragment of the glutamate dehydrogenase gene (gdh). The amplified fragments were subjected to restriction analyses and direct sequencing of purified DNA gel bands for the genotyping assays.
RESULTS Microscopic examination found 56 of 240 (23.3%) sheep and goats infected with Giardia. Based on molecular identification, the frequency of Giardia was 49.2% (118/240). Restriction analyses of the gdh fragments showed 44 (37.3%) assemblage E, 25 (21.2%) assemblage AI and 14 (11.9%) assemblage AII. Eighty one (68.6%) isolates were mixed genotypes (assemblage E with BIII, AI or AII). The potential zoonotic assemblages of *G. duodenalis* were found in 64.4% (76/118) of sheep and goats.
CONCLUSION The molecular identification revealed Giardia as a common parasite in sheep and goats in Tehran slaughterhouses. The presence of zoonotic assemblages (AI, AII, and BIII) in sheep and goats suggests their possible role as reservoirs of human giardiasis.

P.1.10.2.006 (A)
An investigation of Giardiasis and Cryptosporidiosis in Malawi and Cambodia

C. Nuchjangreed[1], D. Winifred[2], C. Probert[3], N. Cunliffe[2] and J. Wastling[1]

[1]*Department of Infection Biology, Institute of Infection and Global health, Faculty of Health and Life Sciences, University of Liverpool, UK;* [2]*Department of Clinical Infection, Microbiology and Immunology, Institute of Infection and Global health, Faculty of Health and Life Sciences, University of Liverpool, UK;* [3]*Institute of Translational Medicine, Department of Gastroenterology, University of Liverpool, UK*

The parasites, *Giardia* sp. and *Cryptosporidium* sp. infect both humans and animals and are considered to have the potential for zoonotic transmission. Giardiasis, caused by *Giardia duodenalis*, is one of the most common intestinal protozoal infections reported worldwide particular in children. At least seven morphologically identical genetic assemblages (A to G) of G. duodenalis have been categorised. Cryptosporidium is a protozoan parasite and emerging pathogen that has become recognised as a significant cause of protracted diarrhoea in both immunocompetent and immunocompromised individuals worldwide. At least seven *Cryptosporidium* species have been reported to infect humans. The two species of greater significance in terms of public health are *C. parvum* and *C. hominis*. Multilocus sequence typing (MLST) is a useful approach for detecting the presence of genotypes of these parasites. Genotyping of human isolates of both parasites from the Malawi and Cambodia can provide crucial information about transmission routes and epidemiological differences between Giardia assemblages and Cryptosporidium species. The purpose of this study was to determine the prevalence and range of *G. duodenalis* assemblages and *Cryptosporidium* species infecting children from Malawi and Cambodia and investigate the use of Gas Chromatography and Mass Spectrometry (GCMS) as a novel method for studying the volatile organic compounds in faeces of patients with *Giardia* and *Cryptosporidium* infection. Faecal samples were collected from children under 5 years of age, living in diverse geographical regions in Malawi and Cambodia. Parasite isolates were typed by using a combination of both PCR and restriction fragment length polymorphism (RFLP) and/or sequencing of SSU-rRNA, Î²-giardin, tpi and gdh genes. Initial results confirmed the occurrence of mixed infections with assemblage A and B genotypes, and also mixed infection with *C. hominis* and *C. parvum*.

1.11 Yellow fever

P.1.11.002 (B)
Yellow fever: threat to Europe

J. P. Woodall

Director, Nucleus for the Investigation of Emerging Infectious Diseases (retired), Institute of Medical Biochemistry, Centre for Health Sciences, Federal University of Rio de Janeiro, Brazil

The last epidemic of yellow fever in Europe was in 1861 in St. Nazaire, a port city in France. But in the last 10 years, cases of yellow fever have been imported from Africa or South America into Belgium, the Netherlands and Switzerland. These countries are north of the range of the urban vector, *Aedes aegypti*, so there was no epidemic risk from that mosquito. But another urban vector, *Ae. albopictus*, has become established in those 3 and 12 more European countries. In 2007, a single individual infected with chikungunya virus arrived from India in northern Italy, outside the range of *Ae. aegypti*. He sparked an epidemic vectored by *Ae. albopictus*. Europe is now vulnerable to importations of yellow fever. Non-stop airline flights between endemic areas of South America and Africa can bring passengers incubating the virus to major European cities within 24 h, where they can fall ill and infect local mosquitoes. There have recently been urban outbreaks of yellow fever in the capital cities of Asuncion, Paraguay and Abidjan, Cote d'Ivoire, which have international airports serving intercontinental flights. Countries in Europe where those and similar flights land should be on the lookout for cases. Unless the physician seeing a case elicits a travel history from an endemic country, yellow fever would never be suspected. ProMED <www.promedmail.org> was searched for up-to-date news of yellow fever outbreaks in the endemic zones, and the spread of the vector mosquito species. The results will be presented. Insecticide spraying of aircraft cabins is not sufficient alone. The conclusion is that the present risk of a yellow fever epidemic in Europe is real, and contingency planning is urgently needed.

