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sequences were detected by PCR. After sequencing of the 16S rDNA gene 3 dominant sequences were found to be present and were tentatively identified to be *H. bizzozeronii*, *H. felis* or *Helicobacter sp.*, originally isolated from a tiger with gastritis. Only one of these types was found per individual.

Conclusions: Bacteria belonging to the genus *Helicobacter* were found in all 9 exotic carnivore species examined. This proves the wide distribution of these microorganisms. Sequence identities between 96% and 99% would indicate that some of these organisms may be new *Helicobacter species*. The presence of *Helicobacter sp.* in the stomach was associated with a generally mild lympho-follicular gastritis in most cases. It is not yet clear whether the organisms were causing these minimal histological tissue changes. Whether the frequent colonisation of zoo-kept carnivores with several phylogenetically distinct helicobacters may reflect special characteristics in feeding and/or social behaviour of captive carnivores will be the subject of further investigations into animal species in the wild.

A-11

***Helicobacter pylori* transmission between spouses in Western Australia**

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Objective: The aim of this investigation was to track the transmission of *H. pylori* between spouses, using couples from the rural town of Busselton, Western Australia, as the subject group. **Patients and Methods:** Serum collected in 1994 from a subject group of 1000 married individuals was tested for *H. pylori* infection using an in-house ELISA test. Serum from the spouses of 200 seropositive patients was also analysed and 83 couples in which both spouses were seropositive for *H. pylori* were identified. Contact with these couples by mail, identified 50 potential study couples. Urea breath tests were used to ascertain which of the 50 couples still had current infections, 26 couples qualified to proceed in the investigation. Twenty-three of the 26 couples chose to proceed. Using the non-invasive string test method, *H. pylori* was isolated from both spouses of 15 couples. Three single isolates from each of these 15 couples were the focus of molecular typing experiments. **Results:** Serological analysis found that although the prevalence of *H. pylori* in the general married population was only 25.1%, in the spouses of infected individuals, the prevalence increased to 41.5% ($p < 0.0001$). Using AFLP and RAPD analysis, it was shown that seven (46.7%) of the 15 couples were infected with identical strains of *H. pylori*. Only one patient was simultaneously infected with more than one strain. **Conclusion:** Serological evidence showed that having a spouse infected with *H. pylori* was a significant risk factor for infection and indirectly inferred that spouse to spouse transmission may have occurred. Molecular typing of the bacterial isolates demonstrated that in Australia, unlike in developing countries, the transmission of *H. pylori* between spouses is common.

A-12

Clinical identification of *Helicobacter pylori* strains

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Introduction: It was stated that relapse of ulcer disease, despite of administered eradication therapy, is connected with repeated *Helicobacter pylori* (Hp) infection. Whether it is a result of insufficient treatment or new infection, remains uncertain. **Aim:** To analyse genotypes of H.p. strains isolated from patients before and after eradication during 12 months. **Methods:** PCR – RAPD finger- printing with the use of single starter T7 RNA POL-1 to differ Hp genotypes. **Results:** 52 patients with diagnosed ulcer disease were enrolled into study. They all underwent eradication treatment (PPI + Amoxy + Klar). Control examination was performed within 12 months. 10 patients (19,2%) were still Hp positive. The infection in 3 of them proved to be a new one with strains of bacteria different than before therapy, in 4 patients we observed persistent Hp infection, in 1 patient the presence of the same strain in two successive isolations was proved while the 3ed time it was a new strain. In 2 patients of the same family the strains were different. **Conclusion:** Our results confirm the possibility of reinfection with a new Hp strain. They do not exclude, however, persistent infection or infection with the same strain but from extraventricular sources.