SoIPa

SOCIETÀ ITALIANA DI PARASSITOLOGIA

XXVIII CONGRESSO NAZIONALE

ROMA, 24-27 giugno 2014

LETTURE
RELAZIONI DEI SIMPOSI
COMUNICAZIONI SCIENTIFICHE

Casa dell'Aviatore, Viale dell'Università, 20 - Roma

O11A.1
MOLECULAR EVIDENCE OF POLYMORPHISM IN PNEUMOCYSTIS FROM WILD MICE AND SHREWS IN THE EASTERN ALPS, ITALY

Da Rold G.[1], Rizzoli A.[2], Hauffe H.C.[2], Arnoldi D.[2], Tagliapietra V.[2], Demanche C.[3], Guillot J.[4], Capelli G.[1], **Danesi P.*[1]**

[1]Istituto Zooprofilattico delle Venezie, Parasitology Laboratory ~ Legnaro (PD) ~ Italy, [2]Fondazione E. Mach, Research and Innovation Centre, Department of Biodiversity and Molecular Ecology, S. Michele all'Adige ~ Trento ~ Italy, [3]Parasitology Dept, Faculty of Biological and Pharmaceutical Sciences ~ Lille ~ France, [4]Parasitology-Mycology Dept, Dynamyc research group, National Veterinary College of Alfort ~ Maisons-Alfort ~ France

INTRODUCTION:
Pneumocystis organisms are considered as major opportunistic fungal pathogens that infect humans and a wide range of other mammalian host species. The genus comprises uncultured, host-specific parasites adapted to the alveolar epithelial cells type I where they may proliferate provoking severe pneumonitis. Thus far, five species have been described: P. carinii and P. wakefieldiae in brown rats, P. jirovecii in humans, P. murina in common mice and P. oryctolagi in rabbits.
In the present study, we detected and characterised Pneumocystis organisms in wild mice and shrews from eastern Alpes. Our objective was to assess whether Pneumocystis organisms could be used as phylogeographic markers for these mammalian species.
MATERIALS AND METHODS:
A total of 96 lung tissue samples from wild rodents and insectivores were analyzed. Specimens of Apodemus flavicollis (n=30), Apodemus sp (n=1), Myodes glareolus (n=3), Sorex antinorii (n=61), and Sorex sp (n=1) were captured as part of an large collaborative European project (EDENext) by Fondazione Edmund Mach. After DNA extraction, samples were analyzed by nested PCR, using primers for the gene encoding the mitochondrial large subunit rRNA (mtLSU rRNA) (Derouiche et al. 2009) and sequenced. The mtLSU sequences were aligned with already known Pneumocystis sequences using Clustal X (version 1.63b) and a phylogenetic analysis was performed using Neighbour Joining integrated in Mega 4 software (version 4.0).
RESULTS:
Pneumocystis DNA was detected in 58 of 96 samples (60%). Lung tissues from Apodemus flavicollis (12/30; 40%), Sorex antinorii (44/61, 72%) and Myodes glareolus (2/3; 67%) were positive. The mtLSU sequences showed marked polymorphism with seven Pneumocystis sequence types representing three distinct major clades according to the three animal species. Among Sorex genus all sequences presented a similarity of 100%, whereas six different sequence types were obtained for the genera Apodemus (n=4) and Myoedes (n=2).
CONCLUSIONS:
These preliminary observations are in agreement with previous findings, which reported similar prevalence of Pneumocystis in Apodemus and Myodes animals as well as the highest prevalence in Sorex spp., when compared with other wild mammals (Laakkonen et al., 1995, Can J Zoology, 73:961-966). The genetic polymorphism in Apodemus and Myodes has already been described and seem to be a general tendency for rodent-derived Pneumocystis. The unique sequence type detected among Sorex shrews from the eastern Alpes suggests that Pneumocystis from insectivores display a lower level of genetic polymorphism.
This study was supported by Veneto Region and partially supported by EU grant FP7-261504 EDENext (http://www.edenext.eu) and the Fondazione E Mach.
The presentation of this work is sponsored by Cutech srl BIOTECHNOLOGY

Keywords:
Pneumocystis, wild mice, Molecular polymorphism

O11A.2
SURVEY ON YEASTS IN MUCOSAE OF DOGS WITH AND WITHOUT WEAKENING PATHOLOGIES

Galuppi R.*[1], Garutti S.[1], Fracassi F.[1], Capitani O.[1], Tampieri M.P.[1]

[1]Dipartimento di Scienze Mediche Veterinarie - Università Di Bologna ~ Bologna ~ Italy

INTRODUCTION:
In human medicine many studies point out as yeasts, commensals on mucosae, can became pathogens in course of immunodeficiency, chemotherapy, cortisone therapy, endocrinopathies (Bulacio et al, 2012, J. Mycol. Med., 22: 348-353). Such risk factors were also suggested in Veterinary Medicine but, so far, only few studies about this topic were made (Tampieri et al 2008, Parassitologia, 50: 95; Bieganska et al., 2012, 18th congress ISHAM, p.177). In this paper, the yeast flora of oral, conjunctiva and rectal mucosae of dogs was examined, in relation to presence ("sick dogs") or absence ("healthy dogs") of predisposing factors such as endocrinopaty, neoplasy, cortisone therapy or other weakening pathologies.
MATERIALS AND METHODS:
One hundred eight dogs (61 "healthy" and 47 "sick") were examined; from each dog 4 swabs from oral, conjunctival and rectal mucosae were collected and inoculated in duplicate on Sabouraud Dextrose Agar (BBL) with 0.05g/ chloramphenicol (Sigma). The plates were incubated both at 25°C and 37°C ad observed daily for 7 days. The yeasts isolated were identified microscopically for Malassezia pachydermatis and with Api 20C AUX (Biomerieux Italia S.p.a, Firenze, Italy) and Dalmau plates on Yeast Morphology Agar DIFCO (Becton Dickinson Italia S.p.a, Milano, Italy) for the other yeasts.
RESULTS:
Yeasts were found in 83 dogs out of 108 examined (76.8%). M. pachydermatis was isolated in at least one sample from 78/108 dogs (73.2%), especially in rectal mucosae where also the major number of yeast species was present. Conversely, lowest yeasts isolation was from conjunctival swabs. The other yeasts isolated were: Rhodotorula spp (8.34%), Candida albicans (3.7%), C. glabrata (2.78%), Cryptococcus laurentii (1.85%), C. guilliermondii, C. parapsilosis, C. boidinii, Saccharomyces cerevisiae and Cr. albidus (0.92%). M. pachydermatis was found more frequently in healthy dogs (83.6%) compared to sick dogs (57.4%) ($X^2y = 6.18$, $p>0.05$). On the contrary, other yeasts were found more frequently in sick dogs (15.22%) than in healthy dogs (6.2%) (Fisher exact $p<0.05$). In particular C. albicans, isolated only in 4 sick dogs (8.7%), was not found in healthy ones (Fisher exact $p<0.05$). In one dog with parvovirosis, C. albicans was isolated from an ulcer of oral mucosa that resolved without specific treatment after healing.
CONCLUSIONS:
M. pachydermatis was the yeast most frequently present on dogs mucosae, according to Tampieri et al. (2008 l.c.), Brito et al. (2009, Vet. J., 182: 320-326) and Santin et al. (2013, Braz. J. microbiol., 44: 139-143) and can be considered an usual component of mucosal microflora of dog. The isolation of S. cerevisiae could be explained by the administration of probiotics. C. boidinii, C. parapsilosis, Cr. laurentii, Cr albidus and Rhodotorula spp. isolated, with low number of colonies, only at 25°C, could be considered as environmental contaminants and not colonizer, contrary to C. glabrata and, especially, C. albicans that were isolated both at 25°C and 37°C, only in sick dogs and in high number of colonies. From these observations we can suppose that may be a real colonization of mucous membranes. Unlike what happens in humans, where C. albicans is a frequent commensal in the mucosa of healthy subjects, in the dog the finding of such yeast is occasional and could be a proof of organic imbalance.

Keywords:
Yeast, Mucosae, Dog