

热带病学术热点追踪报告

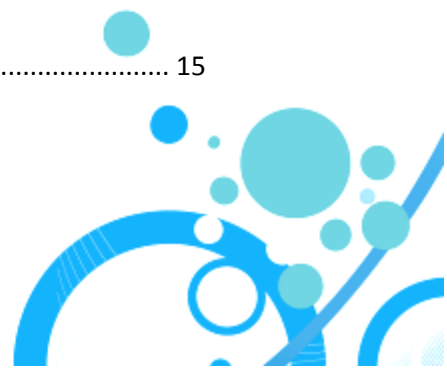
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一、国际热带病热点研究

1. 疟疾相关

(1) *Population genetics and drug resistance markers: an essential for malaria surveillance in Pakistan*

Abstract*

Plasmodium (P.) vivax is the prevalent malarial species accounting for 70% of malaria cases in Pakistan. However, baseline epidemiological data on P. vivax population structure and drug resistance are lacking from Pakistan. For population structure studies, molecular genetic markers, circumsporozoite protein (csp) and merozoite surface protein-1 (msp-1) are considered useful as these play an important role in P. vivax survival under immune and environmental pressure. Studies on drug resistance are necessary so that anti-malarial treatment strategies can be structured and implemented accordingly by the Malaria Control Program, Pakistan. This review aims to provide information on genetic markers of P. vivax population structure and drug resistance and comment on their usefulness in molecular surveillance and control ^[1].

(2) *Habitat hydrology and geomorphology control the distribution of malaria vector larvae in rural Africa*

Abstract

We conducted the first catchment scale study of fine resolution spatial and temporal variation in Anopheles habitat and productivity in relation to rainfall, hydrology and geomorphology for a high malaria transmission area of Tanzania.

* 为了给读者提供更简明扼要的信息，本报告中的英文摘要均经过编辑和精简。

Monthly aggregates of rainfall, river stage and water table were not significantly related to the abundance of vector larvae. However, these metrics showed strong explanatory power to predict mosquito larval abundances after stratification by water body type, with a clear seasonal trend for each, defined on the basis of its geomorphological setting and origin. Hydrological and geomorphological processes governing the availability and productivity of *Anopheles* breeding habitat need to be understood at the local scale for which larval source management is implemented in order to effectively target larval source interventions. Mapping and monitoring these processes is a well-established practice providing a tractable way forward for developing important malaria management tools^[2].

(3) Serum lipids and lipoproteins in malaria - a systematic review and meta-analysis

Abstract

The aim of this paper is to provide an overview on those serum lipid profile changes, and to discuss possible underlying biological mechanisms and the role of lipids in malaria pathogenesis. A systematic review and meta-analysis to determine lipid profile changes during malaria was conducted, following PRISMA guidelines. This meta-analysis suggests that the observed lipid profile changes are characteristic for malaria. Although a definite link with the pathogenesis of malaria cannot yet be demonstrated, plausible hypotheses of biological mechanisms involving host lipid alterations and the pathogenesis of malaria exist. An increased research effort to elucidate the precise pathways is warranted, since this could lead to better understanding of malaria pathophysiology and consequently to novel treatment approaches^[3].

(4) Mosquito transmission, growth phenotypes and the virulence of malaria parasites

Abstract

A series of elegant experiments was recently published which demonstrated that transmission of malaria parasites through mosquitoes elicited an attenuated growth



phenotype, whereby infections grew more slowly and reached peak parasitaemia at least five-fold lower than parasites which had not been mosquito transmitted. Using previously published data, the impact of mosquito transmission on parasite growth rates and virulence of six *Plasmodium chabaudi* lines was analyzed. The effect of mosquito transmission varied among strains, but did not lead to pronounced or consistent reductions in parasite growth rate. Mosquito-induced attenuated growth phenotype is sensitive to experimental conditions^[4].

(5) Efficacy and Safety of Dihydroartemisinin-Piperaquine for Treatment of *Plasmodium vivax* Malaria in Endemic Countries: Meta-Analysis of Randomized Controlled Studies

Abstract

This study aimed to synthesize available evidence on the efficacy of dihydroartemisinin-piperaquine (DHP) in treating uncomplicated *Plasmodium vivax* malaria in people living in endemic countries. This is a meta-analysis of randomized controlled trials (RCT). We searched relevant studies in electronic databases up to May 2013. RCTs comparing efficacy of (DHP) with other artemisinin-based combination therapy (ACT), non-ACT or placebo were selected. The primary endpoint was efficacy expressed as PCR-corrected parasitological failure. Findings document that DHP is more efficacious than CQ and AL in treating uncomplicated *P. vivax* malaria. The better safety profile of DHP and the once-daily dosage improves adherence, and its fixed co-formulation ensures that both drugs (dihydroartemisinin and piperaquine) are taken together^[5].

2. 血吸虫相关

(1) Genetic and Molecular Basis of Drug Resistance and Species-Specific Drug Action in Schistosome Parasites

Abstract

We crossed parental parasites differing 500-fold in drug response, determined drug sensitivity and marker segregation in clonally derived second-generation



progeny, and identified a single quantitative trait locus (logarithm of odds score = 31) on chromosome 6. A sulfotransferase was identified as the causative gene by using RNA interference knockdown and biochemical complementation assays, and we subsequently demonstrated independent origins of loss-of-function mutations in field-derived and laboratory-selected resistant parasites. These results demonstrate the utility of linkage mapping in a human helminth parasite, while crystallographic analyses of protein-drug interactions illuminate the mode of drug action and provide a framework for rational design of oxamniquine derivatives that kill both *S. mansoni* and *S. haematobium*, the two species responsible for >99% of schistosomiasis cases worldwide^[6].

(2) Regulation of innate responses during pre-patent schistosome infection provides an immune environment permissive for parasite development

Abstract

We show that repeated stimulation of innate immunity by an endogenous danger signal can restore parasite development, when administered repeatedly, lead to the regulation of innate responses. Supporting a role for regulation of innate responses in parasite development, we show that regulation of inflammation by neutralizing anti-TNF antibodies also restores parasite development in immunodeficient mice. Finally, we show that administration of IL-4 to immunodeficient mice to regulate inflammation by induction of type 2 responses also restores parasite development. These findings suggest that the type 2 response driven by CD4⁺ T cells during pre-patent infection of immunocompetent hosts is exploited by schistosomes to complete their development to reproductively mature adult parasites^[7].

(3) Activation of an innate immune response in the schistosome-transmitting snail *Biomphalaria glabrata* by specific bacterial PAMPs



Abstract

It is not known if mitogenic activity resides in the lipid A or O-polysaccharide component of LPS. Moreover, the possible role of substances that commonly contaminate crude LPS and that are known to stimulate innate immune responses in mammals, e.g., peptidoglycan (PGN), protein, or bacterial DNA, is unclear. Therefore, we tested the effects of the following injected substances on the snail APO: crude LPS, ultrapurified LPS (lacking lipoprotein contamination), two forms of lipid A, (diphosphoryl lipid A and Kdo2-lipid A), O-polysaccharide, Gram negative PGN, both crude and ultrapurified (with and without endotoxin activity, respectively), Gram positive PGN, PGN components Tri-DAP and muramyl dipeptide, and bacterial DNA. Whereas crude LPS, ultrapurified LPS, and crude PGN were mitogenic, ultrapurified PGN was not. Moreover, LPS components, PGN components, and bacterial DNA were inactive. These results suggest that it is the intact LPS molecule which stimulates cell division in the APO^[8].

(4) Prevalence and effect of schistosome and soil-transmitted helminth infection on labour input in rice-growing communities of Ogun State, Nigeria

Abstract

*Studies were carried out to determine the prevalence and effect of schistosomes and soil-transmitted helminths infection on labour input on rice production in 9 rice-growing communities of Ogun State. Parasitological examinations of urine and faecal samples, and structured questionnaires were conducted on 243 consented individuals from May 2009 to March 2010. The results showed an overall prevalence of 17% for *Ascaris lumbricoides*, 12% for hookworms, 2% for *Trichuris trichiura*, 1% for *Schistosoma haematobium* and 1% for *Schistosoma mansoni*. Infections among the gender were varied as 26.3 % of males and 33.8 % of females had an overall prevalence of: *A. lumbricoides* (16.8%), hookworms (11.8%), *T. trichiura* (1.6%), *S. haematobium* (1.1%) and *S. mansoni* (1.1%). Understanding the effect of these two diseases will not only improve the health status of residents but also increase their productivity and ensure food security^[9].*



(5) Characteristics of the Human Host Have Little Influence on Which Local *Schistosoma mansoni* Populations Are Acquired

Abstract

The variables sex, age, intensity of infection, socio-economic index, lifetime spent on site, previous infection, and trips outside the district were used to group parasites infecting individuals. Schistosoma mansoni infection status was determined by examination of stools submitted on 3 different days. The aggregate of eggs collected from the whole stool was used to determine degree of population differentiation from allele frequencies for 15 microsatellites. Those most heavily infected best reflected the communities' overall parasite diversity. The lack of differentiation within villages suggests that individuals are likely to get infected at the same sites or that the same parasite multilocus genotypes can be found at most sites^[10].

3. 其他寄生虫相关

1. Use of Anti-Aedes aegypti Salivary Extract Antibody Concentration to Correlate Risk of Vector Exposure and Dengue Transmission Risk in Colombia

Abstract

In this study, we examined the serum concentration of anti-Aedes salivary gland extract (SGE) antibodies as a biomarker of DENV infection and transmission, and assessed the duration of anti-SGE antibody concentration after exposure to the vector ceased. We also determined whether SGE antibody concentration could differentiate between positive and negative DENV infected individuals and whether there are differences in exposure for each DENV serotype. We observed a significant decrease in the concentration of IgG antibodies at least 40 days after returning to an "Ae. aegypti-free" area. In addition, we found significantly higher anti-SGE IgG concentrations in DENV positive patients with some difference in exposure to mosquito bites among DENV serotypes. We conclude that the concentration of IgG

antibodies against SGE is an accurate indicator of risk of denguevirus transmission and disease presence^[11].

2. Flavonoid from *Carica papaya* inhibits NS2B-NS3 protease and prevents Dengue 2 viral assembly

Abstract

Dengue hemorrhagic disease caused by dengue virus is a public health problem worldwide. The viral non structural 2B and 3 (NS2B-NS3) protease complex is crucial for virus replication and hence, it is considered to be a good anti-viral target. Leaf extracts from *Carica papaya* is generally prescribed for patients with dengue fever, but there are no scientific evidences for its anti-dengue activity; hence we intended to investigate the anti-viral activity of compounds present in the leaves of *Carica papaya* against dengue 2 virus (DENV-2). We analysed the anti-dengue activities of the extracts from *Carica papaya* by using bioinformatics tools. Interestingly, we find the flavonoid quercetin with highest binding energy against NS2B-NS3 protease which is evident by the formation of six hydrogen bonds with the amino acid residues at the binding site of the receptor. Our results suggest that the flavonoids from *Carica papaya* have significant anti-dengue activities^[12].

3. Percutaneous nephroscopic management of an isolated giant renal hydatid cyst guided by single-incision laparoscopy using conventional instruments: The Santosh-PGI technique

Abstract

We report our experience with a novel technique involving percutaneous management of a giant renal hydatid cyst with single-incision laparoscopic assistance. First we performed retrograde ureteropyelogram, which did not show any communication between the cyst and the calyceal. A Veress needle was used for pneumoperitoneum. Three conventional laparoscopic trocars used. Under laparoscopic guidance, we punctured the cyst. The scolicidal solution used was 10% povidone-iodine. The endocyst was removed under vision with grasping forceps through the nephroscope. A Portex drain was placed into the cyst cavity. We believe



this is the first reported case of its kind in the world. Not only this technique is minimally invasive, it is also cost-effective, as only conventional laparoscopic ports and instruments are used during the procedure^[13].

4. Comparative evaluation of PCR and imprint smear microscopy analyses of skin biopsy specimens in diagnosis of macular, papular, and mixed papulo-nodular lesions of post-kala-azar dermal leishmaniasis

Abstract

Diagnosis of post-kala-azar dermal leishmaniasis (PKDL), particularly the macular form, is difficult when based on microscopy. This study compared the results of nested PCR (91.9% positive samples) with imprint smear microscopy (70.9% positive samples) for 62 PKDL samples. We found that nested PCR, which indicated 87.5% positivity for the macular lesions, compared to 41.6% positivity by imprint smear microscopy, is an efficient method for early diagnosis of PKDL^[14].

5. Cerebellar Cysticercosis Caused by Larval Taenia crassiceps Tapeworm in Immunocompetent Woman, Germany

Abstract

Human cysticercosis caused by Taenia crassiceps tapeworm larvae involves the muscles and subcutis mostly in immunocompromised patients and the eye in immunocompetent persons. We report a successfully treated cerebellar infection in an immunocompetent woman. We developed serologic tests, and the parasite was identified by histologic examination and 12s rDNA PCR and sequencing^[15].



二、国内热带病热点研究

1. 疟疾相关

(1) 新疆输入性疟疾 13 例临床特征分析

【摘要】*

探讨新疆输入性疟疾的临床特征,为临床医师早期诊治该疾病提供依据。回顾性分析新疆 13 例输入性疟疾的临床资料。输入性疟疾以恶性疟疾多见,发热多不规则,前期伴有头痛、肌肉酸痛、咳嗽等症状以及腹痛、腹泻、呕吐等消化道症状,可并发肝肾功能损害;实验室检查白细胞可明显升高,以中性粒细胞比值升高为主(7/13,53.85%),有(9/13,69.23%)的患者出现血小板下降;30.77%的输入性疟疾患者治愈后会出现再燃。5 例患者表现为谷丙转氨酶(ALT)和谷草转氨酶(AST)的升高。5 例患者表现为肌酐或尿素氮的升高。2 例有肝肿大,6 例有脾肿大。经蒿甲醚治疗后,13 例患者均治愈。结论为输入性疟疾临床表现复杂,并发症多,应对临床拟诊病人采取多次查找疟原虫的措施以及早期实验性抗疟治疗^[16]。

(2) 南通市通州区 21 例输入性疟疾流行病学分析

【摘要】

了解和掌握通州区疟疾流行特征。对 2009~2011 年通州区输入性疟疾病例的流行病学特征进行分析。结果为 2009~2011 年共有 21 例输入性疟疾,占全部疟疾病例 80.77%,其中恶性疟 16 例,间日疟 5 例。病例分布于全区 10 个镇;发病季节呈全年分布;男女性别比为 9.5 : 1;年龄在 5~55 岁之间;职业主要为民工,感染来源主要为非洲及南亚等国外疟疾高发区。结论为输入性疟疾病例是通州区疟疾的主要疫情特点,病例感染来源主要为非洲及南亚等国外疟疾高发区^[17]。

*为了给读者提供更简明扼要的信息,本报告中的中文摘要均经过编辑和精简。

(3) 2012 年广东省疟疾疫情流行病学分析

【摘要】

分析 2012 年广东省疟疾流行特点, 为该省消除疟疾提供参考依据。方法资料来自中国疾病预防控制中心疾病监测信息报告管理系统, 采用描述性流行病学方法, 分析 2012 年广东省网络报告疟疾病例的流行病学特点。结果从总体情况、病例地理分布、男女比例、年龄分布、职业类别、输入来源等方面进行了阐述。结论为 2012 年广东省疟疾疫情相对稳定。但是由于输入性疟疾病例增多, 因此应加强疟疾的诊断、治疗和疫情处置能力, 加强监测和防控^[18]。

(4) ABO 血型与疟疾易感性: 基于中国人群的 Meta 分析

【摘要】

研究中国人群 ABO 血型与疟疾易感性之间的关系。通过查询重庆维普、Medline 数据库收集国内外 1980 年 1 月 1 日至 2013 年 3 月 1 日之间公开发表的关于 ABO 血型与疟疾易感性的中英文文献资料, 采用荟萃分析软件 RevMan 5 进行 Meta 分析。Meta 分析结果显示, A 型血与非 A 型血人群相比, 疟疾的发病风险合并相对危险度(RR)及(95%)CI 为 1.27(1.03~1.57); B 型血与非 B 型血人群相比, 为 0.97(0.80~1.17); AB 型血与非 AB 型血人群相比, 为 0.92(0.80~1.06); O 型血与非 O 型血人群相比, 为 0.80(0.73 ~ 0.88)。各亚组研究通过 Egger 回归法进行发表性偏倚分析, P 值分别为 0.32、0.87、0.30、0.72, 均 >0.10。结论为各亚组研究可认为无发表性偏倚, 对于中国人群, A 型血较之其他血型对疟疾多 27% 的感染可能, 而 O 型血较之其他血型少 20% 的感染可能^[19]。

2. 血吸虫相关

(1) 血吸虫病治疗性抗体的研发

【摘要】



血吸虫病仍是影响我国人民群众身体健康和社会经济发展的重大公共卫生问题。随着大型水利工程造成生态环境的改变及流动人口的剧增,将可能导致钉螺面积回升和人、畜感染机会增加,我国血吸虫病防治工作面临严峻的挑战^[20]。

(2) 晚期血吸虫肝病的 B 超诊断分析

【摘要】

探讨 B 超在晚期血吸虫肝病诊断中的应用价值。对 2012 年 6 月-2013 年 6 月 B 超诊断的晚期血吸虫肝病的 10 例患者的临床资料进行回顾,分析其 B 超影像特点。结果为血吸虫肝病典型病例有 8 例,伴有门静脉扩张、腹水、脾脏肿大,1 例患者伴慢性胆囊炎,见胆囊径线变小,囊壁增厚,胆汁透声较差。1 例伴有胆囊多发结石。2 例为非典型病例,超声检查均不伴有门静脉扩张。结论是 B 超诊断血吸虫肝病的特异性和灵敏性较好,对晚期血吸虫肝病诊断鉴别具有重要意义^[21]。

(3) 日本血吸虫尾蚴生态的研究进展

【摘要】

尾蚴是血吸虫病传播的唯一途径,也是血吸虫病流行的关键阶段,研究血吸虫尾蚴的形态、生态及查蚴、灭蚴方面的知识,对预防血吸虫病的感染、检查、监测、灭蚴和预警、预报具有重要的科学意义。本文就日本血吸虫尾蚴的有关研究进展进行简略的介绍^[22]。

(4) 日本血吸虫 T2 核酸酶的原核表达及活性分析

【摘要】

构建日本血吸虫 T2 核酸酶表达载体,并进行体外表达和酶活性分析。从日本血吸虫基因组数据库中找到与曼氏血吸虫虫卵抗原 Omega-1 同源性最高的蛋白 AY814845,设计引物并通过 PCR 技术扩增得到该基因,将其成熟编码区连入 pET32a 表达载体,转化大肠杆菌并用 IPTG 诱导其表达,最后对表达产物的核



酸酶活性进行分析。结果为成功的构建了日本血吸虫 T2 核酸酶的表达载体，其编码区能够在大肠杆菌中表达，且表达产物具有一定的核酸酶活性。结论是从体外扩增了日本血吸虫 T2 核酸酶 AY814845，明确其表达产物具有核酸酶活性，为今后深入研究该蛋白的功能打下了基础^[23]。

3. 其他寄生虫相关

(1) 广东省 2006-2011 年登革热时空分布特征

【摘要】

分析 2006-2011 年广东省登革热的时空分布特征，为登革热防控提供科学依据。计算 2006-2011 年广东省登革热县(区)级年发病率水平，利用空间自相关分析确定登革热高风险地区。结果是广东省珠江三角洲和韩江三角洲登革热发病率分别为 $>4/10$ 万和 $>2.5/10$ 万，Moran' s I 统计量在 2006-2007 年($P=0.005$)和 2009-2011 年($P=0.001$)有统计学意义，2007-2008 年无统计学意义($P=0.814$)。结论为广东省登革热分布是非随机的，珠江三角洲和韩江三角洲是登革热的高危地区^[24]。

(2) 一类具有饱和发生率的包虫病传播模型研究

【摘要】

研究一类具有饱和发生率的包虫病模型，分别讨论了无病平衡点和地方病平衡点的稳定性。分析结果表明模型的动力学行为完全由基本再生数 R_0 决定。最后，在讨论部分根据 R_0 的表达式对疾病给出一些控制策略^[25]。

(3) 细粒棘球绦虫 5 种天然抗原制剂诊断效能的初步评价

【摘要】

对细粒棘球绦虫 5 种天然抗原制剂的诊断效能进行评价。从绵羊肝棘球蚴囊中收集囊液和原头节，制备细粒棘球蚴原头节虫体可溶性抗原 (EgPS)、囊液部分纯化抗原 (EgBu)、囊液粗制抗原 (EgHF) 和天然抗原 B (EgAgB)。从



实验感染的家犬肠道中收集细粒棘球绦虫成虫，制备成虫虫体可溶性抗原（EgAS）。对 369 例细粒棘球绦病患者，99 例其他寄生虫病患者和 366 名健康体检者共 834 份血清样品，用间接 ELISA 技术检测抗体。检测结果经统计学处理后进行综合性分析和评价。结论显示，不同抗原 ELISA 检测结果之间存在着明显差异。以 EgPS 抗原的诊断效能最佳，其次为 EgBu 和 EgAgB 抗原^[26]。

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(如需参考文献中论文全文，请发送论文标题至 yaoyaoyu1987@163.com)

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