热带病学术热点追踪报告

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目　录

一、国际热带病热点研究

1. 疟疾相关

（1）*Impact of malaria related messages on insecticide-treated net (ITN) use formalaria prevention in Ghana.*

Abstract[*]

Media messages have been used in Ghana to promote insecticide-treated net (ITN)/bed net usage in an effort to impact on malaria prevention. The aim of this study was to assess the effect of such malaria-related messages delivered through electronic/print media and by volunteers/health workers on the use of ITNs by children living in a household. Data was collected from September to November of 2008 using a structured, interviewer-administered questionnaire by the Ghana Statistical Service as part of a national demographic and health survey (DHS). Efforts to relate ITN messages to the public are very useful in increasing use of bed nets and having multiple ways of reaching the public increases their effect, with the biggest effect seen when health workers and volunteers were used to deliver malaria-related messages to the public [1].

（2）*Plasma advanced oxidative protein products are associated with anti-oxidative stress pathway genes and malaria in a longitudinal cohort.*

Abstract

Advanced oxidation protein products (AOPP) are newly identified efficient oxidative stress biomarkers. In a longitudinal birth cohort the effects were investigated of genetic polymorphisms in five oxidative pathway genes on AOPP levels. This study is part of a three-arm randomized, double-blind, placebo-controlled trial. Twelve polymorphisms were genotyped in five oxidative stress pathway genes: glutathione reductase (GSR), glutamylcysteine synthetase (GCLC), glutathione

[*] 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。

S-transferase (GST) P1, haem oxygenase 1 (HMOX1) and superoxide dismutase 2 (SOD2) in 298 children. Plasma AOPP levels were predictive for anaemia and oxidative stress markers for clinical malaria infection in two year old children. Several polymorphisms in GCLC, GSR and HMOX1 genes were associated with oxidative stress status of these children [2].

（3）*Proteolysis at a Specific Extracellular Residue Implicates Integral Membrane CLAG3 in Malaria Parasite Nutrient Channels.*

Abstract

The plasmodial surface anion channel mediates uptake of nutrients and other solutes into erythrocytes infected with malaria parasites. We used proteases to examine the channel's composition and function. Chymotrypsin-induced inhibition depended on parasite genotype, with channels induced by the HB3 parasite affected to a greater extent than those of the Dd2 clone. Inheritance of functional proteolysis in the HB3×Dd2 genetic cross, DNA transfection, and gene silencing experiments all pointed to the clag3 genes, providing independent evidence for a role of these genes. Protease protection assays with a Dd2-specific inhibitor and site-directed mutagenesis revealed that a variant L1115F residue on a CLAG3 extracellular loop contributes to inhibitor binding and accounts for differences in functional proteolysis. These findings indicate that surface-exposed CLAG3 is the relevant pool of this protein for channel function. They also suggest structural models for how exposed CLAG3 domains contribute to pore formation and parasite nutrient uptake [3].

（4）*Understanding private sector antimalarial distribution chains: a cross-sectional mixed methods study in six malaria-endemic countries.*

Abstract

Private for-profit outlets are important treatment sources for malaria in most endemic countries. However, these outlets constitute only the last link in a chain of businesses that includes manufacturers, importers and wholesalers, all of which influence the availability, price and quality of antimalarials patients can access. We

conducted nationally representative surveys of antimalarial wholesalers during 2009-2010 using an innovative sampling approach that captured registered and unregistered distribution channels, complemented by in-depth interviews with a range of stakeholders. The conclusion is that the structure and characteristics of antimalarial distribution chains vary across countries; therefore, understanding the wholesalers that comprise them should inform efforts aiming to improve access to quality treatment through the private sector [4].

（5）*Synthetic indole and melatonin derivatives exhibit antimalarial activity on the cell cycle of the human malaria parasite Plasmodium falciparum.*

Abstract

Discovering the mechanisms by which cell signaling controls the cell cycle of the human malaria parasite Plasmodium falciparum is fundamental to designing more effective antimalarials. To better understand the impacts of melatonin structure and function on the cell cycle of P. falciparum, we have synthesized two families of structurally-related melatonin compounds (7-11 and 12-16). All synthesized melatonin analogs were assayed in P. falciparum culture and their antimalarial activities were measured by flow cytometry. We have found that the chemical modification of the carboxamide group attached at C-3 position of the indole ring of melatonin (6) was crucial for the action of the indole-related compounds on the P. falciparum cell cycle. Among the melatonin derivatives, only the compounds 12, 13 and 14 were capable of inhibiting the P. falciparum growth in low micromolar IC50. These results open good perspectives for the development of new drugs with novel mechanisms of action [5].

2. 血吸虫相关

（1）*Differences in the Gene Expression Profiles of Haemocytes from Schistosome-Susceptible and -Resistant Biomphalaria glabrata Exposed to Schistosoma mansoni Excretory-Secretory Products.*

Abstract

During its life cycle, the helminth parasite Schistosoma mansoni uses the freshwater snail Biomphalaria glabrata as an intermediate host to reproduce asexually generating cercariae for infection of the human definitive host. Following invasion of the snail, the parasite develops from a miracidium to a mother sporocyst and releases excretory-secretory products (ESPs) that likely influence the outcome of host infection. We determined gene expression profiles of haemocytes from S. mansoni-resistant or -susceptible strains of B. glabrata exposed in vitro to S. mansoni ESPs (20 µg/ml) for 1 h, using a 5K B. glabrata cDNA microarray. Ninety-eight genes were found differentially expressed between haemocytes from the two snail strains, 57 resistant specific and 41 susceptible specific, 60 of which had no known homologue in GenBank. Comparative analysis with other gene expression studies revealed 38 of the 98 identified genes to be uniquely differentially expressed in haemocytes in the presence of ESPs, thus identifying for the first time schistosome ESPs as important molecules that influence global snail host-defence cell gene expression profiles [6].

（2）*An immunomics approach to schistosome antigen discovery: antibody signatures of naturally resistant and chronically infected individuals from endemic areas.*

Abstract

We take advantage of recent advances in systems biology and longitudinal studies in schistosomiasis endemic areas in Brazil to pilot an immunomics approach to the discovery of schistosomiasis vaccine antigens. We selected mostly surface-derived proteins, produced them using an in vitro rapid translation system and then printed them to generate the first protein microarray for a multi-cellular pathogen. We probed arrays for IgG subclass and IgE responses to these antigens to detect antibody signatures that were reflective of protective vs. non-protective immune responses. We showed that PR individuals mounted a distinct and robust IgG1 response to a small set of newly discovered and well-characterized surface (tegument) antigens in contrast to CI individuals who mounted strong IgE and IgG4 responses to many antigens. Herein, we show the utility of a vaccinomics approach

that profiles antibody responses of resistant individuals in a high-throughput multiplex approach for the identification of several potentially protective and safe schistosomiasis vaccine antigens [7].

（3）*Novel expression profiles of microRNAs suggest that specific miRNAs regulate gene expression for the sexual maturation of female Schistosoma japonicum after pairing.*

Abstract

Parasites isolated from single- and double-sex cercariae-infected mice were analyzed by Solexa to uncover pair-regulated miRNA profiles. To reveal the biological functions of differentially expressed miRNAs among the samples, we predicted the target genes of these differentially expressed miRNAs and compared the gene expression between 23-d-old female schistosomula from double-sex infections (23DSI) and 23-d-old female schistosomula from single-sex infections (23SSI) by analyzing digital gene expression profiling (DGE). KEGG pathway analysis was used to investigate the relevant biological processes of these target genes to understand the significance of differentially expressed miRNAs after pairing. The conclusion is that the differentially expressed miRNAs between 23SSI and 23DSI and their different functions indicated that more genes or metabolic pathways in paired mature females were inhibited than those in unpaired ones. The results suggested that after pairing, specific miRNAs regulated gene expression to lead to female sexual maturation [8].

3. 其他寄生虫相关

（1）*Fusion of Protegrin-1 and Plectasin to MAP30 Shows Significant Inhibition Activity against Dengue Virus Replication.*

Abstract

This study presents a new strategy for inexpensive production of anti-DENV peptide-fusion protein to prevent and/or treat DENV infection. Antiviral cationic peptides protegrin-1 (PG1) and plectasin (PLSN) were fused with MAP30 protein to produce recombinant antiviral peptide-fusion protein (PG1-MAP30-PLSN) as inclusion bodies in E. coli.

High yield production of PG1-MAP30-PLSN protein was achieved by solubilization of inclusion bodies in alkaline buffer followed by the application of appropriate refolding techniques. Antiviral PG1-MAP30-PLSN protein considerably inhibited DENV protease (NS2B-NS3pro) with half-maximal inhibitory concentration (IC50) 0.5±0.1 μM.The peptide-fusion protein protected DENV2-challeged mice with 100% of survival at the dose of 50 mg/kg. In conclusion, producing recombinant antiviral peptide-fusion protein by combining short antiviral peptide with a central protein owning similar activity could be useful to minimize the overall cost of short peptide production and take advantage of its synergistic antiviral activities [9].

（2）*Prediction of high incidence of dengue in the Philippines.*

Abstract

Accurate prediction of dengue incidence levels weeks in advance of an outbreak may reduce the morbidity and mortality associated with this neglected disease. Therefore, models were developed to predict high and low dengue incidence in order to provide timely forewarnings in the Philippines. Model inputs were chosen based on studies indicating variables that may impact dengue incidence. The method first uses Fuzzy Association Rule Mining techniques to extract association rules from these historical epidemiological, environmental, and socio-economic data, as well as climate data indicating future weather patterns. Selection criteria were used to choose a subset of these rules for a classifier, thereby generating a Prediction Model. The threshold between high and low was determined relative to historical incidence data. This method builds prediction models for future dengue incidence in the Philippines and is capable of being modified for use in different situations; for diseases other than dengue; and for regions beyond the Philippines. The Philippines dengue prediction models predicted high or low incidence of dengue four weeks in advance of an outbreak with high accuracy, as measured by PPV, NPV, Sensitivity, and Specificity [10].

（3）*Bone Marrow Parasite Burden among Patients with New World Kala-Azar is Associated with Disease Severity.*

Abstract

Kala-azar or visceral leishmaniasis, found mostly throughout the Indian Subcontinent, East Africa, and Brazil, kills 20,000-40,000 persons annually. The agents, Leishmania

donovani and Leishmania infantum, are obligatory intracellular protozoa of mononuclear phagocytes found principally in the spleen and bone marrow. Protracted fever, anemia, wasting, hepatosplenomegaly, hemorrhages, and bacterial co-infections are typical features. One hundred and twenty-two (122) in-hospital patients were studied to verify if higher bone marrow parasite load estimated by quantitative polymerase chain reaction is associated with severe disease. The estimated median parasite load was 5.0 parasites/10(6) human nucleated cells. It is much higher in deceased than among survivors (median 75.0 versus 4.2). Patients who lost more weight had a higher parasite burden, as well as patients with epistaxis, abdominal pain, edema, and jaundice. This study suggests that higher parasite load is influenced by wasting, which may lead to more severe disease [11].

（4）*Parasite Fate and Involvement of Infected Cells in the Induction of CD4+ and CD8+ T Cell Responses to Toxoplasma gondii.*

Abstract

During infection with the intracellular parasite Toxoplasma gondii, the presentation of parasite-derived antigens to CD4+ and CD8+ T cells is essential for long-term resistance to this pathogen.An attenuated non-replicating strain of T. gondii (the cpsII strain) was combined with a cytometry-based approach to distinguish active invasion from phagocytic uptake. In vivo studies revealed that T. gondii disproportionately infected dendritic cells and macrophages, and that infected dendritic cells and macrophages displayed an activated phenotype characterized by enhanced levels of CD86 compared to cells that had phagocytosed the parasite, thus suggesting a role for these cells in priming naïve T cells. Indeed, dendritic cells were required for optimal CD4+ and CD8+ T cell responses, and the phagocytosis of heat-killed or invasion-blocked parasites was not sufficient to induce T cell responses. Rather, the selective transfer of cpsII-infected dendritic cells or macrophages (but not those that had phagocytosed the parasite) to naïve mice potently induced CD4+ and CD8+ T cell responses, and conferred protection against challenge with virulent T. gondii. Collectively, these results point toward a critical role for actively infected host cells in initiating T. gondii-specific CD4+ and CD8+ T cell responses [12].

（5）***A new combination and a new species of onchobothriid tapeworm (Cestoda: Tetraphyllidea: Onchobothriidae) from triakid sharks.***

Abstract

The specimens studied by us differ from the original description in the number of proglottids and testes and in the size of the cirrus-sac. However, we consider them conspecific with E. xiamenensis due to the consistent hook morphology and laciniations in both descriptions and believe the differences reflect intraspecific variation. The type-host of E. xiamenensis was reported as Mustelus griseus Pietschmann. However, in the present study, this parasite was found only in H. japanica and never in M. griseus although many specimens of the latter host were examined. This suggests that the type-host in the original description has probably been misidentified. We found another undescribed species in M. griseus, Calliobothrium shirozame n. sp., which is distinguished from the congeners by having a unique combination of the number of laciniations: four in the cephalic peduncle, six in the immature proglottids and four in the mature proglottids [13].

二、国内热带病热点研究

1. 疟疾相关

（1）江苏省疟疾疫情预警系统的建立Ⅲ 传染病自动预警信息系统应用于消除疟疾响应的效果

【摘要】*

本研究旨在评价全国传染病自动预警信息子系统疟疾预警系统的运行效果。方法是收集中国疾病预防控制信息系统传染病自动预警信息子系统的疟疾预警信息，对江苏省疟疾预警信号进行统计，比较疟疾预警信息系统运行前后的 3 d

*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。

内完成个案流调率。结论为 3 d 内完成个案流调率与预警手机短信有关联，传染病自动预警信息子系统的疟疾预警信息能有效提高基层疾控中心对疟疾病例的响应速度，对及时核实和判断疟疾病例具有重要作用[14]。

（2）海南省消除疟疾后期间日疟原虫裂殖子表面蛋白 1 基因（MSP－1 ）多态性检测

【摘要】

本研究旨在比对海南省在消除疟疾前期间日疟原虫裂殖子表面蛋白 1 的基因型。方法是采用 PCR 扩增特异性目的片段，基因测序，序列比对及进化树构建。结论为海南消除疟疾后期（２００９－２０１２）间日疟仍以 Sal－１ 型为主，但仍存在该等位基因的多样性而非单一性[15]。

（3）2005-2012 年上海市疟疾监测结果分析

【摘要】

本研究的目的是了解上海市疟疾监测和疫情变化情况，为评价和推进消除疟疾工作提供科学依据。方法是收集 2005-2012 年上海市疟疾监测年报、疟疾疫情数据和人口资料，分析该市发热病人疟原虫血检情况、血检阳性率、人群疟原虫带虫率、人群疟疾抗体水平，以及传疟蚊媒的种群和密度等。结论为上海市已全方位地开展了疟疾监测工作，并已进入消除疟疾阶段，今后的疟疾监测以有境外疟疾流行病学史的人群为重点监测对象，维持并提高二、三级医疗机构的疟疾血检能力，确保能及时、准确发现疟疾病例[16]。

2. 血吸虫相关

（1）150 例晚期血吸虫病患者临床治疗分析

【摘要】

对晚期血吸虫病的临床治疗进行分析和探讨。方法为选取 2010 年 1 月～2012 年 12 月，我区定点医院木渎人民医院收治的 150 例晚期血吸虫病患者，对其临

床资料进行回顾性分析。结果为 68 例腹水型晚血患者接受吡喹酮病原学治疗，16 例基本治愈，36 例病情基本稳定，16 例未愈。76 例巨脾型晚血患者中，17 例患者已行脾脏切除术，10 例计划行脾脏切除术，另 49 例患者接受内科疗法。结论是应定期实施晚血普查，一方面尽早发现患者，另一方面加强健康教育，提升人们的自我保护意识，尽早诊断、尽早治疗，防止由于延误治疗而导致晚血[17]。

（2）下肢游走性红斑确诊为血吸虫病 1 例报告

【摘要】

患者，男，42 岁，2 年来反复出现下肢游走性红斑，以左下肢为主，面部及手背多发扁平疣，红斑出现时多伴有发热咽痛，扁桃体化脓等呼吸道感染症状。间隔 1 周左右发作 1 次，每次发作持续 4～5 d，使用地塞米松和抗生素后症状消失。发作时全身酸痛，乏力，食欲减退，红斑下有硬结，有压痛，有时疼痛较剧烈，间歇期一切正常患者，2 年来反复出现下肢游走性红斑，以左下肢为主，面部及手背多发扁。两年来曾多次到全国各大型医院皮肤科就诊，一直未能确诊，后于我院完善相关检查后考虑血吸虫病可能性较大，经当地血防站病原学检查证实为血吸虫病[18]。

（3）2011 年四川省血吸虫病监测

【摘要】

分析四川省血吸虫病监测点 2011 年疫情，了解监测点血吸虫病工作防治现状和疫情变化趋势，为全省防治血吸虫病提供科学依据。方法为按照全国和四川省血吸虫病监测方案要求，在四川的 15 个监测点开展 2011 年监测工作。结果是 15 个监测点的居民血阳率为 9.04%，居民感染率为 0.04%，耕牛感染率为 0.45%。共查出钉螺面积 376168 m^2，平均活螺密度为 0.131 只／0.11 m^2，未发现感染性钉螺。结论为四川省血吸虫病已控制在一个较低水平，但高山型少数民族地区疫情仍有波动，应近一步加强健康教育，并管理控制好家畜和钉螺，防止疫情回升[19]。

（4）IHA 和 DIGFA 诊断血吸虫病可靠性分析

【摘要】

目的是分析间接红细胞凝集试验(IHA) 和金标免疫法(DIGFA) 诊断血吸虫病的可靠性。方法为采集经粪便孵化法确诊且未经治疗的血吸虫病患者血清标本 46 份和健康人血清 42 份，分别用 IHA 和 DIGFA 进行检测，观察 2 种方法的敏感度和特异度。IHA 法每份血清做 1:5，1:10，1:20，1:40 共 4 个滴度。结果 46 份血吸虫病患者血清检测结果: IHA 法 1:5，1:10，1:20，1:40 滴度检出率分别为 91. 30% (42 /46) 、76. 09% (35 /46) 、65. 22% (30 /46) 、45. 65% (21 /46) ，DIGFA 法检出率为 69. 57% (32 /46) ; 42 份健康人血清检测结果: IHA 法 1:5，1: 10，1: 20，1: 40 滴度阳性率分别为 7. 14% (3 /42) 、4. 76% (2 /42) 、0% (0 /42) 、0% (0 /42) ，IHA (1:5) 和 IHA (1:10) 特异度分别为 92. 85%、95. 24%，DIGFA 的特异度为 97. 62% (41 /42) 。结论 IHA 和 DIGFA 检测血吸虫病患者血清阳性率(敏感度) 偏低; 用 IHA 和 DIGFA 诊断血吸虫病可信度较差; IHA 的阳性阈值滴度为 1:5 阳性检出率较高[20]。

3. 其他寄生虫相关

（1）深圳市外来劳务人员弓形虫感染情况及知识行为调查

【摘要】

本研究的目的是了解和掌握深圳地区外来劳务人员弓形虫病血清学 IgG 抗体水平、及相关知识、行为现况，为制定弓形虫防治策略提供科学依据。方法为通过整群抽样方法抽取宝安区外来劳务工人员作为调查对象，采用 ELISA 检测弓形虫 IgG 抗体水平，同时对该人群的弓形虫相关知识、行为进行描述性研究。问卷由 Epidata3.0 录入，采用 SPSS16.0 进行统计分析。结果是共调查 642 名劳务工，采集有效血清 532 份，阳性 11 份，阳性率为 2.07%。不同性别、户籍、职业、文化程度的感染率差异均无统计学意义（P＞0.05）。不同职业及户籍的人群弓形虫知晓率差异有统计学意义（P＜0.01）。结论是深圳市外来务工人员弓形虫相关知识知晓率较差，应采取有效的综合防制措施，提高个人弓形虫知识，改变不良生活习惯，减少人群弓形虫感染[21]。

（2）湖南省辰溪县 1988 名城乡中小学生蛔虫感染的调查

【摘要】

研究目的是了解湖南省辰溪县城乡中小学生蛔虫感染情况，以便制订出较为完善的预防和治疗工作方案，以达到国家制订的《2006～2015 年全国重点寄生虫病防治规划》要求。方法为采用随机整群抽样方法对本县 15 所城乡中小学校 1988 名学生蛔虫感染情况进行调查。结果是城区 998 名学生中有 28 名出现蛔虫感染， 感染率为 2.81%；乡村 990 名学生中有 30 名出现蛔虫感染，感染率为 3.03%；其中，小学生占 4.77%，中学生占 0.13%，农村学生的蛔虫感染率与城区学生比较差异无统计学意义（$\chi 2=0.089$，$P>0.05$）。结论为本县中学生蛔虫防治工作成效显著，但小学生较差，需进一步加大防治工作力度[22]。

（3）2012 年河南省首例输入性登革热病例的快速诊断与基因分型

【摘要】

随着国内国际交流、劳务输入输出日益频繁，越来越多的省份有输入性登革热病例的报告，再加上其主要传播媒介的蚊种在我国广泛分布，人群又普遍易感，因而对于输人性登革热病例的研究对疫情的防控尤为重要。本次报告了 1 例 2012 年菲律宾输入的疑似登革热病例，采用血清学方法进行实验室快速确诊，并用分子生物学方法进行分型和溯源的描述性研究，对于此次登革热疫情的预防控制起到了重要作用[23]。

（4）新疆内脏利什曼病流行区人群免疫状况调查

【摘要】

了解新疆喀什人源型利什曼病流行区人群的免疫状况，为当地开展内脏利什曼病的防治工作提供参考信息。方法是选择喀什市利什曼病发病率较高的 3 个大队为调查点，人户调查时，除老人与<2 岁婴幼儿外，，LI 内成员均开展利什曼素皮内试验(LDT)。要求皮试数不得低于该小队总户数的 50%。记录皮试者的年龄、性别、文化程度及患病情况。运用 SPSS 13．0 软件对调查结果进行统计分

析。结果 LDT 总计人数 1 126 人，阳性人数 435 人，阳性率为 38.63%(435／1 126)。皮试阳性率与年龄有密切关系(x2=34．29，P<0．05)，皮试阳性率随年龄的增加有逐渐增高的趋势。结论随着年龄的增加，人群的免疫水平增加。低年龄组人群的免疫人口所占比例较低，应重点加强低年龄组人群的监测和防治力度[24]。

【参考文献】

（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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