TIME TO TRACK ALL MALARIA PARASITES IN NIGERIA

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ABSTRACT

This report seeks to draw attention to marginalized human malaria parasite species. There is a need to elucidate their various contribution to malaria burden in other to advise policy and control strategy. Of the six Plasmodium species known to cause human malaria, two are the central focus of research and control; with robust literature available on both. The other four seem neglected, have lean attention and sparse literature. Venous blood was collected in specimen tubes with ethylene diamine tetra acetic acid (Edta) tubes and used for Rapid Diagnostic Test, Microscopy and Polymerase Chain Reaction test. Hospital attendance records were accessed on a monthly basis and collated. Of the four Plasmodium species encountered Plasmodium falciparum peaked with 95.9%, Plasmodium vivax (2.9%), Plasmodium ovale (1.0%) and Plasmodium malariae (0.2%). The presence of P. vivax, P. ovale and P. malariae calls for further investigation to clarify their status. To accelerate to zero and ably prevent malaria resurgence, marginal human malaria parasites should be tracked and treated.

Keywords: Malaria, elimination, *Plasmodium* species, neglect, Nigeria

INTRODUCTION

The Sixty-eighth World Health Assembly, adopts the global technical strategy for malaria 2016–2030 envisioned in a malaria free world. This is the malaria control community's second attempt at eradicating the malaria parasite from planet earth. Major landmarks and failures were recorded in the course of the first attempts at malaria control and elimination (Gilles, 2002). The first attempt at eradication was in the 1950s as Global Malaria Eradication Campaign (GMEP).While it eliminated malaria from some regions it failed in some other regions. Several reasons were given for its failure and eventual abandonment (Kileen, 2013; Najera *et al*, 2011). Among the lessons from the GMEP failure are: one size no longer fits all and minor malaria outcomes should be acknowledged.

Within the complex mosquito-human life cycle are six species of malaria parasites infecting humans (*Plasmodium falciparum*, *Plasmodium vivax*, *Plasmodium ovale wallickeri*, *Plasmodium ovale curtisi*, *Plasmodium malariae*, and *Plasmodium knowlesi*. (Milner, 2017). Of this six two- *Plasmodium falciparum and Plasmodium vivax* account majorly for the yearly morbidity and mortality record by the World Health Organisation (WHO, 2018; Lim *et al*, 2017). Malaria research and literature abounds for both species but limited for the other four species. The question to ask is, in the absence of the major species can the minor species over-run a community? Further research is needed into their bionomics and to elucidate their various contribution to malaria burden in other to advise policy and control strategy.

There are renewed efforts at attaining a malaria free world. In

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view of elimination and prevention of re-establishment of malaria: All human malaria parasites should be tested for, treated and tracked concurrently. This paper argues for more attention to be given to hitherto neglected human malaria parasite species in and out of expected distinct geographical regions.

MATERIALS AND METHOD

Line list for confirmed malaria cases and deaths from hospital attendance records using standard forms (WHO, 2013) tagged annex 8 and 9 ANI 8 & 9] were accessed on a monthly basis. A cross sectional survey of 272 apparently healthy symptomless children and adults (willing participants age 18months and above) was carried out in selected communities in two local governments in Benue State (<u>7°20'N 8°45'E</u>). Venous blood was collected in specimen tubes with ethylene diamine tetra acetic acid (Edta) tubes and used for Rapid Diagnostic Test-RDT, Microscopy and Polymerase Chain Reaction- PCR test (Snounou, 1996; Bereczky & Mårtensson, 2005). All 272 blood samples were soaked (Dry Blood Spot-DBS 60 µl each) onto Whatman filter paper (GE Healthcare, UK, Grade 3 MM CHR CAT No: 3030–861) and air dried then kept in individual sealable sachets of ziplock plastic bags alongside desiccants.

Ethical consideration

Ethical approval (Project Number IRB/15/289) was obtained from the Institutional Review Board (IRB) of the Nigerian Institute for Medical Research (NIMR), Yaba, Lagos. Through a series of advocacy visits verbal consent and community participation were gotten.

Data Analysis

This descriptive survey was analyzed using Microsoft Excel 2013 and expressed in percentages.

RESULT

From the Line list hospital attendance record, four species of *Plasmodium* (Fig. 1) were encountered of which *Plasmodium falciparum* peaked with (95.9 %) 470/490, *Plasmodium vivax* (2.9 %) 14/490, *Plasmodium ovale* (1.0 %) 5/490 and *Plasmodium malariae* (0.2 %) 1/490.



Area of Benue State, North Central Nigeria

Science World Journal Vol. 14(No 3) 2019 www.scienceworldjournal.org ISSN 1597-6343 Published by Faculty of Science, Kaduna State University

KEY TO ABBREVIATIONS

P.f: Plasmodium falciparum P.v: Plasmodium vivax P.o: Plasmodium ovale P.m: Plasmodium malariae

Spread across the hospital record are two forms of test, RDT (81.19 %), RDT/Microscopy (13.48 %) and Microscopy (5.33 %) as shown in Figure 2. From the cross sectional survey due to financial constraints PCR was carried out for only 15 RDT Negative and Microscopy positive samples. Of these 15 two were positive for *Plasmodium falciparum* confirmatory for microscopy positive but RDT false negative. The remaining preserved samples are stored away for further analysis.



Fig. 2: Type of Malaria Test in Gboko Local Government Area of Benue State, North Central Nigeria

KEY TO ABBREVIATIONS RDT: Rapid Diagnostic Test Microscopy: Microscopy Test

DISCUSSION

Available literature now shows presence of *Plasmodium vivax* across parts of sub-Saharan African (Howes *et al.*, 2015; Poirier *et al.*, 2016). With the effect of human movement on malaria (Prugnolle *et al.*, 2013; Martens & Hall, 2000) it will not be farfetched to find *Plasmodium vivax* in Nigeria since an unexpected presence of *Plasmodium vivax* has been reported in neighbouring Benin Republic (Poirier *et al.*, 2016). More so because there is ongoing economic migration between these countries in terms of farming, trading and services.

In malaria heartland mixed infections (two or more species of malaria parasite) are common (Sinden & Gilles, 2002). RDT specific for *P.falciparum* is the common test used to the neglect of microscopy in most health centers. The Pcr test showed RTD false negative result which may be attributed to the missing gene-pfhrp2, poor RDT product design or quality and/or poor transport and storage conditions (WHO, 2016; Tangpukdee, 2009)

RDT specific for *P.falciparum* alone may no longer suffice in the study communities and should be complimented with microscopy especially where RDT specific for *P.falciparum* test is negative for persons with clinical symptoms of malaria. Although PCR is the most sensitive of the three test used in the investigation it is very expensive and requires high level technical expertise in a reference lab. Another molecular test tool - loop mediated

isothermal amplification (LAMP) may be deployed in the setting for preliminary surveys. LAMP is much cheaper, more sensitive than RDT and microscopy and can be used in remote endemic areas (Vásquez *et al.*, 2018).

Highlighting a key lesson from the failure of the Global Malaria Eradication Programme (GMEP) Killeen said,

"The GMEP was defeated by dry season transmission, and by mosquitoes which avoid houses, because it simply ignored them, never took them on, and did not acknowledge their importance until it was too late". (Killeen, 2013)

Nigeria bears the heaviest malaria burden (cases-25%; deaths-19%) in the world, attributable majorly to *Plasmodium falciparum* (WHO, 2018). A country already overwhelmed with P. *falciparum* malaria cannot afford to eclipse or ignore *plasmodium vivax* and other *Plasmodium* species that may be present. Malaria is a focal disease with narratives that vary from place to place. In the face of epidemiological shifts, evolution and human migration careful attention should be paid to incoming information regardless of unexpected geographical boundaries and age long generalizations.

From the Harvard edx lecture series on malaria (Alonso, 2017) highlighted the warning below:

"In the study of malaria problems and in the formulation of control programmes, action based on generalizations is likely to be followed by the most disastrous consequences. It has been well said that the most hazardous of human tendencies is the drawing of general conclusions from limited experience, and in no instance it is more applicable than in the planning of malaria control measures". Sir Gordon Covell (1948) Lectures on Malaria (4th edition) IN: (Alonso, 2017).

Once these generalizations are cast in gold, the silent but strong interplay of position, power and knowledge (Hewett *et al.*, 2004) may impede full disclosure of research outcome which in turn may eclipse critical epidemiological shifts.

Conclusion

Tracking all human malaria parasite species concurrently is crucial to accelerating to zero and preventing re-establishment. Deciphering and giving adequate attention to locale specifics will enhance intervention efficacy and sustain gains. This may help prevent history from repeating itself.

Acknowledgments

I thank the traditional ruler of Otukpo, Chief Dr. John Eyimonye (Och'Otukpo Odu) for access to his immediate community and for participating in the survey. Elder Terwase Tergama and Mrs Arit Tergama are both acknowledged for their immense assistant in gaining participant's consent and field work in Gboko local government area.

Science World Journal Vol. 14(No 3) 2019 www.scienceworldjournal.org ISSN 1597-6343 Published by Faculty of Science, Kaduna State University

REFERENCES

- Alonso, L.P., 2017. Defeating Malaria From Gene to Globe-The Past:A Historical Overview. <u>MalariaX: Defeating Malaria</u> from the Genes to the Globe | Harvard https://onlinelearning.harvard.edu/course/malariax-defeating-malariagenes-globe
- Bereczky, S., MÅrtensson, A., Gil, J.P. and FÄrnert, A., 2005. Rapid DNA extraction from archive blood spots on filter paper for genotyping of Plasmodium falciparum. The American Journal of Tropical Medicine and Hygiene, 72(3), pp.249-251.
- Gilles, H.M., 2002. Historical outline. Essential Malariology, pp.1-7.
- Hewett, A.M., and Foucault, M., 2004. Power/Knowledge and Epistemological Prescriptions". Honours Theses. Paper 534.University of Richmond Virginia,USA
- Howes, R.E., Reiner Jr, R.C., Battle, K.E., Longbottom, J., Mappin, B., Ordanovich, D., Tatem, A.J., Drakeley, C., Gething, P.W., Zimmerman, P.A. and Smith, D.L., 2015. Plasmodium vivax transmission in Africa. PLoS Neglected Tropical Diseases, 9(11), p.e0004222.
- Killeen, G.F., 2013. A second chance to tackle African malaria vector mosquitoes that avoid houses and don't take drugs. The American Journal of Tropical Medicine and Hygiene, 88(5), pp.809-816.
- Lim, C., Dankwa, S., Paul, A.S. and Duraisingh, M.T., 2017. Host Cell Tropism and Adaptation of Blood-Stage Malaria Parasites: Challenges for Malaria Elimination. *Cold Spring Harbor Perspectives in Medicine*, p.a025494.
- Martens, P. and Hall, L., 2000. Malaria on the move: human population movement and malaria transmission. Emerging Infectious Diseases, 6(2), p.103.
- Nájera, J.A., González-Silva, M. and Alonso, P.L., 2011. Some lessons for the future from the Global Malaria Eradication Programme (1955–1969). PLoS Medicine, 8(1), p.e1000412.

- Poirier, P., Doderer-Lang, C., Atchade, P.S., Lemoine, J.P., de l'Isle, M.L.C., Abou-bacar, A., Pfaff, A.W., Brunet, J., Arnoux, L., Haar, E. and Filisetti, D., 2016. The hide and seek of Plasmodium vivax in West Africa: report from a large-scale study in Beninese asymptomatic subjects. Malaria Journal, 15(1), p.570.
- Prugnolle, F., Rougeron, V., Becquart, P., Berry, A., Makanga, B., Rahola, N., Arnathau, C., Ngoubangoye, B., Menard, S., Willaume, E. and Ayala, F.J., 2013. Diversity, host switching and evolution of Plasmodium vivax infecting African great apes. Proceedings of the National Academy of Sciences, 110(20), pp.8123-8128.
- Sinden RE, Gilles HM. The Malaria Parasites. In Warrell DA, Herbert MG, editors. Essential Malariology, London: Hodder Arnold Press; 2002. p. 8-34.
- Snounou, G., 1996. Detection and identification of the four malaria parasite species infecting humans by PCR amplification. In Species Diagnostics Protocols (pp. 263-291). Humana Press.
- Tangpukdee, N., Duangdee, C., Wilairatana, P. and Krudsood, S., 2009. Malaria diagnosis: a brief review. The Korean journal of parasitology, 47(2), p.93.
- Vásquez, A.M., Zuluaga, L., Tobón, A., Posada, M., Vélez, G., González, I.J., Campillo, A. and Ding, X., 2018. Diagnostic accuracy of loop-mediated isothermal amplification (LAMP) for screening malaria in peripheral and placental blood samples from pregnant women in Colombia. Malaria Journal, 17(1), p.262.
- World Health Organisation, 2013. Epidemiological approach for malaria control 2nd ed. Guide for participants.
- World Health Organisation, 2016. WHO investigates reports of missing gene among malaria parasites and possible impact on RDT performance. <u>https://www.who.int/malaria/news/2016/missing-gene-rdt-</u> performance/en/ Accessed 02- 05- 2019
- World Health Organisation, 2018. https://www.who.int/malaria/publications/world-malariareport.2018/en/ (2018) Accessed 19 Dec 2018.