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CONFLICT OF INTEREST DECLARATION

I am employed as Managing Director of F1000 that could be perceived as a direct conflict of interest in the content of this presentation.
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RESEARCH ARTICLE

Geographic-genetic analysis of *Plasmodium falciparum* parasite populations from surveys of primary school children in Western Kenya [version 1; referees: awaiting peer review]

Irene Omedo, Polycarp Mogendi, Kirk Rockett, Alice Kamau, Christina Hubbar, Anna Jeffreys, Lynette Isabella Ochola-Ogier, Etienne P. de Villiers, Caroline W. Gitonga, Abdisalan M. Noor, Robert W. Snow, Dominic Kwiatkowsk, Philip Bojar

Abstract

**Background.** Malaria control, and finally malaria elimination, requires the identification and targeting of residual foci or hotspots of transmission. However, the level of parasite mixing within and between geographical locations is likely to impact the effectiveness and durability of control interventions and thus should be taken into consideration when developing control programs.

**Methods.** In order to determine the geographic-genetic patterns of *Plasmodium falciparum* parasite populations at a sub-national level in Kenya, we used the Sequenom platform to genotype 111 genome-wide distributed single nucleotide polymorphic (SNP) positions in 2486 isolates collected from children in 95 primary schools in western Kenya. We analysed these parasite genotypes for genetic structure using principal component analysis and assessed local and global clustering using statistical measures of spatial autocorrelation. We further examined the region for spatial barriers to parasite movement as well as directionality in the patterns of parasite movement.

**Results.** We found no evidence of population structure and little evidence of spatial autocorrelation of parasite genotypes (correlation coefficients <0.03 among parasite pairs in distance classes of 1km, 2km and 5km; p value<0.01). An analysis of the geographical distribution of allele frequencies showed weak evidence of variation in distribution of alleles, with clusters representing a higher than expected number of samples with the major alleles being identified for 5 SNPs. Furthermore, we found no evidence of the existence of spatial barriers to parasite movement within the region.
Free serum haemoglobin is associated with brain atrophy in secondary progressive multiple sclerosis [version 2; referees: 3 approved]

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Grant information

Abstract

Background: A major cause of disability in secondary progressive multiple sclerosis (SPMS) is progressive brain atrophy, whose pathogenesis is not fully understood. The objective of this study was to identify protein biomarkers of brain atrophy in SPMS.

Methods: We used surface-enhanced laser desorption-ionization time-of-flight mass spectrometry to carry out an unbiased search for serum proteins whose concentration correlated with the rate of brain atrophy, measured by serial MRI scans over a 2-year period in a well-characterized cohort of 140 patients with SPMS. Protein species were identified by liquid chromatography-electrospray ionization
LSR – HOW COULD ‘TRADITIONAL’ JOURNALS KEEP UP-TO-DATE
situation is further complicated by the ever-growing body of literature. A single clinical trial can result in multiple publications: the study protocol and traditional results paper or papers, as well as commentaries, secondary analyses and, eventually, systematic reviews, among others [8].
REPURPOSING ERRATA/RETRACTION SYSTEM
Especially useful for:

→ Updating Systematic Reviews, Protocols & Guidelines – no need to rewrite introduction etc

→ Rapid peer review feedback on Protocols before start the study
A CRISPR/Cas9-based method and primer design tool for seamless genome editing in fission yeast

María Rodríguez-López, a, 1, Cristina Cobobal, 1, Oscar Fernández-Sánchez, 1, Natalia Borbarán Bravo, 1, Risky Oktiani, 1, Heike Abendroth, 1, Dardan Uke, 1, Mirnoza Holt, 1, Jin Wang, 1, Mikel Zarategui, 2, and Jürg Bähler 4, 1

Abstract

In the fission yeast Schizosaccharomyces pombe the prevailing approach for gene manipulations is based on homologous recombination of a PCR product that contains genomic target sequences and a selectable marker. The CRISPR/Cas9 system has recently been implemented in fission yeast, which allows for seamless genome editing without integration of a selection marker or leaving any other genomic ‘scars’.
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From Dinas et al, 2017: https://f1000research.com/articles/6-286/v2

Can update date if rerun the search & no new data to add
LIVING FIGURES

https://f1000research.com/articles/3-176/v2
CONCLUSION

• There are existing mechanisms that can be repurposed by traditional journals to link updates & cross-publisher

• The technology is now available to update through versioning and living elements within articles that
  o minimise time/effort for authors & reviewers
  o enable timely updates
  o retain archival record
  o ensure transparency of changes across all major sites
QUESTIONS

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