Identification of Important Interacting Proteins responsible for Merozoites Invasion in Human RBCs

Jumoke Soyemi, Itunuoluwa Isewon, Jelili Oyelade & Ezekiel Adebiyi

Jumoke.soyemi@federalpolyilaro.edu.ng[1,3] itunu.isewon@covenantuniversity.edu.ng[2,3] ola.oyelade@covenantuniversity.edu.ng [2,3] ezekiel.adebiyi@covenantuniversity.edu.ng[2,3]

[1]Department of Computer Science , Federal Polytechnic, Ilaro [2] Department of Computer and Information Sciences, Covenant University, Ota
[3] Covenant University Bioinformatics Research (CUBRe), Ota, Nigeria.

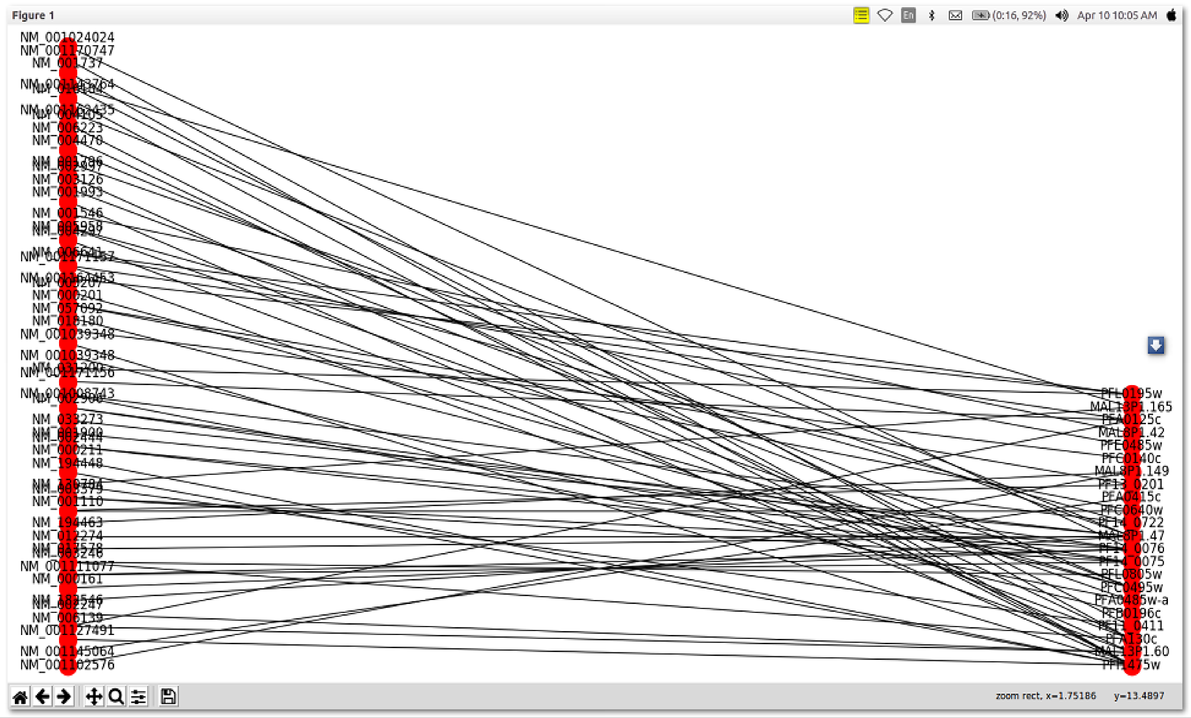
INTRODUCTION

Prevention of infectious disease requires better insight into the molecular crosstalk between host and parasite. Unfortunately, experimental identification of host-parasite protein interaction remains very challenging and hence the computational prediction becomes essential (Liu *et al.*, 2014). Merozoites invasion of the Red Blood Cells (RBCs) has been identified as an essential stage crucial to the survival and pathogenesis of the parasite and a stage in which clinical manifestation occurs (Wright *et al.*, 2014; Soyemi *et al.*, 2018). New interest has also been built to identify and develop vaccines and drugs that target RBCs invasion because some proteins and processes needed for invasion are unique as well as essential to the parasite (Bhattacharyya and Chakrabarti, 2015). This study, therefore, predicted important interacting proteins between human Red Blood Cells and *Plasmodium falciparum* merozoites based on RNA-Seq gene expression profiles (Otto et al., 2010; Yamagishi et al., 2014) using K-nearest neighbour supervised machine learning algorithm. The predicted results were also validated against computational predictions from literature with 63% of the result being consistent with literature and 37% novel to this study. The important interacting proteins could be used as drug targets for vaccine development against the parasite invasion of the red blood cells

AIM

✓ to predict important interacting protein between human red blood cells and Plasmodium falciparum at the Schizont

RESULTS



Bipartite Graph of the host-parasite Important interacting Proteins Predicted

Discussion

From the implementation carried out in this study, sixty-three host-parasite protein interactions were predicted at the Schizont stage of *Plasmodium falciparum* and human RBCs. Forty of the sixty-three host-parasite proteins predicted were consistent with predictions from Literature while twenty-three of the sixty-three host-parasite proteins predicted are novel

Predictions Consistent with Literature

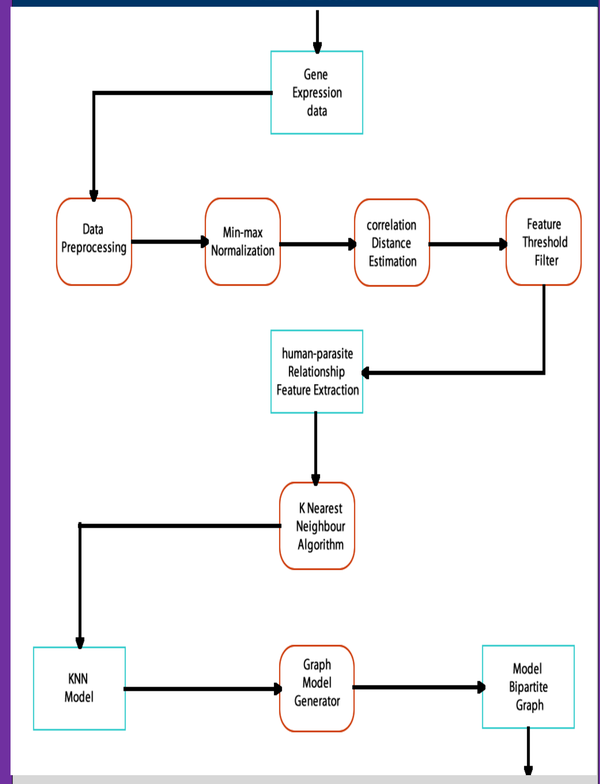
The following important protein interactions were discovered among several others; CSP and Trap-related proteins of *P. falciparum* interacted with CAM-1 and CAM-4 proteins of human. Merozoite surface protein 1 interacted with Coagulation factor III precursor protein, Complement 9 protein and EGF-containing fibulin-like extracellular matrix protein 1 precursor. Also Erythrocyte binding antigen-181 interacted with Cluster differentiation 28, Salia binding Ig-like lectin 10 and Junctional adhesion molecule A. Merozoite surface protein 4 also made clear interaction with Thrombospondin-1 and several others whose functions are implicated in the invasion process

Novel Predictions in the study

Among the novel predictions in this study is **MAL8P1.47** (with uncharacterized function), this protein seems promising with several interactions made with about seven human proteins. Also, **MAL8P1.149** also having interactions with two other human proteins. Special attention should be give to this two key proteins among others when taken for experimental validation.

PRESENTED AT 11TH CONFERENCE OF THE AFRICAN SOCIETY OF HUMAN GENETICS (AFSHG) AND H3AFRICA CONSORTIUM, KIGALI, RWANDA. SEPT 19-21, 2018

METHOD



CONTRIBUTION

Here, KNN algorithm has been put to use to elucidate the mechanism of host-parasite protein interaction between human host and *Plasmodium falciparum*. The study was able to capture several predictions that corroborate with those predicted from previous studies, and novel host-parasite proteins interactions were also established. The important interacting proteins and novel HPPI predicted are recommended for further experimental validation for use as drug targets.

BIBLIOGRAPHY

1. Bhattacharyya, M. & Chakrabarti, S. (2015). Identification of important interacting proteins (IIPs) in Plasmodium falciparum using large-scale interaction network analysis and in-silico knock-out studies. *Malaria Journal*, 14(1):1
2. Liu, X. (2014) Computational prediction of protein interactions related to the invasion of erythrocytes by malaria parasites. BMC Bioinformatics. 15:393
3. Otto, T.D. Wilinski, D. Assefa, S. Keane, T.M. Sarry, L.R. Bohme, U. Lemieux, J. Barrell, B. Pain, A. Berriman, M. Newbold, C. Llinas, M. (2010) New insights into the blood-stage transcriptome of Plasmodium falciparum using RNA-Seq. Mol. Microbiol. 76: 12-24
4. Soyemi, J., Isewon, I., Ogunlana,O., Rotimi, S., Oyelade, O.J. & Adebiyi, E.F. (2018). Computational analysis of Plasmodium falciparum RNA-Seq data reveals PPIs that might be implicated in the invasion of RBCs. *IEEE Computational Intelligence in Bioinformatics and computational Biology (CIBCB)*
5. Yamagishi J., Natori A. Tolba E.M., Mongan A. E. Sugimoto C., Katayama T., Kawashima S., Makalowski W., Maeda R., Eshita Y. Tuda, J. and Suzuki, Y. (2014) Interactive transciptome analysis of malaria