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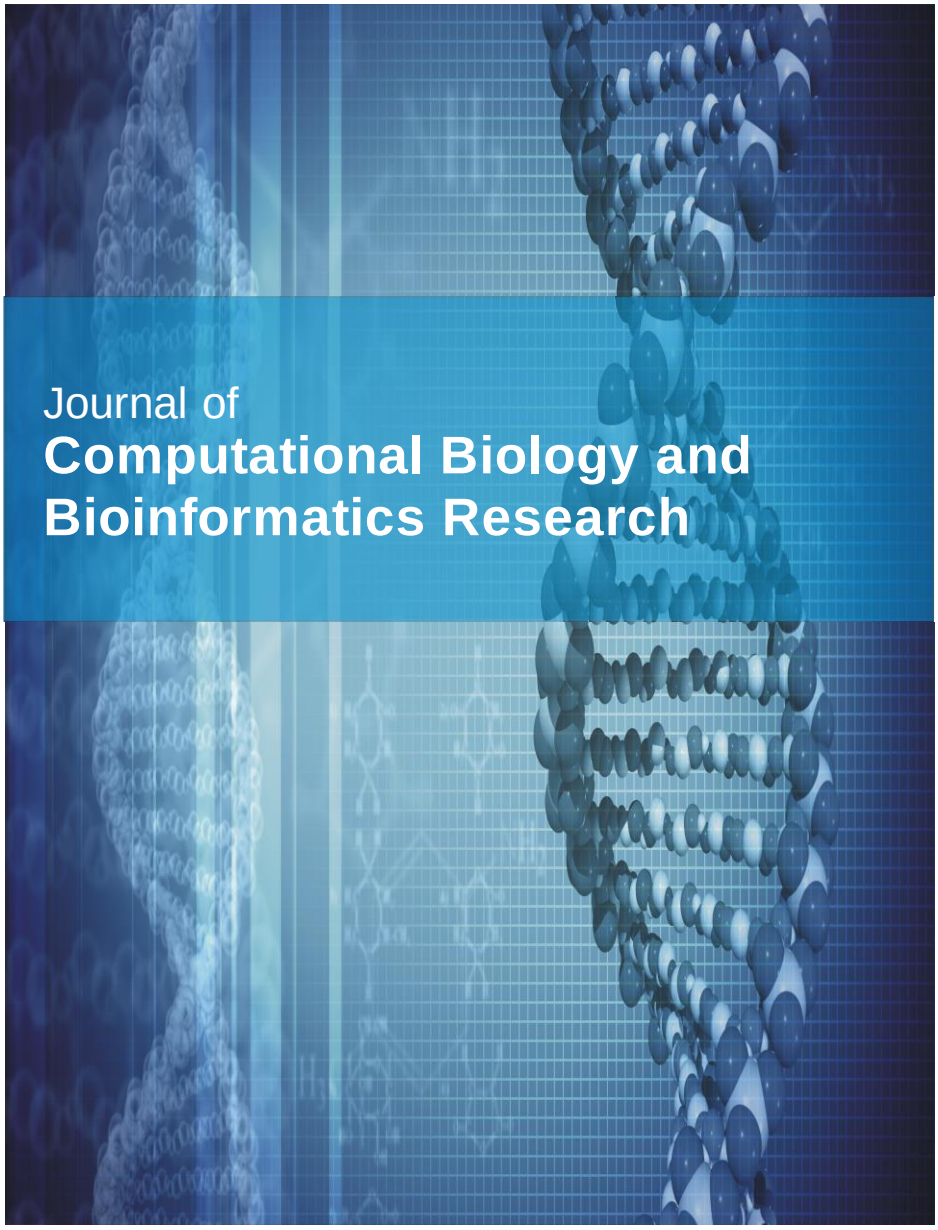

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Full Length Research Paper

A bioinformatics analysis and homology modeling of polyadenylate binding protein of *Plasmodium falciparum* 3D7

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Malaria is one of the major causes of morbidity and mortality in tropical and sub-tropical parts of the world. *Plasmodium falciparum* polyadenylate binding protein (PABP) plays a vital role in the stable RNA accumulation of host cells during *P. falciparum* malaria parasite infection. This protein mediates the liver stage invasion of the parasite by binding to poly-A tail of the mRNA using its globular domains that contain RNA-recognition motifs (RRMs) which regulate mRNA stability and protein translation. An *in-silico* analysis and modeling of the *P. falciparum* PABP was carried out to elucidate the physicochemical properties, disease-causing regions, the protein-protein interactions as well as the predicted structure of the protein. The primary and secondary structural features of the protein were calculated by ProtParam and SOPMA, respectively, which revealed the protein is composed of random coils (41.71%), α-helix (36.23%), extended strand (14.06%), and β turn (8.00%). The three-dimensional structure of *P. falciparum* PABP was not available as yet at PDB. Therefore, homology models for these proteins were developed using SWISS-MODEL, PHYRE2, and I-TASSER Web Server. The models were visualized with RASMOL and validated using PROCHECK, Verify3D, and QMEAN for reliability. 92.64% of the residues in the predicted model have averaged 3D-1D score ≥ 0.2 which indicates that the predicted model is compatible with the sequence. Protein-protein and residue-residue interaction networks were generated by the STRING and RING servers, respectively. 3DLigand server was used to analyze binding sites of the modeled PABP. This predicted structure of *P. falciparum* PABP will make an important contribution towards better understanding of the functions of the protein in translation regulation in the parasite and may also provide targets for novel therapeutic candidates.

Key words: Malaria, poly A-binding protein, bioinformatics analysis, *Plasmodium falciparum, Pf*PABP.

INTRODUCTION

Malaria is an infectious disease that is highly distributed in the tropical and subtropical regions of the world, and it is caused by the parasite of the genus *Plasmodium.* Malaria is one of the leading causes of death by a communicable infectious agent, claiming 405,000 lives globally in 2018 with 67% of the total mortality being children under 5 years (WHO, 2019). The malaria parasite has a complex life cycle, involving an invertebrate vector (mosquito) and a vertebrate host. Each stage of the parasite's life cycle involves arrays of

genes whose expressions are tightly regulated.

The regulation of gene expression and the synthesis of proteins is pertinent for the parasite to carry out its sophisticated developmental program since the parasite does not know when it would be transmitted from the mosquito to the human host and vice versa (Coulson et al., 2004; Cui et al., 2002). The genome of the parasite is deficient in transcriptional regulators (Coulson et al., 2004), which implies that post-transcriptional regulation are important in regulating the expression of the parasite's genes as well as in protein synthesis (Reddy et al., 2015). Gene regulation via a post-transcriptional mechanism is dependent on RNA-binding proteins, which play important roles in the parasite's biology especially during the transmission stage (Bunnik et al., 2016). The transmission stages (sporozoites and gametocytes) must remain inactive, stable, and infectious in the vector or host for an extended period before a mosquito may bite and pick them up again (Minns et al., 2018). At these stages, mRNA which is important for development in the host or vectors are kept translationally repressed (Reddy et al., 2015) so that rapid protein synthesis can occur presumably when the opportunity to infect arises (Cui et al., 2015). These translationally repressed transcripts are stored in punctate storage granules within the cytoplasm (Minns et al., 2018). Phosphorylation of initiation factors such as eIF2-α, eIF4E, and Poly-Adenylate Binding Protein is an important mechanism of regulating mRNA translation (Hay and Sonenberg, 2004). For instance, the phosphorylation of poly A-binding proteins (PABP) improves its interaction with eIF4G and enhances the rate of mRNA translation (Le et al., 2000).

PABP is a post-transcriptional RNA binding protein which binds to the adenine-rich sequences in mRNA and *acts* as a scaffold for protein-protein interactions (Mangus et al., 2003). In model eukaryotes, translationally repressed proteins interact with and are influenced by PABPs. In the nucleus, PABP play a role in polyadenylation; it determines the length of the poly(A) and may be involved in mRNA export (Minns et al., 2018). While in the cytoplasm, they participate in the regulation of translation initiation and either protect mRNAs from decay through binding to their poly(A) tails or stimulate this decay by promoting mRNA interactions with deadenylase complex proteins (Eliseeva et al., 2013). Non-nuclear PABP plays a surprise role outside the parasite's cell. For example, when the parasite develops into a sporozoite in the mosquito, PABP accumulates at the surface of the sporozoite and is shed when the parasite moves (Minns et al., 2018). The accumulation of this protein on the surface of the sporozoite may be involved in the binding of exogenous RNAs that accumulate as stress granules or help the parasite interact with its environment (host or vector) (Mair, 2013; Minns et al., 2018) . PABP also plays a role in the interaction of poly(A) tail with translation initiation complex, and subsequent binding of eukaryotic initiation factor 4E (eIF4E) and PABP to eIF4G, which is pertinent for efficient translation (De Gregorio et al., 1999; Mangus et al., 2003; Preiss and Hentze, 2003). Using bioinformatics tools, *P. falciparum* PABP has been characterized and shown to have the characteristics of a cytosolic PABP with additional sequence inserted between RNA-recognition motif (RRM) III and IV (Tuteja, 2009; Tuteja and Pradhan, 2009).

It is important to regulate the expression of PABP because of the multiple roles it plays in mRNA metabolism and stored PABP mRNA is believed to be activated by growth stimuli (Bag and Bhattacharjee, 2010). Hence, factors or agents that can interfere with the functions or expression of this RNA binding protein may disrupt the parasite life cycle and result in processes such as premature hepatic sporozoite formation. For example, studies have shown that Ik2 kinase knockout sporozoite lacks phosphorylated eIF2α (which keeps mRNAs in a translationally repressed state) and the parasites develop prematurely into the liver stage and lose its infectivity (Zhang et al., 2010). Understanding the malaria parasite's biology and the functions of its proteins may help provide insights that would be useful in antimalarial drug discovery. In other to eliminate malaria, innovative malaria intervention strategies aimed at the transmission stages of the parasite would play a pertinent role. Though the mechanism of PABP has been reported (Bag and Bhattacharjee, 2010; Eliseeva et al., 2013), detailed computational studies to validate the chemical and structural properties, as well as compounds that may interfere with the functions of *Plasmodium falciparum* PABP is yet to be elucidated. In this study, we predicted the structure of *P. falciparum* PABP using homology modeling and also carried out active site prediction and docking simulation to provide insights on this protein as a potential antimalarial drug target.

MATERIALS AND METHODS

Sequence acquisition

The amino acid sequence of PABP of *P. falciparum* (Accession No: ABL63812.1) was obtained from the National Center for Biotechnology Information (NCBI); a comparison of this sequence with those of RCSB-PDB (Protein Data Bank) was performed.

Physiochemical characterization

The physiochemical parameters were computed using

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PROTPARAM, which includes amino acid composition, molecular weight, theoretical pl, total number of negatively charged residues (Asp + Glu), total number of positively charged residues (Arg + Lys), extinction coefficient, estimated half-life, instability index and grand average of hydropathicity (GRAVY). These parameters are essential for studying protein physiochemical properties (Gasteiger et al., 2003).

Secondary structure prediction

The secondary structure of the *P. falciparum* PABP was predicted using the SOPMA tool (Geourjon and Deléage, 1995). This was done by making a consensus prediction from multiple sequence alignments. The positional possibility of the α-helix, β-strands, turns, and random coils of the *P. falciparum* PABP was assessed using default parameters with a window width of 17, number of states of 4 and similarity threshold of 8.

Network interaction

STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) was used to identify protein-protein interactions (Szklarczyk et al., 2018). STRING is a biological database and web resource for constructing different known and predicted protein interactions networks based on functional association.

Residue Interaction Network Generator (RING) was used to analyze the residue-residue interaction of Polyadenylate-Binding Protein (Piovesan et al., 2016).

Disease-causing region prediction

Disease-causing region prediction using PONDR, DISOPRED, and PRDOS web-based servers was analyzed to find out the regions that are intrinsically disordered in the protein. These web services look for order/globularity or disorder tendency in the query protein based on a running sum of the propensity for an amino acid to be in the ordered or disordered state by searching domain databases and known disorders in proteins.

Selection of template

Template protein is selected on sequence similarity bases. The template was searched against the PDB database using the protein-Basic Local Alignment Search Tool (BLASTp). Using the default parameters, that is, BLOSUM 62 matrix, word size 3, and an E-value threshold 10. Chain D. PABP of *Saccharomyces cerevisiae* (PDB ID: 6R5K_D) at a resolution of 4.8 Å sharing 51.54% identity with *P. falciparum* PABP was selected for structural modeling.

Structural prediction and validation

Modeling of the 3D structure of *P. falciparum* PABP was performed by three web-based homology modeling programs, SWISS-MODEL, PHYRE2 and, I-TASSER to compare for accuracy. The derived models were visualized using RASMOL. PROCHECK was used to check for the quality of the modeled 3D structure of *P. falciparum* PABP. For structure validation, the .pdb file of the modeled *P. falciparum* PABP was uploaded on the PDB sum web server 3.0 of European Bioinformatics Institute (EBI) to obtain both the Ramachandran plot and the Ramachandran plot statistics. While the Ramachandran plot is used in accessing the quality of a modeled protein or an experimental structure, the Ramachandran plot statistics provide information on the total number of amino acid residues found in the favorable, allowed and disallowed regions. Also, Verify3D was used to validate the structure of the modeled protein, determine how compatible a 3D structure is to its amino acids, and compare the result with that of known structures.

Binding site identification

3DLigand was employed for the identification of binding sites in the derived structure that might be responsible for interaction with eIF4G (Wass et al., 2010).

RESULTS AND DISCUSSION

Sequence acquisition

P. falciparum PABP has been identified as an important post-transcriptional component of the organism especially in RNA metabolism and in the translational repression involved in the regulation of the parasite's growth, development and transmission. Hence, it is an attractive target candidate for antimalarial drug discovery. The amino acid sequence of PABP of *P. falciparum* 3D7 with accession number ABL63812.1 was obtained from the NCBI protein database in FASTA format. The protein has a total of 875 aa with a molecular weight of 97 kD. Interpro database analysis suggests that the protein consists of RNA recognition motif domains with 16-527 aa; four Nucleotide-binding Alpha-Beta domain superfamily with 5-103, 104-177, 183-275 and 354-537 aa, Polyadenylate-binding protein/*hyperplastic* disc protein domain (PABP-HDP) with 799-875 aa found at the conserved C-terminal domain of the protein and functions to recruit several different translational factors to the mRNA poly (A) tail.

Physicochemical characterization

Physicochemical characterization of the protein sequence was done using the Expasy PROTPARAM tool (Gasteiger et al., 2003) to gain an insight into the PABP (Table 1). The analysis revealed an instability index of 33.43, indicating that the protein will be stable *in vitro* because proteins with values over 40 are considered to be unstable (Anayet et al., 2011). A low GRAVY value of -0.880 reflects the hydrated state of the protein and a high aliphatic index, calculated as the total volume occupied by the aliphatic side chains, is considered a positive physicochemical factor for increased thermostability. The high extinction coefficient also points to the stability of the protein.

Secondary structure prediction

The secondary structural features indicate whether a given amino acid lies in α-helix, β-strand, or random coil. SOPMA (self-optimized prediction method with alignment)

Table 1. Important physiochemical properties of *Pf*PABP as determined using PROTPARAM.

S/N	Property	Value
1	Number of amino acids	875
2	Molecular weight	97229.71
3	Theoretical Pi	8.96
4	Total number of negatively charged residues (Asp + Glu)	78
5	Total number of positively charged residues (Arg + Lys)	88
6	Extinction coefficient	42540
7	Extinction coefficient	42290
8	Instability index	33.43
9	Aliphatic index	62.63
10	Grand average of hydropathicity (GRAVY)	-0.880

Table 2. The secondary structure prediction result from SOPMA indicating the secondary structure features.

Secondary structure prediction	Percentage
A-helix	317 (36.23)
3_{10} helix	0 (0.00)
Pi helix	0 (0.00)
B-bridge	0 (0.00)
Extended strand	123 (14.06)
β-turn	70 (8.00)
Bend region	0 (0.00)
Random coil	365 (41.71)
Ambiguous states	0 (0.00)
Other states	0 (0.00)

servers was used for secondary structure prediction and the features showed domination of random coils 41.71% followed by α-helix (Hh) 36.23%, extended strand (Ee) 14.06%, and β-turn (Tt) 8.00% (Table 2). The abundance of random coils could be important in the formation of the protein's 3D structure and also indicates a high level of stability and conservation of the protein structure (Ullah et al., 2012). Interactions between side chains within a random coil sometimes lead to the formation of hydrophobic clusters which acts as initiation or nucleation sites for protein folding (Nain et al., 2020; Smith et al., 1996). It has also been shown that random coils act as 'connecting bridges' for the alpha-helix and beta-strands, with the amino acid content of the random coils depending on the flanking structures (Khrustalev et al., 2013, 2014).

Network analysis

The protein-protein interaction (PPI) of PABP of *P. falciparum* with other proteins was determined using STRING (Szklarczyk et al., 2018). PPIs are very indicative of certain events in a cell and usually form the basis for several transcriptional regulatory networks and help elucidate signal transduction pathways in a cell (Raman, 2010). PPI of *P. falciparum* PABP generated through STRING is presented in Figure 1. The PPI network result shows that *Pf*PABP interacts with other proteins in a high confidence score, among which eukaryotic initiation factors EIF4A, EIF4E, and EIF4G, members of the multi-subunit translation initiation complex EIF4F were identified to interact with *P. falciparum* PABP (represented as PFL1170w on the STRING result).

EIF4A (H45) is an ATP-dependent RNA helicase involved in unwinding of the inhibitory secondary structures present in the 5'-UTR of the mRNA and also aids in the binding and scanning of the ribosomes for the initiator codon due to its single-stranded form (Rogers et al., 2001). EIF4E (PFC0635c) functions in the recognition of the mRNA 5'-cap structure and also necessary for cap-dependent translation (Gingras et al., 1999). EIF4G (MAL13P1.63) is an adapter protein that is required to mediate ribosome recruitment as well as circularization of the mRNA via interaction with PABP (Tuteja, 2009).

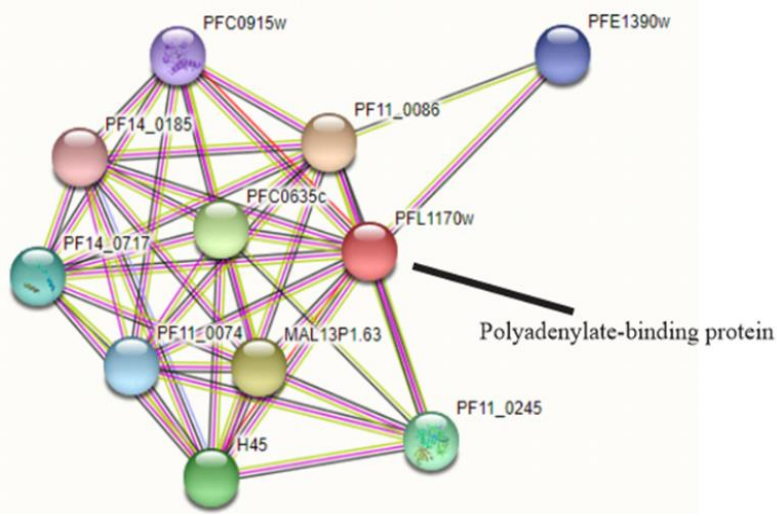

Figure 1. Protein-protein interaction network of PABP (*P. falciparum* 3D7) detected through STRING.

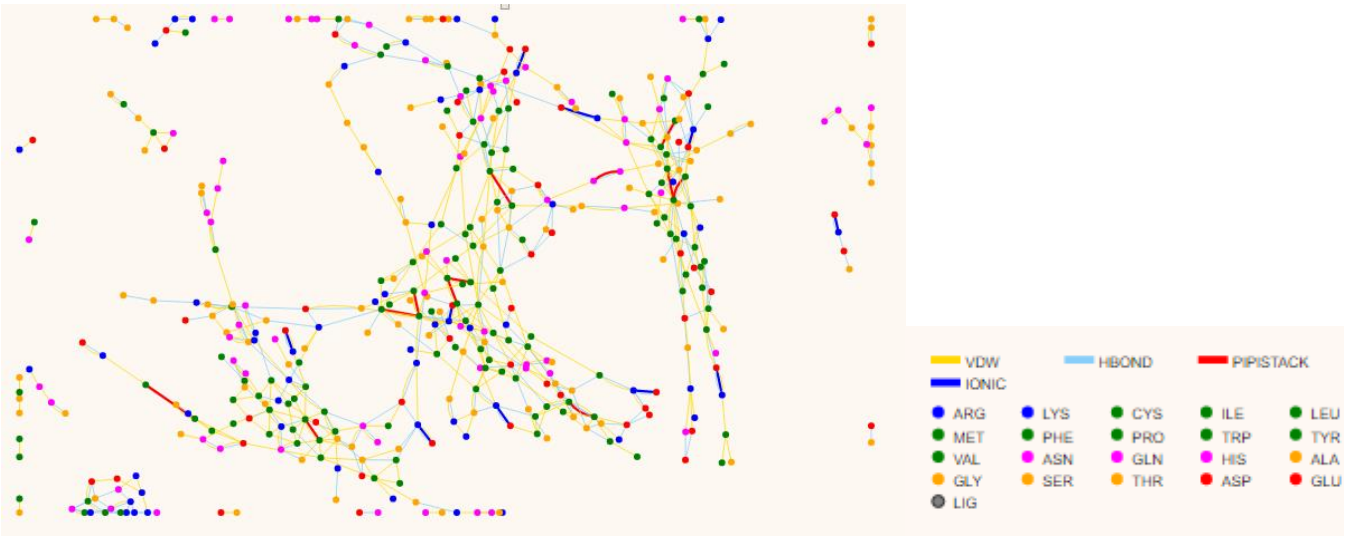

Figure 2. Residue interaction network generated by RING, nodes represent amino acids and edges represent interaction.

Other proteins identified to have a network PPI interaction with *P. falciparum* PABP includes the ATP-dependent RNA helicases DDX6, SPB4 and DDX41 (PFC0915w, PF14_0185, and PFE1390w); the PABP-interacting protein 1 (PF11_0086) which mediates binding between PABP and EIF4A (Minns et al., 2018); the translation elongation factor subunit alpha (PF11_0245), etc.

To analyze residue interaction within the *P. falciparum* PABP molecule, the residue interaction network was generated by RING (Piovesan et al., 2016). This describes the protein's 3D structure as a graph where nodes represent residues and edges represent physiochemical characterization (Anayet et al., 2011). RING uses the standard programs to create network interactions. The residue-residue interaction network of PABP indicates the probable active site of the protein (Figure 2).

Disease-causing region prediction

The results from the 3 servers showed the regions that are intrinsically disordered in the protein (Figure 3). Disordered regions of proteins are important and necessary for performing many functions such as DNA binding, binding to other proteins such as to kinases, transcription factors and translation inhibitors or mRNAs

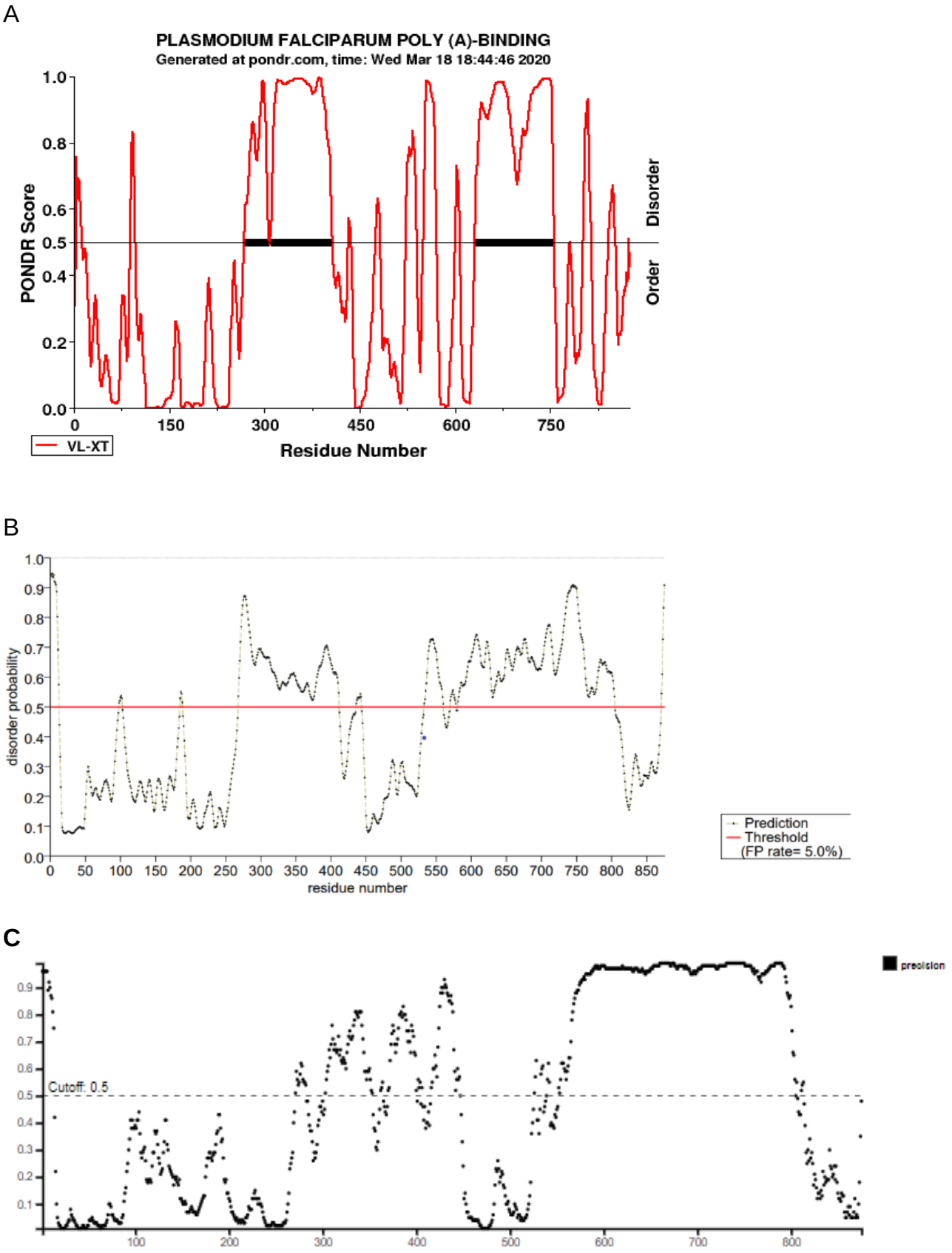

Figure 3. Disease-causing regions prediction results from A) PONDR, B) PRDOS and C) DISOPRED showing the disease-causing regions of *PfPABP.*

Table 3. Ramachandran plot calculation and comparative analysis of the models from the Swiss-model, Phyre2, and I-TASSER computed with the PROCHECK program.

Protein	Swiss model (%)	Phyre2 (%)	I-TASSER (%)
Residues in the most favored region	67.6	57.9	45.0
Residues in additionally allowed region	26.3	28.4	39.6
Residues in generously allowed region	3.9	6.3	11.4
Residues in disallowed region	2.1	7.4	3.9

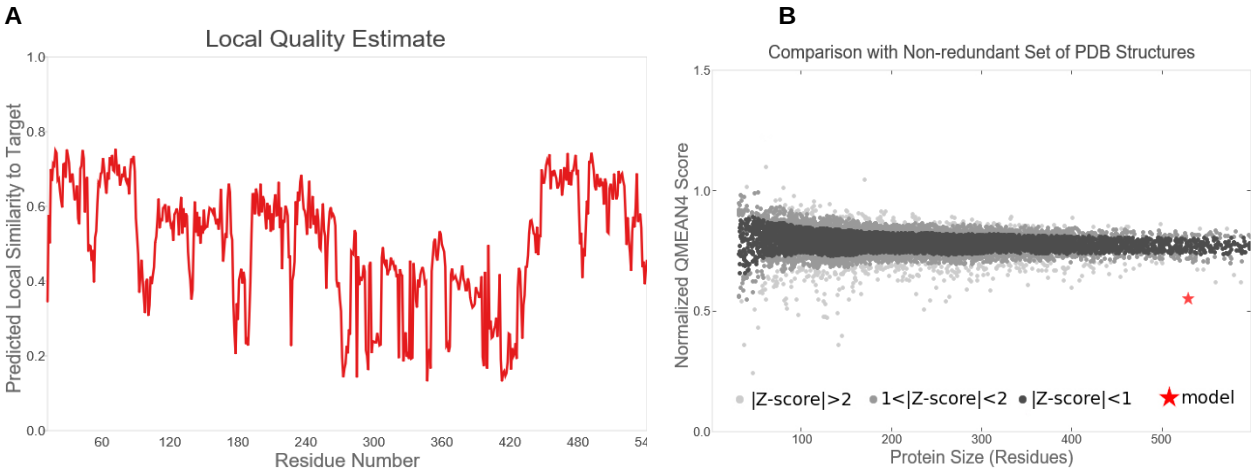

Figure 4. Structure validation of modeled PfPABP: (A) Local quality estimate of the residues of the predicted PfPABP model; (B) comparison of the predicted PfPABP structure with a nonredundant set of PDB structures. *Abbreviation: PfPABP Plasmodium falciparum* polyadenylate binding protein, PDB, Protein Data Bank.

(Anayet et al., 2011; Dunker et al., 2002; He et al., 2009). These disordered regions might contain functional sites or linear motifs such as molecular recognition domains, protein folding inhibitors, flexible linkers, etc. (Dunker et al., 2001). This correlates with the results from the Interpro prediction of the various domains found in the *P. falciparum* PABP as well as the results from the protein-protein interaction which predicted that the *P. falciparum* PABP has a network of PPI with other proteins involved in binding PABP and EIF4A as well as with other proteins.

Template selection

To find a suitable template for the protein model based on sequence similarity, a BLASTp search was conducted using default parameters. From the result, Chain D PABP of *Saccharomyces cerevisiae* (PDB ID: 6R5K_D) at a resolution of 4.8 Å, sharing 51.54% identity with *P. falciparum* PABP was selected for the structural modeling.

Structure prediction and validation of modeled protein

The three-dimensional structure of *P. falciparum* PABP performed by three homology modeling programs generated a refined 3D homology model of the protein sequence based on the given sequence alignment and the selected template (Table 3). 3D protein structures provide insight into the function of a protein since protein sequences with >20% identity may have identical structure and function. The SWISS-MODEL model web server which automatically calculates the QMEAN scoring function of the protein model, producing a z-score ranging from 0 to 1 (Arnold et al., 2006; Bordoli et al., 2009) was able to generate a better-quality 3D model with a GMQE of 0.32 and QMEAN of -6.5 (Figure 4). Ramachandran plot was done by PROCHECK to measure the accuracy of the modeled protein. About <70% of the residues were in the favored region and 2.1% of amino acids in the disallowed region (Figure 5). This also validates the modeled structure as a good quality protein model.

Binding site identification

3DLigand predicted 9 binding sites in the modeled structure. Out of which the largest site having a volume of 233 $Å^3$ was selected as the active site. Important residues identified in the active site were ASN14, ARG 49, ASP 50, SER 51, THR 53, ARG 76, LYS 55, ARG 55,

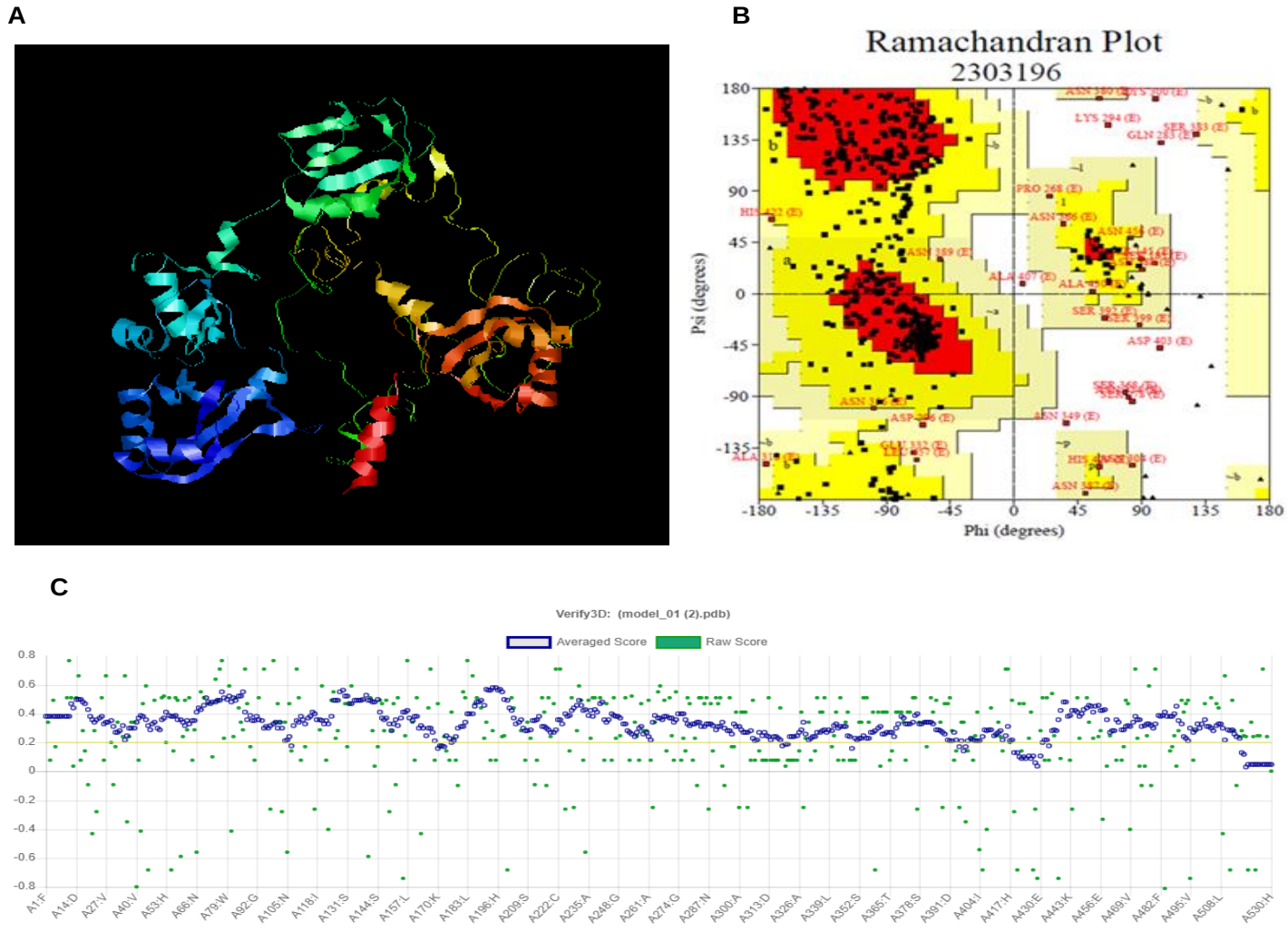

Figure 5. (A) 3D model of *Pf*PABP representation of the generated model by Rasmol. (B) Ramachandran plot of the modeled *Pf*PABP. (C) Verify3D. *Pf*PABP, *Plasmodium falciparum* polyadenylate binding protein.

HIS 85, GLN104 and ARG167. These residues located at the RRM1 and 2 regions of the modeled *PfPABP* have previously been reported to interact with eIF4G in animals and yeast (Imataka et al., 1998; Kessler and Sachs, 1998).

Conclusion

The setback in the war against malaria is caused mainly by the increasing number of vectors resistant to insecticides, dirty environments, limited primary healthcare facilities as well as lack of affordable cheap/effective drugs and the spread of multidrug resistance *Plasmodium* species. These situations have strengthened the need for search of new drug targets and understanding the basic biology of the malaria parasite. Hence, our findings would help broaden understanding of *P. falciparum* PABP, in particular, understanding its structure, binding sites, conformational changes, protein-protein/residue interaction, diseases causing regions as well as its physicochemical properties. These data would be valuable in structure-function interventions and identifying molecular targets for designing drugs applicable to *P. falciparum.* The authors have identified *P. falciparum* PABP as a potential antimalarial drug target and they recommend *in vitro* and *in vivo* experimentation to further justify its potential.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Development of information system for tracking breeding traits of improved crops

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Plant breeding involves application of a group of systems targeted at transporting collected decent parents' traits to produce an improved crop in the offspring. Cross-breeding and selection in plant breeding has been able to considerably improve yields as well as pest and disease resistance of crops. Efficiency in crop breeding research programs is contingent upon the aptitude of breeders making it possible to successfully produce, classify, store, track and choose recombinant genetic constitution with a determined number of required traits. It is not easily done with the manual system to store and manage large volumes of data generated in all research institutions. Locating files among tons of data is a tedious and time-consuming process for researchers. The importance of keeping track of research data is becoming vital in agricultural research institutions. A study was conceived in response to the need to improve the storage, tracking and dissemination of research data collected during the breeding of improved crops. It was conducted to develop a system for tracking breeding records, at the National Agricultural Research Laboratories (NARL) in Uganda. This was motivated by the increasing need to develop high yielding yet resilient crop varieties due to the constantly changing climate amid other socio-economic changes like population pressure and loss of soil fertility. Different methods were used to design such systems which included data-flow diagrams (DFDs) and entity relationship diagrams (ERDs). An ERD was used to recognize the data to be apprehended and deposited, and regained in order to accomplish the process of storing and tracking files. As a result, a breeding tracking system was developed as an application tool that can manage the creation and tracking of records. The advanced system supports information sharing between scientists and easy access to the trait information in improved crops.

Key words: Data, tracking, plant, breeding.

INTRODUCTION

Plant breeding is recognized as genomic enhancement within plants' presentation to collectively regulate required genetic factor and decrease the incidence of the unwanted genes in plants (Lance et al., 2020). This conserves the veracity of the parental genotype, inserting only a minor supplementary section of evidence that

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pedals a precise trait. A gene is a classification of deoxyribonucleic acid (DNA) that comprises evidence that determines a particular characteristic (Sarkar and Plutynski, 2010). Genes are located in chromosomes and are units of legacy that are accepted from one generation to the next and provide directions for expansion and function of the organism. Crops with genetic improvement are referred to as genetically enhanced crops. A better plant comprises a gene or genes, which has been artificially inserted in the process of conventional breeding.

Agriculture and biotechnology are critical contributors to solving the global problems of hunger, poverty and environmental degradation (Tonukari and Omotor, 2010). Although major scientific breakthroughs have been realized in engineering, electronics, information technology and medical research, advances in agricultural technologies, particularly agricultural biotechnology, hold a great potential for economic growth, crop productivity, nutritional quality necessary for reducing poverty and associated challenges in developing countries (Ivar et al., 2007). In Uganda, the land area under agriculture has been steadily declining due to population growth that was 40.0 million in 2019 (UBOS, 2019). At the global level, the world population was 7.7 billion in 2019 and is predictable to range almost to 9 billion in the year 2045 (UNDP, 2012). Therefore, a wide assortment of agricultural hereditary variety requirements to be taken, availed and used in order to feedstuff this rising population. Climate alteration is an additional risk to biodiversity that will meaningfully influence genetic resources for food manufacture (Lidder and Sonnino, 2012). Crop production must double by 2050 to encounter the foretold production stresses of the worldwide population. However, attaining this goal will be an important challenge for plant breeders for the reason that crop yields would consume to upsurge at a rate of 2.4% per year, yet the regular rate of increase is only 1.3%, with yields festering in up to 40% of land below cereal construction.

Tracking and tracing of improved crops

According to the new guideline (applicable since 2015) in the European Union, traceability is mandatory in all phases of the supply chain, cover all food and feedstuff as fit as commercial operators without preconception to current lawmaking on exact segments such as grains (European Union, 2015). A plant research institute must record and have information such as name, location, status, nature of plant consignment number and a more comprehensive explanation of the crop (Luca et al., 2013). Unless detailed requirements for additional traceability exist, the obligation for traceability is incomplete to safeguarding that researchers are at least able to classify the immediate source of the crop as well as immediate subsequent receiver. Handling the enormous quantity of data and processing them is a challenge that needs to be answered by emerging data management and tracking system for managing upgraded crops (Adetunji and Izang, 2018).

METHODOLOGY

System design is the process of turning the abstract solution into a practical specification suitable for implementation. The system was designed based on the functional and nonfunctional requirements obtained during requirements collection which described the parameters and the data to be incorporated into the system. Different methods were used to design the system which included data flow diagrams (DFDs) and entity relationship diagrams (ERDs).

To release the purpose of this paper, we begin with modelling the projected tracking system using the data flow diagram and context diagram. A data flow diagram (DFD) is a graphical illustration of the flow of data and modelling its procedural aspects. A DFD is often used as an initial stage to generate a summary of the system without going into details. Data flow illustrations show the purposes to be accomplished by a system and the data flow in the system, what alterations are made on the data. They similarly give graphic representations of the system's mechanisms, procedures and the boundaries. The excellent data flow diagram is based on the detailed information to be comprehended by practical and non-technical spectators. It can deliver a high-level system overview with limitations and influences to other systems, and lastly, it can deliver a comprehensive representation of the system mechanism. It uses diagram to document an object-based rottenness of systems and to show the communication amongst these objects and the dynamic forces of these objects. The information tracking system was developed as a web request with three tier construction. Hypertext Pro-processor (PHP) handles data transmission from the user boundary to the database and query demand to the database from the user interface Entity Relationship Diagrams (ERDs) were used to perfect together with the rational and physical database construction projects. The entity relationship data model shows the relations among the objects complicated in the system composed of their qualities and designates the number of incidences an entity can exist for a single incidence of the related entity. ERDs aid the imprisonment of additional details such as data about entities (attributes and constraints on entities) and their relations. An ERD was used to classify the data to be taken, stored and retrieved in order to provide the activities completed in the procedure of filing and paying taxes. ERDs are comparatively humble, user friendly and can provide a unified view of data which is independent of any data model (Tiberiu and Liviu, 2010)

The reason for choosing PHP is that it is not only a broadly used open-source scripting language but also PHP is free software and turns on numerous platforms making it platform independent. PHP is companionable with almost all web servers in use today. PHP supports an extensive variety of databases. It can open, read, write, remove and close files on the server. It can gather the form information and can send and obtain cookies. PHP can add, remove, modify data in a database and can limit users from retrieving some pages on your website. PHP can encode data with PHP varied output users produced.

The database management system used is MySQL. It is one of the world's greatest popular open databases, allowing the cost-effective distribution of reliable, high-performance, and climbable web-based and entrenched database application. It is perfect for both small and big applications. MySQL is very fast, dependable and easy to use. It chains standard SQL.MySQL accumulates on a number of platforms. It is free to transfer and use and is established, distributed, and supported by Oracles Corporation.

Cascading style sheets (CSS) come in handy for styling the user interfaces, creating them appealingly pleasing to users of the system.

Germplasm tracking

Information technology (IT) benefits crop growth by helping data management and operation across corrections and software systems. Efforts to advance new crops must grow from individual, inaccessible data sets to a realm where information flows easily from field and laboratory trainings to a systematic tracking system.

Some systems accomplished linking crop-specific data to crop development information (Seelye et al., 2016). This ranges from possession of source germplasm to misuse of indigenous knowledge about potential uses (Subramanian and Pisupati, 2010). Careful documentation of the crop growth procedure will deliver shareholders the information needed to achieve and track the information about enhanced crops.

The documentation of the complete plant breeding procedure and tracking information in breeding segment, emphasizes mostly on crossing, selection, increase, embryo rescue, micro-propagation and field testing. Each genetic entity, whether a single cell, seed packet, and tissue culture, is uniquely recognized, and the identifies can be associated with alternative names as needed. Sequences of generations are flawlessly linked, letting historic pedigrees to be traced as far back as archives allow. Genetic entities may be considered using user-specified attributes ranging from origin of germplasm, to plant signifiers (White et al., 2007).

Benefits of information systems for tracking information about improved crops

The role of Management Information System (MIS) in an organization can be compared to the role of a heart in the body. The data is to the blood and Management Data System (MIS) is to the heart. In the body, the heart acts the role of providing blood to all the essentials of the body together with the brain. It regulates and controls the inward impure blood, processes it and sends it to the end point in the quantity needed. It accomplishes the needs of blood supply to human body.

An MIS plays exactly the same role in the association. The system safeguards suitable data that is collected from the various sources, administered, and sent to the required last stop. The system is expected to fulfill the data needs of an individual, a group of individuals, the organization functions- the managers and the top supervisors. Hence, an MIS satisfies the diverse needs through a variety of systems such as Query Systems, Analysis Systems, Modelling Systems and Decision Support Systems. Therefore, MIS helps in Tactical Preparation, Management Control, Operational Controller and Transaction Processing. By contrast with labor-intensive systems, MIS have a variety of benefits to an organization specifically.

Extensive breeding and agronomic efforts over the past 50 years have been accountable for tripling cereal yields. Ongoing advances in the techniques available to breeders offer the possible to increase the rate of genetic improvement.

Plant genetic engineers often need to trace traits in improved crops to their original plant. This is done to track the source of a good trait using the breeding collections in order to get the traits for producing other improved crops. This process requires access to data from the field. The starting materials are taken to the laboratory where they are subjected to a number of experiments, before they are released back to the field as improved plants. Currently at Uganda's National Agricultural Research Organization (NARO), this data is manually collected, entered and stored in personal laboratory books and paper files. As a result, there are a lot of challenges regarding utilization of this data notably: data duplication, difficulty in locating data about specific samples, misinterpretation and wastage of time in locating data. The aim of this project was to develop an information system for tracking information about improved crops. It is hoped that such a system will make it easier to trace some of the good traits found in the improved crops in the process of breeding.

Plant breeding can be measured as an evolutionary procedure between humans and palatable plants. People produced variations in the plants that were used for agriculture and innovative plant. Plants yielding more substantial harvests freed some of the people's time for emerging art, handcrafting, and science, eventually leading to modern human life as recognized. Evolution could not exist deprived of agriculture and agriculture could not sustain the civilized world lacking contemporary crop varieties. From this opinion of view, it grows into making clear that plant breeding is one of the foremost fundamentals of development.

RESULTS AND DISCUSSION

Context diagram (data flow diagrams)

A setting diagram is a data flow diagram that precises all dispensation actions within the system in single process symbol. It defines the maximum level view of the system, shows a system as a whole with inputs and outputs from/to external factors. It was used to describe in general context of the system by identifying all the external entities or users interacting with the improved crop system. The information they feed into the system and the feedback from the system.

Data flow diagrams are a network symbol of a system. They are the keystone for controlled systems analysis and design. The diagrams use four symbols to characterize any system at any level of feature. The four entities that must be signified are the following.

System context diagram

The context-level DFD at Level 0 DFD shows some of the aspect of the system being demonstrated. The Level 0 DFD shows how the system is divided into sub-systems (processes), respectively of which contracts with one or additional of the data flows to or from an outside agent, and which collected offer all of the functionality of the system as an entire. It also classifies interior data stores that must be present in order for the system to do its job, and shows the flow of data between the numerous parts of the system. A context diagram is a data flow diagram that precises all dispensation happenings within the system in single process symbol (Figure 1).

Entity relationship diagram (ERD)/ER model

An entity-relationship diagram is a data modeling technique that creates a graphical representation of the entities, and the relationships between entities within an

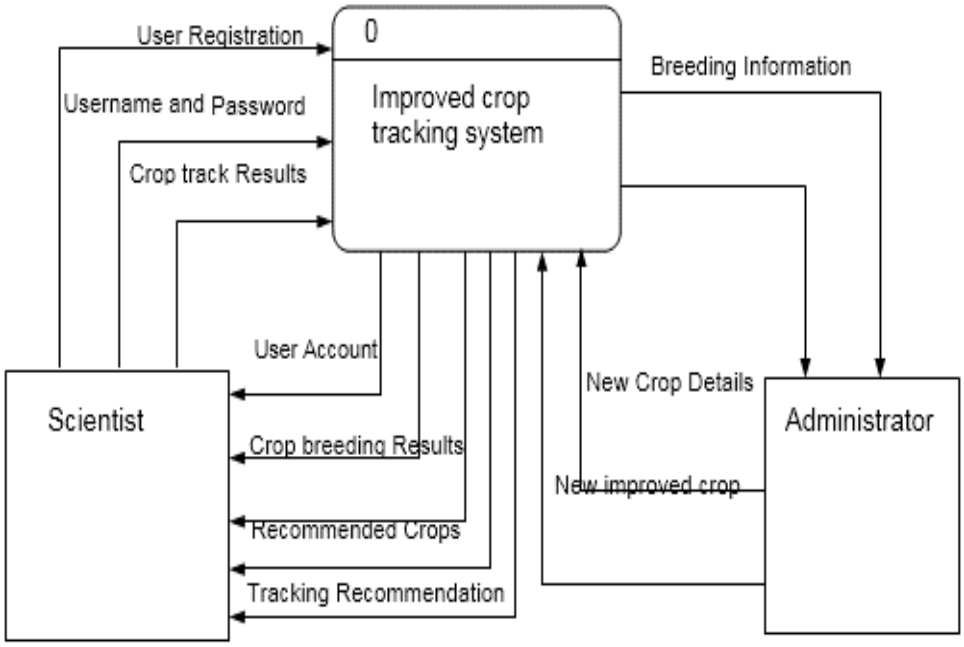

Figure 1. System context diagram.

information system. It represents the logical design of the database for a system. It identifies major entities/ database tables, attributes of the entities and establishes the relationship between the entities.

The entity-relationship diagram for an information system for tracking information about improved crops is as shown in Figure 2.

The ERD was used to illustrate the data model of the tracking system. An ERD comprises entities, identifier and relationships. An entity is a tangible object of interest that exists in the user's domain. It is usually something of interest to the user and they (users) keep track of it. Collective noun, or nouns, are usually used to name (describe) entities. In this case the entities for the system for tracking information about improved crops were germplasm, crops, crossing, users, selection field testing, lab multiplication, field testing and tracking.

Administration user interface

Login page: This is an interface that gives the user access to the system when the application loads it, prompt the login interface which requires the user to enter the username and password and then click the login button. The login page for users is as shown in Figure 3.

Germplasm: Germplasm is a living genetic resource such as seeds or tissues that are maintained for the purpose of plant breeding, preservation, and other research uses. It can be a seed or another plant part like a leaf, a piece of stem, pollen or even just a few cells that can be turned into a whole plant. Germplasm collections can range from collections of wild species to elite, domesticated breeding lines that have undergone extensive human selection. The germplasm component contains information for a plant name, genetic makeup and a valuable natural resource of plant diversity. Genetic diversity of germplasm gives plant breeders the sustained ability to develop new high yielding, high quality varieties that can resist constantly evolving pests, diseases and environmental stresses. This component (Figure 4) allows scientists to capture and store information about germplasm. While entering germplasm records, it has germplasm name. It is a name given to the germplasm generated by the breeder. Institute is the institute where germplasm was generated from. Exact location is the location where the germplasm is located.

Conventional plant breeding: Can be seen as a collection of techniques aimed at bringing together good parents to generate a better crop in the progeny. It is therefore essential for plant breeders to be entirely sure of what the parents of a cross are. Crosses between breeding stocks are generally done manually.

Category of information collected, stored and used on improved crops

As shown in Table 1 and Figure 5, different crop researchers collect different information depending on the research they are conducting. Most researchers collect

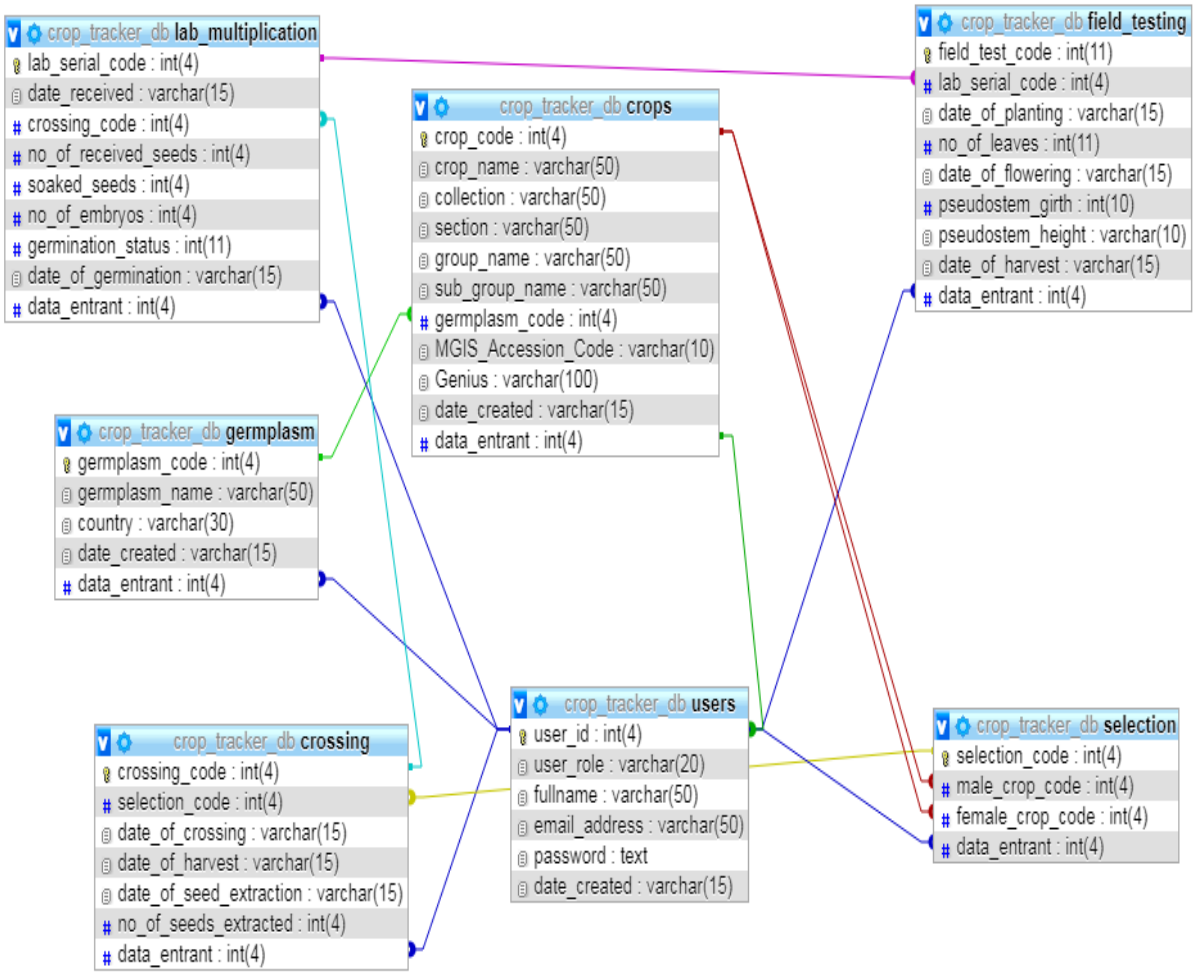

Figure 2. The entity relationship diagram for an information system for tracking information about improved crops.

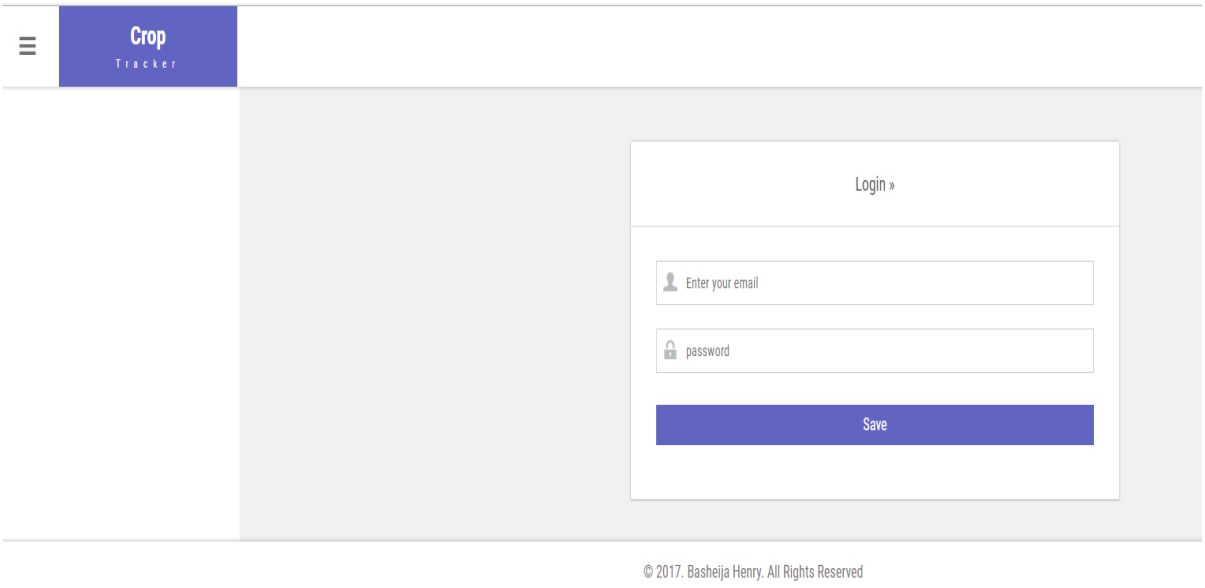

Figure 3. Crop tracker login.

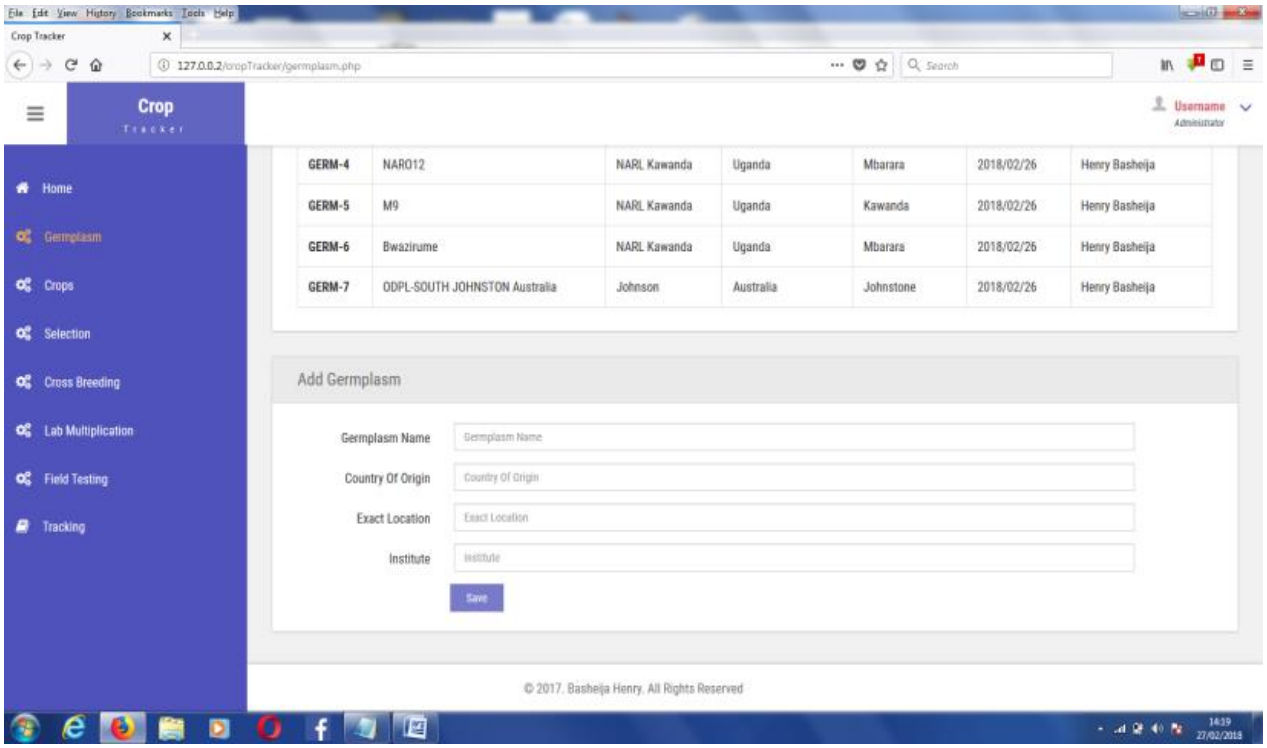

Figure 4. The interface for germplasm crops available in the system.

Table 1. Category of information collected on improved crops.

Information category	Total number of respondents	Frequency	Percent
Breeding	50	40	80
Diseases	50	32	64
Pests	50	31	62
Others	50	13	26

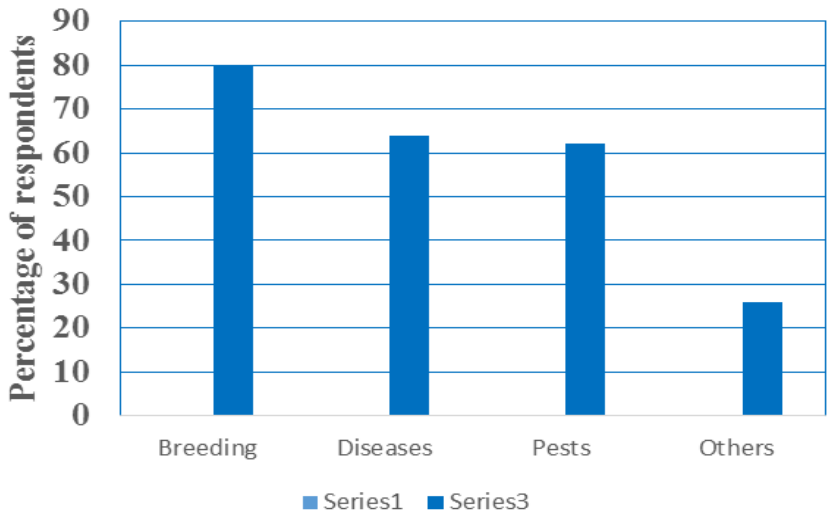

Figure 5. Category of information collected about improved crops.

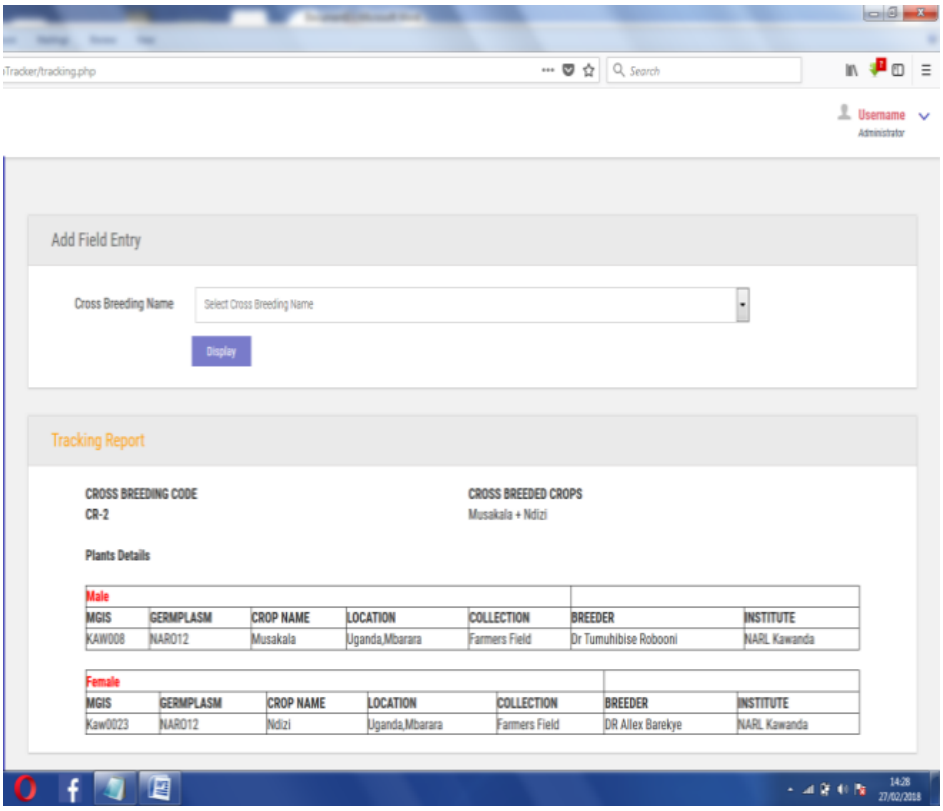

Figure 6. Crop tracking interface.

information about breeding at 80%, 64% collect information about diseases, while 62% collect information about pests.

Tracking: After the plant has gone through the breeding process, users (scientists) can search the system to find the origins of the new crop, that is, the female and male parents. Through this functionality, the user can know the origin of the new crop. This is hoped to help young researchers to know the source of good breeding materials to use in breeding tracking interface. This is hoped to help young researchers to know the source of good breeding materials to use in breeding tracking interface (Figure 6). The system was effective in storage, tracking and dissemination of research data collected during the breeding of improved banana. The system needs validation in different agricultural research programs. Control of entry into the system is based on user names and password. However, the level of security can be increased through adding another layer of security such as encrypting information during transmission and/or biometrics.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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