IN THIS ISSUE

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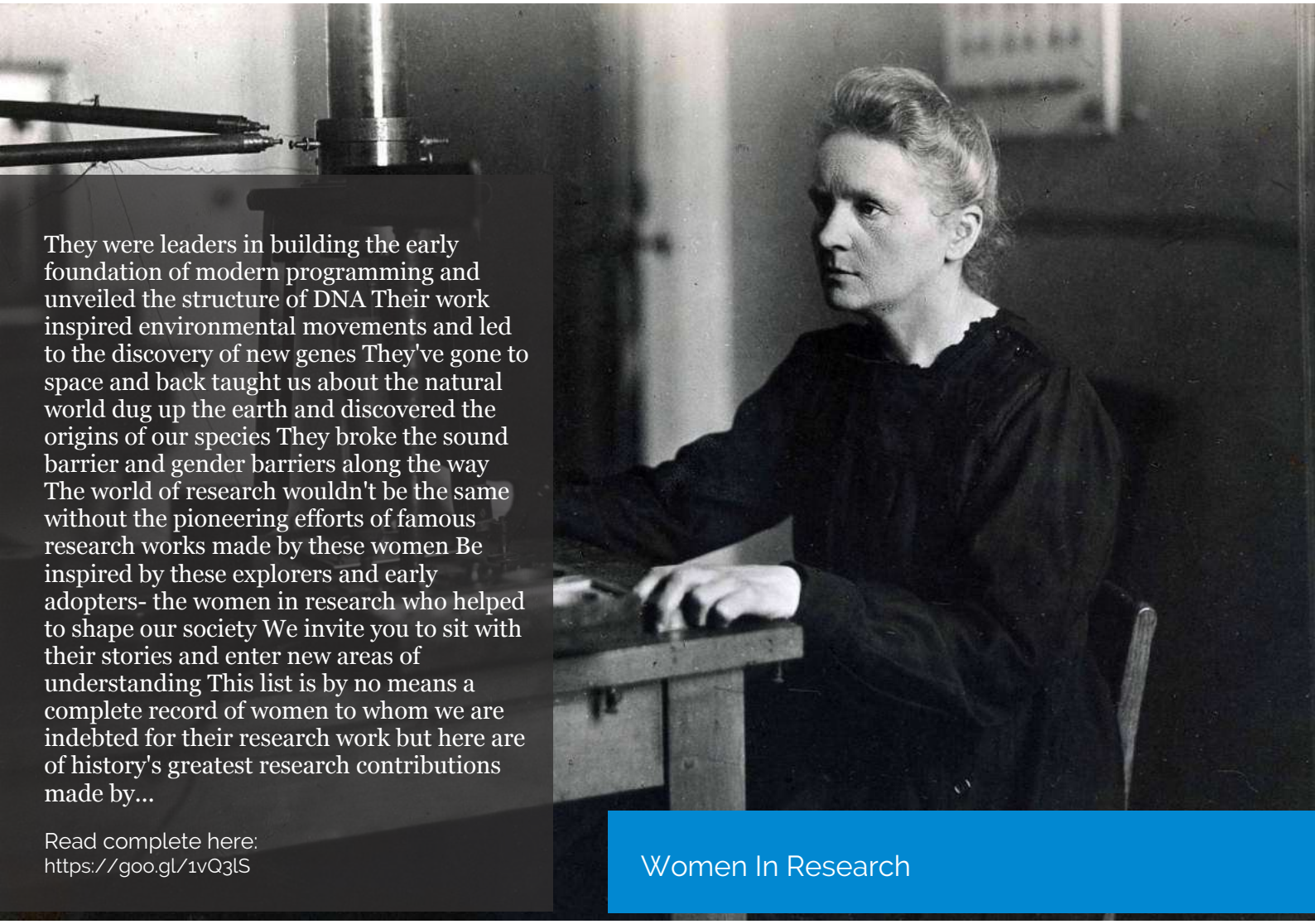

They were leaders in building the early foundation of modern programming and unveiled the structure of DNA Their work inspired environmental movements and led to the discovery of new genes They've gone to space and back taught us about the natural world dug up the earth and discovered the origins of our species They broke the sound barrier and gender barriers along the way The world of research wouldn't be the same without the pioneering efforts of famous research works made by these women Be inspired by these explorers and early adopters- the women in research who helped to shape our society We invite you to sit with their stories and enter new areas of understanding This list is by no means a complete record of women to whom we are indebted for their research work but here are of history's greatest research contributions made by...

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Research papers and articles

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Yonatan Zilpa

ABSTRACT

This paper explores the use of a system of equations to factor semiprime numbers. Semiprime numbers are a special type of composite number that are the product of two prime numbers. Factoring semiprime numbers is important in cryptography and number theory. In this study, we present a method that applies a system of polynomial equations to factor semiprime number M.

Where M can be any semiprime number. In fact, we build a family of systems where each system compose from three polynomial equations with three variables. The results of this study show that a solution for one system results with a complete factorization for a semiprime number. It may be possible to apply well known algorithms, such as Gröbner method [1], to solve one of those systems for a particular semiprime number M.

Keywords: semiprime, factorization, system of equations.

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Keywords: semiprime, factorization, system of equations.

I. INTRODUCTION

Let s_1, s_2, and S be any integers such that $S = s_1 s_2$, then

$$(s_2 - s_1)^2 + 4S$$

is a perfect square. Indeed

$$(s_2 - s_1)^2 + 4S = (s_2 + s_1)^2.$$

Let M be a semiprime number and let p, q be its prime factors, where $q > p$. Let $d = q - p$ and let n and x be any integers, such that n divides $M - x$, then

$$\sqrt{\left(\frac{M-x}{n} - n\right)^2 + 4(M-x)} = \left|\frac{M-x}{n} + n\right| \tag{1.1}$$

is a positive integer. Thus, if $\left(\frac{M-x}{n} - n\right)^2 - 4x$ is a non-negative perfect square, then

$$\left(\frac{M-x}{n} - n\right)^2 - 4x = d^2. \tag{1.2}$$

Equation (1.2) implies that

$$\frac{M-x}{n} - n = \sqrt{4x + d^2}.$$

Hence, x must contain a factor t such that

$$\frac{x}{t} - t = d.$$

The number x must be of the form:

$$(d + j)j$$

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where j is an integer. Let k be a positive integer less than p, then substituting x with $k(d+k)$ in equation (1.2) yields

$$\left(\frac{M-(d+k)k}{n}-n\right)^2-4(d+k)k=d^2 \tag{1.3}$$

Solving equation (1.3) for d we get the following two solutions

$$\begin{aligned} d_0 &= \tfrac{M-k^2+2kn-n^2}{k-n} = \tfrac{M-(k-n)^2}{k-n} \\ d_1 &= \tfrac{M-k^2-2kn-n^2}{k+n} = \tfrac{M-(k+n)^2}{k+n} \end{aligned} \tag{1.4}$$

Since d is a positive integer. The first equality of equation (1.4) implies that $|k-n|=1$ or

$$|n-k|=p \tag{1.5}$$

Substituting k with k_1 and n with $n+1$ in equation (1.3) yields $|k_1-(n+1)|=p$ and from this we get $k_1=k+1$. Similarly, substituting k with k_2 and n with $n+2$ in equation (1.3) yields $|k_2-(n+2)|=p$ which gives us $k_2=k+2$. This gives us the following system

$$\begin{aligned} &\left(\tfrac{M-(d+k)k}{n}-n\right)^2-4k(d+k)=d^2 \\ &\left(\tfrac{M-(d+(k+1))(k+1)}{n+1}-(n+1)\right)^2-4(k+1)(d+(k+1))=d^2 \\ &\left(\tfrac{M-(d+(k+2))(k+2)}{n+2}-(n+2)\right)^2-4(k+2)(d+(k+2))=d^2 \end{aligned} \tag{1.6}$$

System (1.6) has three equations with three variables n,k,d, however this system is dependent. We may overcome this problem by trying other functions. Let $t:\mathbb{Z}\to\mathbb{Z}$ be any function, replace n with $t(n)$ and k with u in equation (1.3). Equality (1.5) implies that $u-t(n)=p$ (or $t(n)-u=p$) and $k-n=p$ (or $n-k=p$), which gives us a system of equations

$$\begin{aligned} u-t(n)&=p \\ k-n&=p \end{aligned}$$

from which we deduce $u-k-t(n)+n=0$ or equivalently $u=k+t(n)-n$. We get the following equality:

$$\begin{aligned} &\left(\frac{M-\Big(d+\big(k+t(n)-n\big)\Big)\big(k+t(n)-n\big)}{t(n)}-t(n)\right)^2+ \\ &-4\big(k+t(n)-n\big)\Big(d+\big(k+t(n)-n\big)\Big)=d^2 \end{aligned} \tag{1.7}$$

II. BUILDING SYSTEMS OF EQUATIONS WITH d_0

Based on equation (1.7) we can deduce a new system of three equations with three variables k,n and, d. We may find three functions $t_1,t_2,t_3:\mathbb{Z}\to\mathbb{Z}$ and replace $t(n)$ with $t_3(n)$ to get the third equation, $t(n)$ with $t_2(n)$ to get the second equation, and finally $t(n)$ with $t_1(n)$ to get the first equation. The key here is to select the functions t_1,t_2, and t_3 in such a way that our system has a unique solution, where $|n-k|\neq 1$. When moving d^2 to the left side of equality (1.7) and multiplying it with $t^2(n)$, the left side of this equality becomes:

$$\phi(t,n,k,d) := \left(\Big(M - \Big(d + \big(k + t(n) - n\big)\Big)\big(k + t(n) - n\big)\Big) - t^2(n)\right)^2$$
$$-4t^2(n)\big(k + t(n) - n\big)\Big(d + \big(k + t(n) - n\big)\Big) - t^2(n)d^2 \tag{2.1}$$

If t is a polynomial function in $\mathbb{R}$ with integral coefficients, then ϕ can be viewed as a polynomial function from $\mathbb{R}^3$ to $\mathbb{R}$. In this case we also denote the function $\phi(t,n,k,d)$ with $\phi_t(x,y,z)$. We thus get a system of polynomial equations:

$$\begin{aligned} \phi_{t_1}(x,y,z) &= 0 \\ \phi_{t_2}(x,y,z) &= 0 \\ \phi_{t_3}(x,y,z) &= 0 \end{aligned} \tag{2.2}$$

III. BUILDING SYSTEMS OF EQUATIONS WITH d_1

The problem with d_0 is that the variant of system (1.7) is infinite, any integer n,k such that $|n-k| = 1$ satisfying this system. However, applying solution d_1 in equality (1.4) and requiring that n,k be positive integers implies that

$$k + n = p. \tag{3.1}$$

Replacing n with $t(n)$ and k with u in equation (1.3) we get the following system

$$\begin{aligned} u + t(n) &= p \\ k + n &= p \end{aligned} \tag{3.2}$$

from which we deduce $u + t(n) - k - n = 0$ or equivalently $u = n + k - t(n)$. Now we can replace k with $n + k - t(n)$ and n with $t(n)$ and d with d_1 in equation (1.3) to get

$$\left(\frac{M - \Big(d + \big(n + k - t(n)\big)\Big)\big(n + k - t(n)\big)}{t(n)} - t(n)\right)^2$$
$$-4\big(n + k - t(n)\big)\big(d + \big(n + k - t(n)\big)\big) = d^2 \tag{3.3}$$

Since $t(n)$ relies on the second equality of (1.4) and since $t(n)$ differs from n, the first solution in (1.4) won't solve equality (3.3). Hence, by replacing $t(n)$ with polynomial $t_1(n)$ with positive coefficients we get two independent polynomials.

Let us denote

$$\Psi_t(n,k,d) := \left(\frac{M - (d + n + k - t(n))(n + k - t(n))}{t(n)} - t(n)\right)^2$$
$$-4\Big(d + (n + k - t(n))\Big)\Big(n + k - t(n)\Big) - d^2$$

then equality (3.3) becomes

$$\Psi_t(n,k,d) = 0. \tag{3.4}$$

If we set $t(n) = n$, then equation (3.4) is equivalent to (1.3). However, if polynomial $t(n)$ differs from n, then solution d_0 is lost. Hence, for any polynomial $t_2(n)$ with positive integers that differs from n, polynomials Ψ_n and $\Psi_{t_2(n)}$ are independent.

We can repeatedly use the result $u = n + k - t(n)$, obtained from system (3.2), to get the following system of three polynomial equations with three variables:

$$\psi_{t_1}(n,k,d) = 0$$

$$\lambda_{t_2}(n,k,d) = \psi_{t_1}(t_2(n), n+k-t(n), d) = 0 \tag{3.5}$$

$$\psi_{t_1}(t_3(n), n+k-t(n), d) + \lambda_{t_2}(t_3(n), n+k-t(n), d) = 0.$$

If polynomials t_1, t_2, and t_3 differ in pairs and having non-negative integers and if none of these polynomial is zero, then none of the polynomial in system (3.5) depends on the other.

IV. CONCLUSIONS

The RSA cryptosystem [4] as well as all public key cryptography implementations rely on the complexity of semiprime factorization. Mathematical attacks based on known relations, such as Pythagorean primes [3] or the use of a polynomial of third degree order [6] have been recently proposed for potential methods for factoring semiprimes numbers. When it comes to factoring large semiprime numbers, well known existing algorithms may consume too much memory and running time. Other algorithms, such as the firefly algorithm [5], may address some of these issues [2].

In this article, we attempt to attack the problem of semiprime factorization by using relationships between M and two different numbers, that are less than M. Using only quadratic relationships, we have constructed a wide variety of systems of three polynomial equations with three variables. A solution of one of one system may lead to a complete factorization of the semiprime number M.

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Special Issue: "Data Science in the Cloud: Overcoming Challenges and Maximizing Opportunities for Machine Learning"

Vinay Singh

INTRODUCTION

As Data Science is a rapidly evolving field in which large amounts of data are analyzed to derive meaningful insights using machine learning-based techniques. In contrast, cloud computing offers a scalable and cost-effective platform for storing and processing data for machine learning-based applications. The combination of data science and cloud computing has emerged as a powerful tool for organizations seeking a competitive advantage through data-driven decision-making. The problem statement is that traditional machine learning approaches frequently involved storing data on local servers and analyzing it with specialized tools. However, this approach can be costly, time-consuming, and unscalable in the face of large data volumes. Many organizations are turning to cloud-based machine-learning platforms to address these challenges.

Several challenges are in the way to overcome to this problem and some of them are the complexity of integrating different tools and technologies is one of the major challenges of machine learning in cloud computing. Data scientists must be skilled in a variety of programming languages, cloud platforms, and machine-learning tools. Furthermore, data scientists may run into compatibility issues with various cloud platforms and services.

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Several challenges are in the way to overcome to this problem and some of them are the complexity of integrating different tools and technologies is one of the major challenges of machine learning in cloud computing. Data scientists must be skilled in a variety of programming languages, cloud platforms, and machine-learning tools. Furthermore, data scientists may run into compatibility issues with various cloud platforms and services.

Another issue to consider is data security and privacy. To protect against data breaches and unauthorized access, sensitive data should be stored in the cloud. Organizations must ensure that adequate security measures are in place to prevent unauthorized access to their data.

Finally, organizations face difficulties in managing and maintaining their cloud-based machine-learning platforms. These platforms' management and maintenance can be complex, necessitating specialized knowledge and skills. Organizations must have the resources in place to effectively manage their cloud-based machine learning platforms.

There will be several benefits for this as cloud-based machine learning platforms are highly scalable and can handle large data volumes, allowing organizations to analyze and process large datasets more easily. Cloud-based platforms also give data scientists access to a wide range of machine learning tools and frameworks, allowing them to experiment and develop models quickly. Furthermore, cloud-based machine learning platforms can assist organizations in lowering costs by eliminating the need for costly hardware and infrastructure. The cloud allows businesses to pay for only what they use, allowing them to scale their computing resources up or down as needed. This scalability also enables organizations to experiment with new machine-learning approaches without incurring significant costs.

How the challenges can be solved:

To address the challenges of machine learning in cloud computing, organizations can implement a number of best practices. To begin, they can invest in training programs to help data scientists learn how to work with cloud-based machine-learning platforms. Specialized courses or training programs provided by cloud vendors may be included in this training.

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Second, organizations can protect sensitive data by implementing strong security measures such as data encryption and access controls. This may entail collaborating with cloud vendors to ensure that the necessary security measures are in place to protect their data.

Finally, organizations can use cloud vendors' managed services to simplify the deployment and management of machine learning platforms. Managed services can provide organizations with pre-configured machine-learning platforms, allowing them to concentrate on analysis rather than infrastructure management.

Machine learning in cloud computing provides many benefits to organizations, including scalability, access to a diverse set of tools and frameworks, and cost savings. To realize these benefits, organizations must overcome several challenges, including integrating various tools and technologies, ensuring data security and privacy, and managing and maintaining their machine-learning platforms. Organizations can overcome these challenges and reap the benefits of machine learning in the cloud by implementing best practices, such as investing in training, implementing robust security measures, and leveraging managed services provided by cloud vendors.

This Special Issue aims at publishing high-quality manuscripts covering new research on topics related to the Integration of cloud computing and Big data for better IOT utilization including but not limited to the *following:-*

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- AI Algorithms for better cloud computing
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- Internet on Things(IoT)

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- Hybrid Cloud
- Cloud architecture
- Virtualization, containerization, and container orchestration
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- Artificial Intelligence
- Machine Learning

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- Communications and networking in Cloud
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- Submission of revised papers: 15/09/2023
- 2nd round of acceptance notification: 15/10/2023
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Epitope - based Peptide Vaccine Against Glycoprotein GPC Precursor of Lujo Virus using Immunoinformatics Approaches

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Africa City of Technology/Applied Bioinformatics Center Biotechnology Park

ABSTRACT

Background: Lujo virus (LUJV) is a highly fatal human pathogen belonging to the Arenaviridae family. Lujo virus causes viral hemorrhagic fever (VHF). An In silico molecular docking was performed on the GPC domain of Lujo virus in complex with the first CUB domain of neuropilin-2.

The aim of this study is to predict an effective epitope-based vaccine against the glycoprotein GPC precursor of Lujo virus using immunoinformatics approaches.

Methods and Materials: A glycoprotein GPC precursor of Lujo virus Sequence was retrieved from NCBI. Different prediction tools were then used to analyze the nominee's epitopes in BepiPred-2.0: Sequential B-Cell Epitope Predictor for B-cell, T-cell MHC class II & I. Later the proposed peptides were docked using the Autodock 4.0 software program.

Keywords: immunoinformatics, glycoprotein GPC precursor, epitope-based vaccine, Lujo virus LUJV, VHF.

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Epitope - based Peptide Vaccine Against Glycoprotein GPC Precursor of *Lujo Virus* using Immunoinformatics Approaches

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ABSTRACT

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Results and Conclusions: The proposed and promising peptides FWYLNHTKL and YMFSVTLCI has shown a very strong binding affinity to MHC class I & II alleles with high population coverage for the world, South Africa, and Sudan. This indicates a strong potential to formulate a new vaccine, especially with the peptide YMFSVTLCI which is likely to be the first proposed epitope-based vaccine against glycoprotein GPC of Lujo virus. This study recommends an in-vivo assessment for the most promising peptides especially FWYLNHTKL, YMFSVTLCI and LPCPKPHRLR.

Keywords: immunoinformatics, glycoprotein GPC precursor, epitope-based vaccine, *Lujo virus* LUJV, VHF.

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I. INTRODUCTION

Arenaviruses are rodent-borne viruses. Where a genetically unique arenavirus called *Lujo virus*, has been discovered as the causal agent of a nosocomial outbreak of acute febrile disease with hemorrhagic manifestations in Zambia and South Africa. The outbreak marked a high case fatality rate of almost 80% [1]. These viruses are genetically and geographically related to the Old World mammarena viruses, endemic to West Africa, and the New World mammarena viruses, endemic to South and North America [2].

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Lujo virus causes viral hemorrhagic fever (VHF) which can be caused by five distinct families of viruses: the filo-, arena-, flavi-, rhabdo- and bunya virus family [3].

Viral hemorrhagic fever (VHF) is an acute systemic illness classically involving fever, a constellation of initially nonspecific signs and symptoms, and a propensity for bleeding and shock.

With *Lujo virus* hemorrhagic fever (LVHF) illness typically begins with the abrupt onset of fever, malaise, headache, and myalgias followed successively by a sore throat, chest pain, gastrointestinal symptoms, rash, minor hemorrhage, subconjunctival injection, and neck and facial swelling over the first week of sickness [4]. No major hemorrhage was noted. Whereas neurological signs were sometimes seen in the late stages, shock and multi-organ system failure, often with evidence of disseminated intravascular coagulopathy, ensued in the second week, with death in four of the five cases [4].

There are currently limited preventative and therapeutic options for patients infected with these highly pathogenic viruses [5].

Arenaviruses are enveloped negative-strand RNA viruses with a genome that is bi- segmented into S and L segments. The S segment encodes a nucleocapsid protein (NP) and an envelope glycoprotein precursor (GPC); the L segment encodes a matrix protein (Z) and an RNA-dependent RNA polymerase (L). The GPC is synthesized as a single polypeptide and undergoes processing by the host cell signal peptidase (SP ase) and subtilisin-like kexinisozyme-1/site-1-protease (SKI-1/S1P), yielding typical receptor binding (G1), transmembrane fusion (G2), and stable signal peptide (SSP) subunits, respectively [6-8]. Viral entry into target cells is initiated by the binding of G1 to appropriate cell surface receptors. The first cellular receptor for arenavirus to be identified was_- dystroglycan (_DG), a ubiquitous receptor for extracellular matrix proteins [9].

The understanding of epitope/antibody interaction is the key to constructing potent vaccines and effective diagnostics. The host defense mechanisms against viruses generally vary from germline-encoded immunity, which present early in the evolution of microorganisms to activation and induction of specific adaptive immune responses by the production of Th-1 andTh-2 cytokines. B-cells recognize antigens via membrane bound antibodies using B-cell receptors (BCRs), resulting in the secretion of antibodies that bind to the antigen and deactivate or remove it. Processing and presentation of peptide epitopes are essential steps in cell-mediated immunity [10]. *Lujo virus* (LUJV) is a highly fatal human pathogen belonging to the *Arenaviridae* family. This virus is unique; as it uses neuropilin-2 (NRP2) as a cellular receptor.

Previous study revealed that the GP1 receptor-binding domain of LUJV (LUJVGP1) recognizes NRP2, where its recognition is metal-ion dependent. The binding of a $Ca2^{+}$ ion stabilizes the conformations of Asp127 and Glu79 from NRP2 pre-organizing them for interaction with Lys110 of LUJVGP1. CUB domain of NRP2 is almost completely conserved among humans, mice, rats and bats, and the only slight variations occur outside of the binding site for LUJV. Hence all of these animal species have a potential to serve as reservoirs for LUJV, considering only the compatibility to NRP2 [2]. *In silico* molecular docking was performed on the GP1 domain of *Lujo virus* in complex with the first CUB domain of neuropilin-2 [2].

The aim of the study is to predict an effective epitope-based vaccine against an envelope glycoprotein precursor (GPC); of *Lujo virus*. The development of immunogenetics approaches will enhance the understanding of the genetic factors impact on the interindividual and interpopulation variations in immune responses to vaccines that could be helpful to progress new vaccine strategies [11]. In silico/reverse vaccinology had replaced conventional culture-based vaccine because it reduces the cost required for laboratory investigation of pathogen, also speeding up the time needed to achieve the results [12,13].

Therefore, using immunoinformatics approaches to predict this new kind of vaccines could be a

magnificently additive in the way forward of preventing *Lujo virus*. Normally, the investigation of the binding affinity of antigenic peptides to the MHC molecules is the main goal when predicting epitopes. The usage of such tools and information leads to the development of new vaccines. While these approaches permit the optimization of a vaccine for a specific population, It's probably can be reformulated to design a "universal vaccine" a vaccine that provides maximum coverage for the whole worlds' population [14-17]. In this study, we focused on both MHC class II and class I with performing of molecular docked in HLA-A0201.

II. MATERIALS AND METHODS

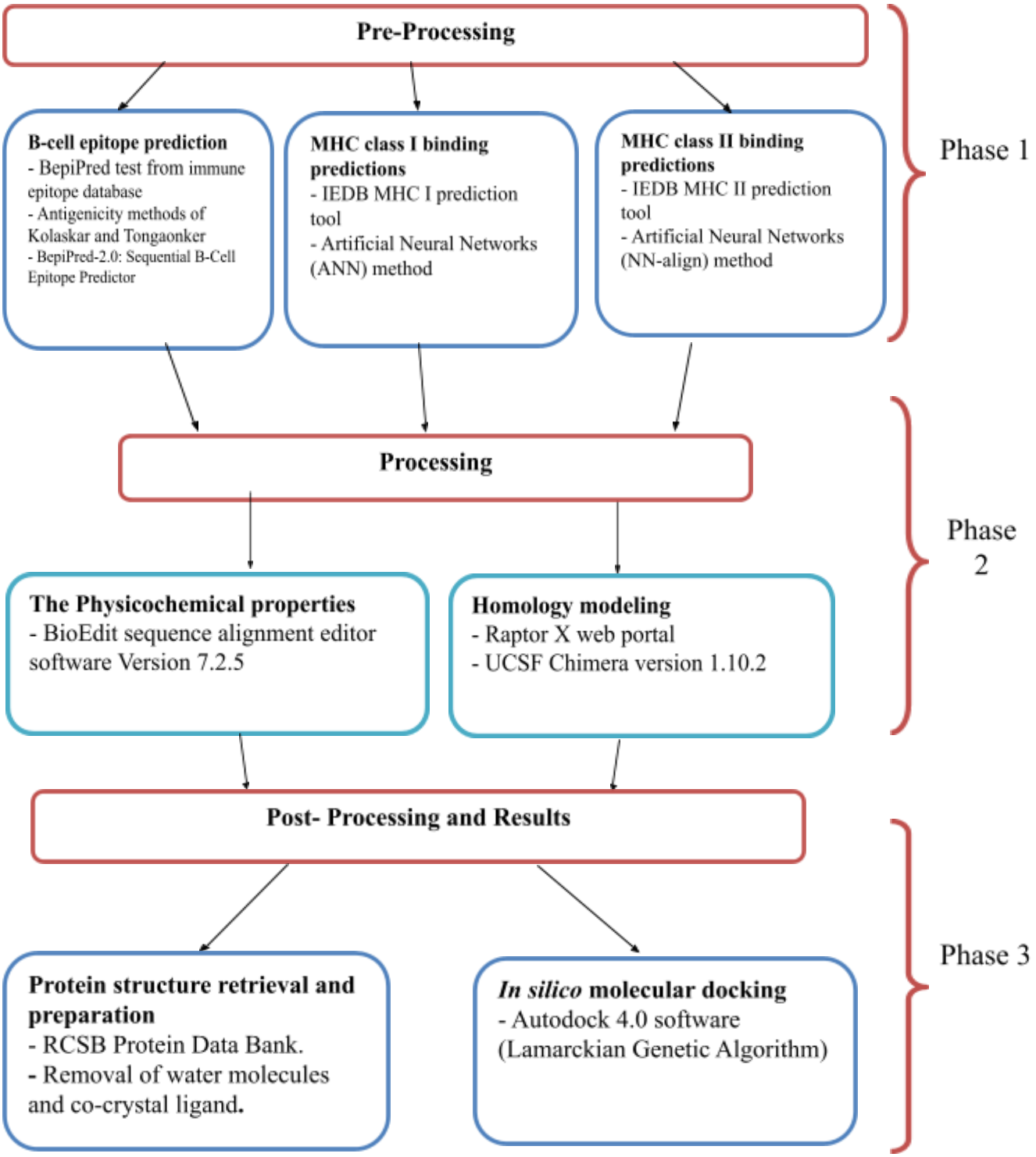

Figure 1: The Three Phases of Material and Method Process

2.1 Sequences Retrieval

The amino acids sequences of Glycoprotein GPC (Glycoside hydrolase family) of *Lujo virus* were retrieved from the NCBI database (https://www.ncbi.nlm.nih.gov/protein) [18] in FASTA format on July 2018. Different prediction tools of Immune Epitope Database IEDB analysis resource (http://www.iedb.org/) [19] were then used to analyze the candidate epitopes as shown on figure (1).

2.2 Conservation Region and Physicochemical Properties

Conservation regions were determined using multiple sequence alignment with the help of Clustal-W in the BioEdit software version 7.2.5 [20]. Epitope conservancy prediction for individual epitopes was then calculated using the IEDB analysis resource. Conservancy can be defined as the portion of protein sequences that restrain the epitope measured at or exceeding a specific level of identity [21]. The physicochemical properties of the retrieved sequence; molecular weight and amino acid composition; were also determined by BioEdit software version 7.2.5 [20].

2.3 B Cell Epitope Prediction Tools

Candidate epitopes were analyzed using several B-cell prediction methods to determine their antigenicity, flexibility, hydrophilicity, and surface accessibility. The linear prediction epitopes were obtained from the Immune epitope database (http://tools.iedb.org/bcell/result/) [22] by using the BepiPred test with a threshold value of 0.149 and a window size of 6.0.

Moreover, surface-accessible epitopes were predicated with a threshold value of 1.0 and window size of 6.0 using the Emini surface accessibility prediction tool [23].

Kolaskar and Tongaonker antigenicity methods (http://tools.iedb.org/bcell/result/) were proposed to determine the sites of antigenic epitopes with a default threshold value of 1.030 and a window size of 6.0 [24].

2.4 T cell epitope prediction tools

2.4.1 Peptide binding to MHC class I molecules

The peptide binding was assessed by IEDB MHC class I prediction tool at http://tools.iedb.org/mhc1. This tool employs different methods to determine the ability of submitted sequence to bind to a specific MHC class I molecule. The artificial neural network (ANN) method [25, 26] was used to calculate IC50 values of peptide binding to MHC- class I molecules. For both frequent and non-frequent alleles, peptide length was set to 9 amino acids earlier to the prediction. The alleles having binding affinity IC50 equal to or less than 500 nM were considered for further analysis. The affinity of 500 nM is routinely used as a threshold for peptide selection and it captures 92% of the epitopes [27- 29].

2.4.2 Peptide Binding to MHC Class II Molecules

MHC class II prediction tool http://tools.iedb.org/mhcII provided by Immune Epitope Database (IEDB) analysis resource and human allele references set was used to predict the peptide binding to MHC class II molecules. Where the Artificial Neural Network prediction method was chosen to identify the binding affinity to MHC class II grooves and MHC class II binding core epitopes. All epitopes that bind to as many alleles at score equal to or less than 1000 half-maximal inhibitory concentration (IC50) were selected for further analysis. [30].

2.5 Population Coverage

Population coverage for each epitope was calculated by the IEDB population coverage tool at http://tools.iedb.org/tools/population/iedb_input [31]. This tool was targeted in order to determine the fraction of individual alleles predicted to respond to a given set of epitopes with known MHC restrictions. For every single population coverage, the tool computed the following information: (1) predicted population coverage, (2) HLA combinations recognized by the population, and (3) HLA combinations recognized by 90% of the population (PC90). All epitopes and their MHC class I and MHC class II

molecules were assessed against a population coverage area selected prior to the submission.

2.6 Homology Modeling

The 3D structure of glycoprotein GPC of *Lujo virus* was predicted using Raptor X web portal (http://raptorx.uchicago.edu/) [32]. The reference sequence was submitted in FASTA format on 14/9/2018 and the structure was received on 15/9/2018. Subsequently the structure was treated with UCSF Chimera 1.10.2 [33] to visualize the position of the proposed peptides.

2.7 In Silico Molecular Docking

2.7.1 Ligand Preparation

In order to estimate the binding affinities between the epitopes and the molecular structure of MHC class I & MHC class II, in silico molecular docking was utilized. The proposed epitopes sequences were then selected from the *Lujo virus* reference sequence using Chimera 1.10 and saved as a "pdb" file. The obtained files were later optimized and energy minimized. The HLA-A0201 was selected as the macromolecule for docking; as HLA-A0201 is considered as the most popular MHC allele and most MHC-I epitopes were nonapeptides [34].

Its crystal structure (4UQ3) was downloaded from the RCSB Protein Data Bank (http://www.rcsb.org/pdb/home/home.do), which was in complex with an azobenzene-containing peptide [35].

The crystal structure of LUJVGP1/NRP2 was retrieved from protein databank (PDB ID: 6GH8) [2].

2.7.2 Molecular Docking

Molecular docking was performed using Autodock 4.0 software, based on Lamarckian Genetic Algorithm; which combines energy evaluation through grids of affinity potential to find the suitable binding position for a ligand on a given protein [36]. Polar hydrogen atoms were added to the protein targets and Kollman united atomic charges were computed. All hydrogen atoms were added to the ligands before the Gastiger partial charges were assigned. The co-crystal ligand was removed and the bond orders were checked. The target's grid map was calculated and set to 60×60×60 points with a grid spacing of 0.375 Å. The grid box was then allocated properly in the target to include the active residue in the center. The default docking algorithms were set in accordance with standard docking protocol [37]. Finally, ten independent docking runs were carried out for each ligand and results were retrieved as binding energies. Poses that showed the lowest binding energies were visualized using the UCSF chimera [38].

III. RESULTS

3.1. Lujo Virus Glycoprotein GPC Physical and Chemical Parameters

The physicochemical properties of the *Lujo virus* glycoprotein GPC protein was assessed using BioEdit software version 7.0.9.0. The protein length was found to be 454 amino acids. The amino acids that form *Lujo virus* glycoprotein GPC protein is shown in Figure (2) along with their numbers and molar percentages in (Mol%).

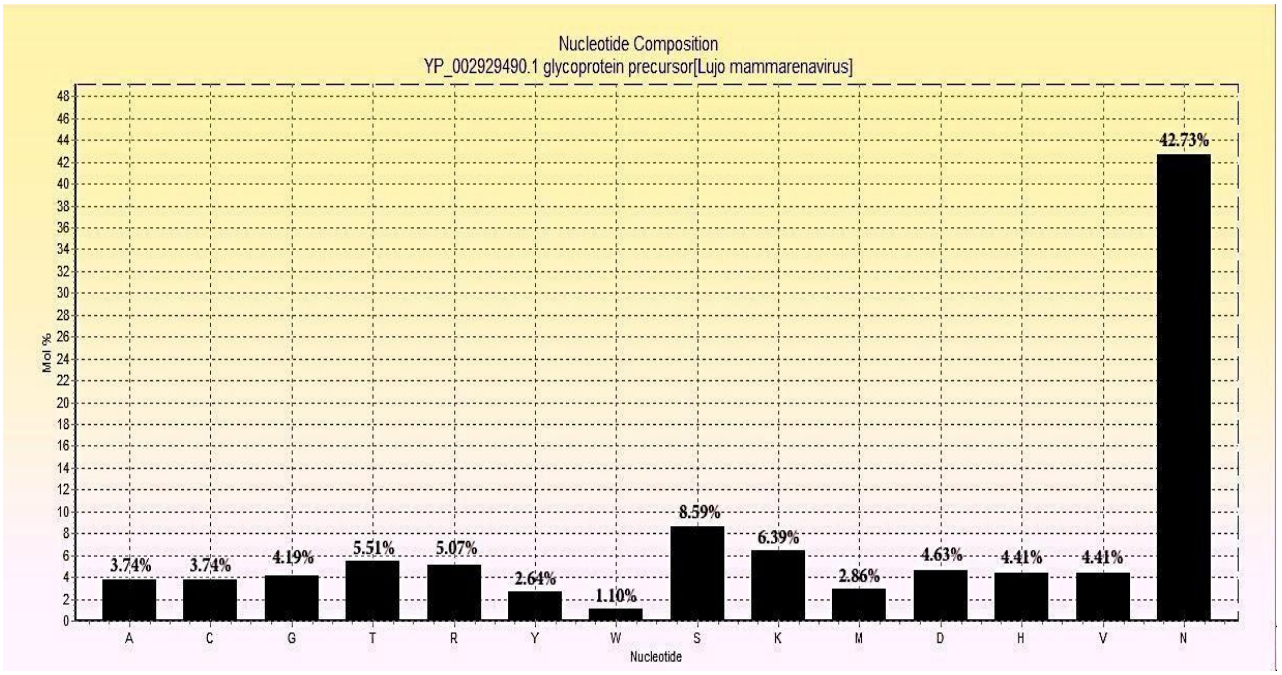

Figure 2: Amino acids composition of *Lujo virus* glycoprotein GPC using Bioedit

3.2 B-Cell Epitope Prediction

The ref sequence of the *Lujo virus* glycoprotein GPC was subjected to a Bepipred linear epitope prediction. Emini surface accessibility, Kolaskar and Tongaonkar antigenicity methods in IEDB were used to determine bindings to the B cell, testing its surface and immunogenicity. The results are shown in Table1.

Table 1: Most Linear Epitopes, High Surface Accessibility and Immunogenicity Bindings to the B Cell

No.	Start	End	Peptide	Length	Emini Surfce	scor	Kolasker & Tongankar	scor
33	423	432	LPCPKP HRLR	10	pass	1.371	pass	1.088
35	423	430	LPCPKP HR	8	pass	1.378	pass	1.095

3.3 Prediction of T Helper Cell Epitopes and Interaction With MHC Class I Alleles

Lujo virus glycoprotein GPC sequence was analyzed using IEDB MHC class I binding prediction tool based on ANN-align with half-maximal inhibitory concentration (IC_{50}) ≤**500**; the least most promising epitopes that had a binding affinity with the Class I alleles along with their positions in the *Lujo virus* glycoprotein GPC are shown in Table 2.

Table 2: Most Potential T-Cell Epitopes With Interacting MHC- Class I Alleles, Their Positions, IC50, Rank and Conservancy

Peptide	Start	End	Allele	IC50	Rank	Conservancy
Ymfsvtlci	403	411	HLA-A*02:01	3.96	0.02	
	403	411	HLA-A*02:06	43.36	0.48	
	403	411	HLA-A*23:01	121.22	0.38	
	403	411	HLA-A*29:02	77.5	0.45	
	403	411	HLA-A*32:01	116.01	0.15	

	403	411	HLA-B*15:01	92.12	0.49	100
	403	411	HLA-B*39:01	56	0.08	
	403	411	HLA-B*58:01	314.96	0.77	
	403	411	HLA-C*03:03	420.85	0.68	
	403	411	HLA-C*07:01	486.45	0.14	
	403	411	HLA-C*12:03	13.35	0.03	
	403	411	HLA-C*14:02	45.86	0.08	
Lmfsvsfym	396	404	HLA-A*02:01	4.29	0.03	100
	396	404	HLA-A*02:06	22.33	0.27	
	396	404	HLA-A*11:01	482.09	2.3	
	396	404	HLA-A*29:02	9.94	0.08	
	396	404	HLA-A*30:02	130.57	0.49	
	396	404	HLA-A*31:01	46.07	0.58	
	396	404	HLA-B*15:01	28.4	0.17	
	396	404	HLA-B*35:01	76.06	0.25	
	396	404	HLA-B*58:01	32.61	0.16	
	396	404	HLA-C*03:03	271.14	0.54	
	396	404	HLA-C*12:03	254.08	0.33	
Rlqeavstl	165	173	HLA-A*02:01	66.37	0.69	100
	165	173	HLA-A*02:06	239.83	1.7	
	165	173	HLA-A*32:01	114.21	0.15	
	165	173	HLA-B*15:01	227.04	0.93	
	165	173	HLA-C*12:03	434.14	0.5	
	165	173	HLA-C*14:02	130.18	0.22	
Fqlviflll	44	52	HLA-A*02:01	160.67	1.5	100
	44	52	HLA-A*02:06	10.35	0.13	
	44	52	HLA-B*27:05	223.21	0.83	
	44	52	HLA-B*39:01	37.81	0.06	
	44	52	HLA-B*40:01	207.49	0.39	
	44	52	HLA-B*48:01	160.64	0.02	
Msllssipm	74	82	HLA-A*02:06	287.92	1.9	100
	74	82	HLA-A*30:01	213.76	0.53	
	74	82	HLA-B*15:01	221.62	0.91	
	74	82	HLA-B*35:01	13.96	0.06	
	74	82	HLA-B*39:01	364.24	0.26	
	74	82	HLA-B*58:01	150.48	0.52	
	74	82	HLA-C*03:03	99.8	0.32	
	74	82	HLA-C*14:02	337.92	0.43	

Vifdlfref	122 122 122 122 122	130 130 130 130 130	HLA-A*02:06 HLA-A*29:02 HLA-A*32:01 HLA-B*15:01 HLA-C*12:03	362.08 430.15 329.32 50.88 424.4	2.2 1.3 0.33 0.3 0.5	100
Itfslltnk	97 97 97 97 97	105 105 105 105 105	HLA-A*03:01 HLA-A*11:01 HLA-A*30:01 HLA-A*31:01 HLA-A*68:01	16.97 9.43 173.26 95.4 14.88	0.06 0.03 0.48 1.2 0.1	100
Ilmfsvsfy	395 395 395 395 395 395 395	403 403 403 403 403 403 403	HLA-A*03:01 HLA-A*11:01 HLA-A*29:02 HLA-A*30:02 HLA-A*68:01 HLA-B*15:01 HLA-B*15:02	25.13 69.52 16.35 23.88 208.18 31.98 289.75	0.1 0.48 0.13 0.04 1.3 0.2 0.11	100
Fwylnhtkl	331 331 331 331 331	339 339 339 339 339	HLA-A*23:01 HLA-C*03:03 HLA-C*07:02 HLA-C*12:03 HLA-C*14:02	278.63 68.25 370.98 413.98 14.88	0.65 0.25 0.09 0.49 0.03	100

3.4 Prediction of T Helper Cell Epitopes and Interaction With MHC Class II Alleles

Lujo virus glycoprotein GPC sequence was analyzed using IEDB MHC class II binding prediction tool based on NN-align with half-maximal inhibitory concentration (IC_{50}) ≤1000. The list of the most promising epitopes, that had a strong binding affinity to MHC class II alleles and depending on the number of their binding alleles are shown in Table 3.

Table 3: Most potential T-cell Epitopes with Interacting MHC- Class II Alleles

Peptide	Allele	No. of Alleles
Fwylnhtkl	HLA-DRB1*01:01, HLA-DRB1*04:04, HLA-DRB1*04:05, HLA-DRB1*07:01, HLA-DRB1*08:02, HLA-DRB1*09:01, HLA-DRB1*15:01, HLA-DRB4*01:01, HLA-DRB5*01:01, HLA-DPA1*01/DPB1*04:01, HLA-DPA1*01:03/DPB1*02:01, HLA-DPA1*02:01/DPB1*01:01, HLA-DPA1*02:01/DPB1*05:01, HLA-DPA1*03:01/DPB1*04:02	14

Fnmsllssi	HLA-DRB1*04:01, HLA-DRB1*04:04, HLA-DRB1*04:05, HLA-DRB1*07:01, HLA-DRB1*09:01, HLA-DRB1*11:01, HLA-DRB3*01:01, HLA-DRB5*01:01, HLA-DPA1*01/DPB1*04:01, HLA-DPA1*01:03/DPB1*02:01, HLA-DPA1*02:01/DPB1*01:01, HLA-DPA1*03:01/DPB1*04:02, HLA-DQA1*05:01/DQB1*03:01	13
Inaiisdtl	HLA-DRB1*01:01, HLA-DRB1*03:01, HLA-DRB1*04:01, HLA-DRB1*04:04, HLA-DRB1*04:05, HLA-DRB1*07:01, HLA-DRB1*09:01, HLA-DRB1*13:02, HLA-DRB1*15:01, HLA-DRB4*01:01, HLA-DQA1*01:02/DQB1*06:02, HLA-DQA1*05:01/DQB1*02:01, HLA-DQA1*05:01/DQB1*03:01	13
Lmklfqwsl	HLA-DRB1*01:01, HLA-DRB1*04:01, HLA-DRB1*04:05, HLA-DRB1*07:01, HLA-DRB1*09:01, HLA-DRB1*15:01, HLA-DRB4*01:01, HLA-DRB5*01:01, HLA-DPA1*01/DPB1*04:01, HLA-DPA1*01:03/DPB1*02:01, HLA-DPA1*02:01/DPB1*01:01, HLA-DPA1*03:01/DPB1*04:02, HLA-DQA1*01:01/DQB1*05:01	13
Vfqaipeil	HLA-DRB1*03:01, HLA-DRB1*07:01, HLA-DRB1*09:01, HLA-DRB1*13:02, HLA-DRB4*01:01, HLA-DRB5*01:01, HLA-DPA1*01/DPB1*04:01, HLA-DPA1*01:03/DPB1*02:01, HLA-DPA1*02:01/DPB1*01:01, HLA-DPA1*03:01/DPB1*04:02, HLA-DQA1*01:01/DQB1*05:01, HLA-DQA1*05:01/DQB1*02:01, HLA-DQA1*05:01/DQB1*03:01	13
Ymfsvtlci	HLA-DRB1*01:01, HLA-DRB1*04:01, HLA-DRB1*07:01, HLA-DRB1*13:02, HLA-DRB1*15:01, HLA-DRB3*01:01, HLA-DRB5*01:01, HLA-DPA1*01/DPB1*04:01, HLA-DPA1*01:03/DPB1*02:01, HLA-DPA1*02:01/DPB1*05:01, HLA-DPA1*03:01/DPB1*04:02, HLA-DQA1*01:02/DQB1*06:02, HLA-DQA1*05:01/DQB1*03:01	13

3.5 Population Coverage

A population coverage test was performed to detect all the epitopes that bind to MHC class I alleles and MHC class II alleles available in the database in relation to the world, South Africa, and Sudan.

Table 4: APopulation Coverage for All Epitopes That Bind to MHC Class I and II Alleles From Different Parts of the World

MHC classes	Population	World	South Africa	Sudan
Class I	Coverage[a]	99.83%	99.4%	99.41%
	Average_hit[b]	32.5	25.45	28.25
	PC90[c]	13.28	8.99	8.76
Class II	Coverage[a]	68.23%	32.1%	56.38%
	Average_hit[b]	55.22	10.89	34.14
	PC90[c]	-6.57	4.71	5.57

[a] projected population coverage
[b] average number of epitope hits / HLA combinations recognized by the population
[c] minimum number of epitope hits / HLA combinations recognized by 90% of the population.

Table 5: Population Coverage of the Proposed Peptides in MHC Class I and MHC Class II in Five Areas

Peptide	Population coverage %/ Area								
	World			South Africa			Sudan		
	MHC I	MHC II	MHC I & II	MHC I	MHC II	MHC I & II	MHC I	MHC II	MHC I & II
Ymfsvtlci	73.92%	56.92%	88.77%	63.56%	5.91%	65.72%	75.17%	21.85%	80.6%
Fwylnhtkl	42.99%	55.84%	74.82%	41.97%	1.79%	43.01%	35.12%	25.35%	51.56%

3.6 3D Structure

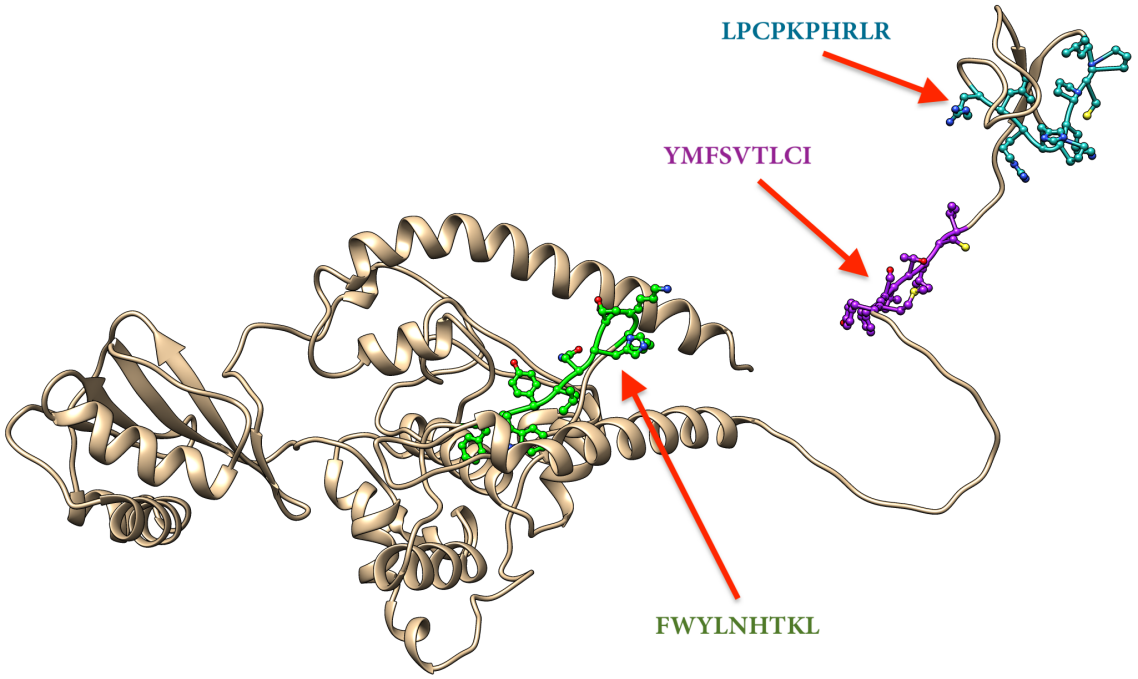

Figure 3: The Four Potential Peptides Bound to MHC Class I, MHC Class II and B Cell Visualized by Chimera 1.10.2

3.7 Molecular Docking

Three peptides; FWYLNHTKL, LPCPKPHRLR and YMFSVTLCI were docked onto protein target of GP1 domain of *Lujo virus* in complex with the first CUB domain of NRP2.

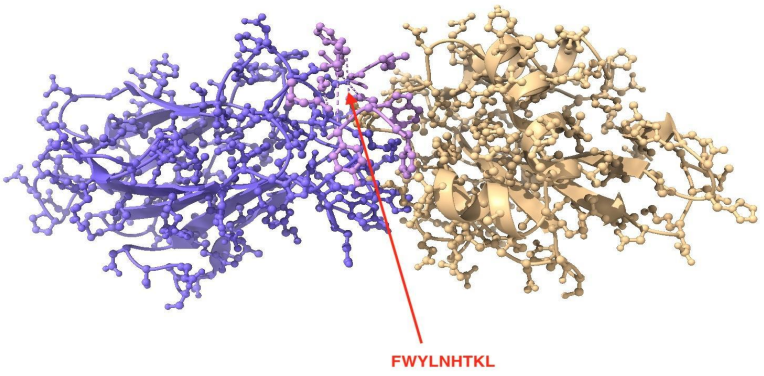

Figure 4: Peptide-1 FWYLNHTKL

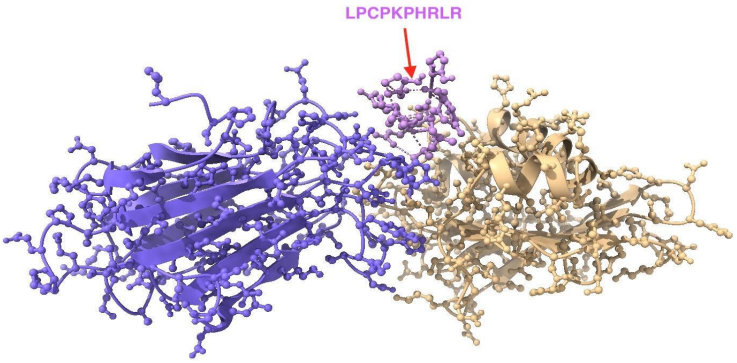

Figure 5: Peptide-2 LPCPKPHRLR

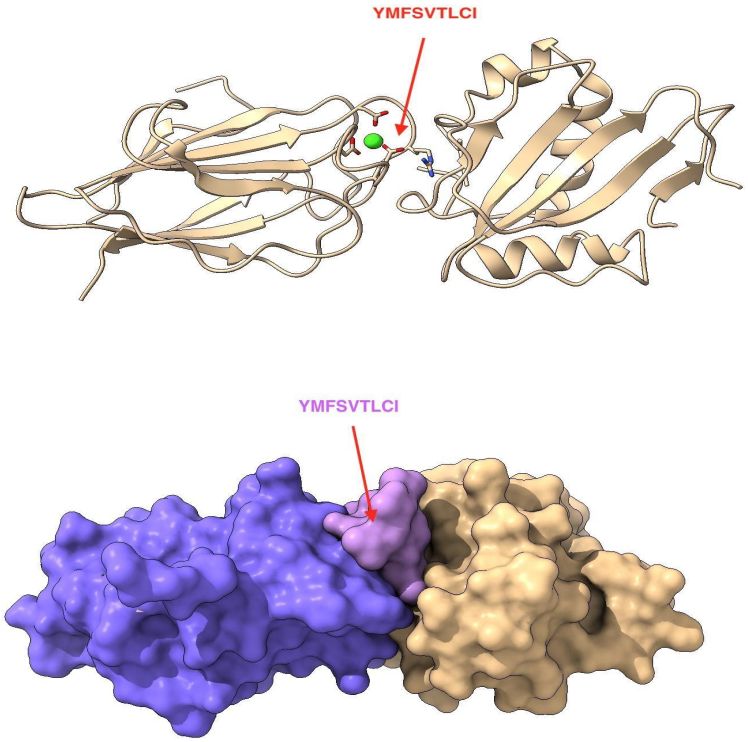

Figure 6: Peptide-3 YMFSVTLCI

IV. DISCUSSION

In this computational immunoinformatic study we suggest a new promising highly selective peptides vaccine against *Lujo virus* for the first time according to our findings. We expect to obtain a peptide-based vaccine which implies a high antigenicity and a minimum allergic outcome that is more accurate than the currently used vaccines. The analytical process started after having adequate information on the protein structure of *Lujo virus* according to the literature review. Simultaneously, though the 3D structure was previously available on the database with all its prospects, we produced our own structure using Raptor X web portal to utilize its complete physiochemical properties information file to confirm our results, and it's a technique we have pursued. The reference sequence of *Lujo virus* glycoprotein GPC was obtained from the NCBI database. To determine the binding affinity of the

conserves epitopes to B-cell and to examine the immunogenicity several tests on the IEDB database were used; the Bepipred linear epitope prediction test, Emini surface accessibility test, and Kolaskar and Tongaonkar antigenicity test were examined. For the Bepipred test of B-cell, the total number of epitopes was 39. For Emini surface accessibility prediction, 29 conserved epitopes were passing the default threshold of 1.0.

In Kolaskar and Tongaonkar antigenicity, 7 epitopes provided a score above the default threshold 1.045. However, there are only two epitopes that passed our three tests, which were (LPCPKPHRLR, LPCPKPHR). The reference glycoprotein GPC strain was analyzed using IEDB class MHC- class I binding prediction tool to predict T cell epitope. 165 peptides were predicted to interact with different class MHC- class I alleles. For class MHC- class II binding prediction, there were 315 epitopes found to interact with class MHC- class II alleles. The peptides YMFSVTLCI, LMFSVSFYM, RLQEAVSTL, FQLVIFLLL, MSLLSSIPM, VIFDLFREF, ITFSLLTNK, ILMFSVSFY and FWYLNHTKL had the affinity to bind with the highest number of class MHC- class I alleles. The peptides FWYLNHTKL, YMFSVTLCI, FNMSLLSSI, INAIISDTL, LMKLFQWSL and VFQAIPEIL had the affinity to bind with the highest number of class MHC- class II alleles.

The most promising three peptides for both class MHC- class I and MHC- class II were FWYLNHTKL, LPCPKPHRLR and YMFSVTLCI as shown on figure (3). On the other hand, the world Population coverage of all epitopes that bind to MHC- class I were found to be 99.83%, while the world population coverage of all epitopes that bind to MHC- class II were 68.23% as presented in table 4. For the binding affinity to MHC- class I and MHC- class II the peptide FWYLNHTKL was found to bind 14 different alleles of MHC- class II & five alleles of MHC- class I, that gave a world population coverage of 74.82% , 43.01% for South Africa and 51.56% for Sudan of both MHC class I and II as shown on table 5. This finding shows a very strong potential to formulate an epitopes-based peptide vaccine for *Lujo virus*. The binding affinity of the peptide YMFSVTLCI to both class MHC- class I and MHC- class II alleles were found to be 13 different alleles with world population coverage 88.77%, 65.72% for South Africa and 80.6% for Sudan of both MHC class I and II as shown on table 5.

According to these interesting findings, a very promising vaccine against *Lujo virus* can potentially be formulated. The most promising three peptides; FWYLNHTKL, LPCPKPHRLR and YMFSVTLCI were docked on to protein target of GPC domain of *Lujo virus* in complex with the first CUB domain of NRP2 as shown on figure (4 – 6). All peptides were docked on the interface of *Lujo virus* GPC/NRP2 and scored binding energies of -5.84, -3.88 and -8.20 Kcal/mol for peptides 1, 2 and 3, respectively. As the docking results from the analysis of peptide-1 showed binding hydrogen bonding with two amino acid residues: SER-51 and GLN-131 of NRP2. While, Peptide-2 showed a bonding affinity to hydrogen with residues HIS-131 and PHE-137 of *Lujo virus* GPC and ARG-432 of NRP2, whereas peptide-3 formed hydrogen bonds with PHE-137 of *Lujo virus* GPC.

Only Peptide-2 and 3 interact by forming hydrogen bonding with residues on *Lujo virus* GPC (HIS-131 and PHE-137). These residues are located at a hydrophobic pocket and adjacent to both residues Val139 and Thr140 of the α2β4 loop which participates in Van der Waals interactions with NRP2 residues. In addition, histidine residues in the *Lujo virus* GPC/NRP2 complex are obvious candidates for controlling pH-dependent protein-protein interactions.

As for peptide-1, it has formed hydrogen bonds with GLN-131 of NRP2, which is adjacent to the key residue Arg130 that is important for NRP2-fc to recognize *Lujo virus* GPC-bearing cells and cell entry of *Lujo virus* [2]. The overall docking results analysis has revealed that the peptides are docked at *Lujo virus* GPC/NRP2 binding surfaces, in which these peptides would serve as potential inhibitors for blocking binding to NRP2 and thus may neutralize the virus.

V. CONCLUSIONS

To the best of our knowledge, this study is considered to be the first to propose an epitope-based peptide vaccine against glycoprotein GPC of *Lujo virus*, which is expected to be highly antigenic with a minimum allergic impact. Furthermore, this study proposes a promising peptide FWYLNHTKL with a very strong binding affinity to MHC1 and MHC11 alleles. This peptide shows exceptional population coverage results for both MHC1 and MHC11 alleles.

In-vivo and in-vitro assessments for the most promising peptides namely, FWYLNHTKL, LPCPKPHRLR and YMFSVTLCI are recommended to be explored and studied on their ability to be developed into vaccines against *Lujo virus* glycoprotein GPC.

Competing Interests

The authors declare that they have no competing interests.

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ABSTRACT

The current study aims to build an objective tool using the computer to diagnose psychotic disorders and mental illness among university students, provided that the battery paragraphs are prepared from the exploratory study of measures of psychotic disorders and mental illness according to the fifth Diagnostic and Statistical Manual DSM-5. The study also aims to verify the criteria for the stability and validity of the computerized scale applied to a sample of undergraduate students with special needs and normal according to the specification features contained in the fifth Diagnostic Statistical Manual DSM-5, which is the stage in which students are in dire need of identifying and diagnosing psychotic disorders and mental illness, without the need for an experienced and trained specialist in the diagnosis process, and so that it can be applied by non-specialist caregivers, and at the same time obtain a diagnosis Specific and precise mental illness or disorder.

Keywords: psychotic disorders, mental illness, special needs.

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I. INTRODUCTION

Many college students may experience the persistence, exacerbation, or first onset of mental health and substance use problems, while possibly receiving no or inadequate treatment. With the increasing recognition of child mental health issues and the use of more psychotropic medications, the number of young adults with mental health problems entering college has significantly increased. For example, in a survey of 274 institutions, 88 % of counseling center directors reported an increase in "severe" psychological problems over the previous 5 years including learning disabilities, self-injury incidents, eating disorders, substance use, and sexual assaults. Thus, there is an increase in demand for counseling and specialized services. However, the increase in demands has not always corresponded to an increase in staff. In particular, counseling centers are in need of psychiatrists with expertise in treating traditional as well as non-traditional college students, two groups with specific age-related characteristics and challenges. In this commentary, the prevalence of psychiatric and substance use problems in college students, as well as their common onset, will be described. Next, the worrisome persistent nature of mental health problems among college students and its implication will be discussed. Finally, important treatment considerations for traditional and non-traditional college students will be outlined. (Pedreli et al., 2015:503).

1.1 Purpose of the Study

The current study aims to build an objective tool using the computer to diagnose psychotic disorders and mental illness among university students, provided that the battery paragraphs are prepared from

the exploratory study of measures of psychotic disorders and mental illness according to the fifth Diagnostic and Statistical Manual DSM-5.

The inventory will contain the following subtests:

- Scale of neurodevelopmental disorders.
- Scale of Bipolar and related disorders.
- Anxiety Disorders scale.
- Scale of Trauma and stressor- Related disorders.
- Dissociative Disorders.
- The scale of problem solving disabilities.
- Scale of Feeding and eating disorders.
- Scale sleep – Wake disorders.
- Scale of Disruptive impulsive- Control and Conduct Disorders.
- Neurocognitive Disorders Scale.
- Personality Disorders Scale.

1.2 Significance of the Study

Theoretical importance: The theoretical importance of the current study lies in its handling of a new concept in contemporary psychological literature, which is the assessment of psychotic disorders and mental illness using a computer, according to the fifth Diagnostic and Statistical Manual as follows:

- Scale of neurodevelopmental disorders.
- Scale of Bipolar and related disorders.
- Anxiety Disorders scale.
- Scale of Trauma and stressor- Related disorders.
- Dissociative Disorders.
- The scale of problem solving disabilities.
- Scale of Feeding and eating disorders.
- Scale sleep – Wake disorders.
- Scale of Disruptive impulsive- Control and Conduct Disorders.
- Neurocognitive Disorders Scale.
- Personality Disorders Scale.

Which the Arab studies did not adequately address - as within the limits of the researcher's knowledge - and because of the importance of this computerized scale in the diagnostic curve of psychotic disorders and mental illnesses, and what it entails in reducing the impact of these disorders at the university level.

1.3 Practical Importance

The applied importance of the current study lies in the possibility of using the list of psychotic disorders and computerized mental illnesses at the university stage, so that it can be developed and benefited from in the field of early diagnosis of these disorders and identifying their causes as a first step in diagnosis, and then preparing for the preparation of appropriate treatment programs and early intervention.

II. REVIEW OF LITERATURE

Attending college can be a stressful time for many students. In addition to coping with academic pressure, some students have to deal with the stressful tasks of separation and individuation from their family of origin while some may have to attend to numerous work and family responsibilities (Pedreli et al., 2015:503).

McMillan et al. (2013: 3) have found that Students with disabilities are at increased risk of experiencing mental health difficulties, but may not be recognized as an at-risk population in the design of school-based prevention and intervention efforts.

Studies of the prevalence of personality disorders have been fewer and smaller-scale, but one broad Norwegian survey found a five-year prevalence of almost 1 in 7 (13.4%). Each year 73 million women are affected by major depression, and suicide is ranked 7th as the cause of death for women between the ages of 20–59. Psychotropic medications are available in Bangladesh but psychotherapy is hardly available

Cadge et al. (2019) attempted to explore lay understanding and perceptions of schizophrenia in university students using Qualitative study using semi-structured interviews and thematic analysis at The University of Birmingham, West Midlands. The study was applied on 20 UK home students of white British (n=5), Indian (n=5), Pakistani (n=5), African Caribbean (n=4) and dual white British and African Caribbean ethnicity (n=1). Findings revealed a lack of knowledge about schizophrenia, particularly the negative symptoms that were not mentioned.

Kabir and Ashraful (2017) conducted a study that is an attempt to explore an empirical investigation on the search for psychological problems among the students in Bangladesh. The sample was composed of 300 respondents. A 2× 2×2 factorial design involving 2 levels of gender (male vs. female), 2 levels of residence (urban vs. rural) and 2 levels of students' category (science vs. humanities) were used. It was to study the psychological problems of 17 to 18 years old students. Four psychological problems such as anxiety, depression, obsessive compulsive disorder and eating disorder were found. These four problems are related with mentioned six categories at P at $P<0.01$ level and ANOVA were significant at $P<0.05$ level. It was found that students of humanities group were more vulnerable with these problems as compared to the students of science group.

On the other side, Furnham et al. (2011) had a study to explore the mental health literacy of students. This study is part of the growing interest in mental health literacy among young people. Design/methodology/approach – Over 400 university students indicated their knowledge of over 90 psychiatric illnesses labels derived from DSM:IV. They rated disorders on six questions concerning whether they had heard of the disorder; knew anybody with it; could define or describe it; knew what causes it; whether those with it can be cured; and whether it is common.

Findings – On average, participants had heard of just over one-third of the various illnesses. Those who rated the conditions as more common deemed them to have more known causes and to be more curable. Emotionally intelligent, open-to-experience females who had studied relevant academic subjects claimed to be better informed. The participant's age and personality.

III. METHODOLOGY

The study will be carried out in university and will be applied on a sample of students with or without special needs. the study will adopt the descriptive method.

Study group: The population of the study will be from university students
Study sample: The researcher will choose two samples of university students: a group of university students with special needs, and a group of normal.
Tools: A battery of psychotic and mental illness using a computer that contains the following tests:

- Scale of neurodevelopmental disorders.
- Scale of Bipolar and related disorders.
- Anxiety Disorders scale.

- Scale of Trauma and stressor- Related disorders.
- Dissociative Disorders.
- The scale of problem solving disabilities.
- Scale of Feeding and eating disorders.
- Scale sleep – Wake disorders.
- Scale of Disruptive impulsive- Control and Conduct Disorders.
- Neurocognitive Disorders Scale.
- Personality Disorders Scale

3.1 Applied Study

This section discusses the descriptive analysis for study sample and study variable as following:

Descriptive analysis for study sample: A sample of 20 university students who suffer from mental disorders and developmental delays was selected as an experimental sample, and 20 university students from normal students were identified as a control sample, and in Table (1) a description of the two groups is presented.

Table 1: Study Groups of Sample

		Frequency	Percent	Chi-Square	df	P-Value
Groups	students with special needs	20	50.0			
	Normal	20	50.0	.000	1	1.000
	Total	40	100.0			

Reliability Tests of the Study Tool: This part presents the test of validity and reliability of the proposed scale for the study, and to what extent this scale can be relied upon and used in diagnosing students' cases. This section will organize as follow:

Reliability Tests: Reliability analysis allows you to study the properties of measurement scales and the items that compose the scales. The Reliability Analysis procedure calculates a number of commonly used measures of scale reliability and also provides information about the relationships between individual items in the scale. Test results shows in table (2).

Table 2: Reliability Statistics

Cronbach's Alpha		N of Items	
.950		68	
Case Processing Summary			
		N	%
Cases	Valid	38	95.0
	Excluded	2	5.0
	Total	40	100.0

From the previous table the Cronbach's alpha was 95% this means that the research tool is reliable, researcher can depend on it and complete the study procedures.

Consistency Tests of the Study tool: The consistency of research tool was test by correlation test to know how every dimension measure the objective which related it. The results of correlation test in table (3)

Table 3: Correlation Matrix

		D1	D2	D3	D4	D5	D6	D7	D8	D9	D10	D11	Y
D1	Pearson Correlation	1											
D2	Pearson Correlation	.729**	1										
D3	Pearson Correlation	.827**	.720**	1									
D4	Pearson Correlation	.647**	.614**	.674**	1								
D5	Pearson Correlation	.746**	.591**	.759**	.727**	1							
D6	Pearson Correlation	.409**	.485**	.573**	.588**	.552**	1						
D7	Pearson Correlation	.668**	.620**	.725**	.596**	.663**	.348*	1					
D8	Pearson Correlation	.679**	.727**	.749**	.747**	.656**	.492**	.756**	1				
D9	Pearson Correlation	.596**	.676**	.667**	.691**	.730**	.698**	.534**	.709**	1			
D10	Pearson Correlation	.629**	.647**	.704**	.710**	.709**	.702**	.540**	.664**	.799**	1		
D11	Pearson Correlation	.647**	.614**	.674**	1.000**	.727**	.588**	.596**	.747**	.691**	.710**	1	
Y	Pearson Correlation	.803**	.794**	.866**	.883**	.857**	.718**	.759**	.863**	.860**	.863*	.883**	1

The previous table shows that the correlation coefficient of the lowest dimensions was 71.8%, means that the research tool is able to measure what it was designed to measure and reliable. The highest correlation coefficient was 88.3%, means that there is a strong relationship between all dimensions of the scale and purpose from measurement.

3.4 Descriptive Analysis for Study Tool Dimensions

Scale of neurodevelopmental disorders: The statistical analysis results of this dimension were as follow: Frequency and Chi-square tests: The results of descriptive tests show in table (4).

Table 4: Descriptive Analysis for D1

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
Intellectual disabilities, Intellectual development disorder	mild disease middle disease strong disease Total	24 11 5 40	13.3 13.3 13.3	14.150[a]	2	.001
Delayed overall growth	mild disease middle disease strong disease Total	19 14 7 40	10.0 10.0 10.0 10.0	19.400[b]	3	.000
Unspecified intellectual disability	mild disease middle disease strong disease Total	16 16 8 40	13.3 13.3 13.3	3.200[a]	2	.202
Communication disorders	mild disease middle disease strong disease Total	21 10 9 40	10.0 10.0 10.0 10.0	20.600[b]	3	.000
Language disorder, Speech sound disorder	mild disease middle disease strong disease Total	26 12 2 40	13.3 13.3 13.3	21.800[a]	2	.000
Infantile onset of stuttering fluency disorder, Practical social communication disorder	mild disease middle disease strong disease Total	28 9 3 40	10.0 10.0 10.0 10.0	47.000[b]	3	.000

Unspecified Communication Disorder, Autism spectrum disorder	mild disease middle disease strong disease Total	24 13 3 40	10.0 10.0 10.0 10.0	35.000[b]	3	.000
Attention Deficit/Hyperactivity Disorder, Other Specific Attention Deficit /Hyperactivity Disorder, Unspecified Attention Deficit/Hyperactivity Disorder	mild disease middle disease strong disease Total	26 11 3 40	10.0 10.0 10.0 10.0	40.200[b]	3	.000
Specific learning disorder	mild disease middle disease strong disease Total	16 16 7 40	10.0 10.0 10.0 10.0	29.000[b]	3	.000
Movement disorders Developmental coordination disorder, stereotyped movement disorder	mild disease middle disease strong disease Total	23 14 3 40	10.0 10.0 10.0 10.0	15.200[b]	3	.002

The previous table shows that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant deficiencies between Study Groups.

T-test for two Groups: The T-test results shown in table (5)

Table 5: T-Test Results for D1

	Study Groups	N	Mean	T-Test for Equality of Means		
				T	Df	Sig. (2-Tailed)
Intellectual disabilities, Intellectual development disorder	students with special needs	20	1.8500			
	Normal	20	1.2000	3.193	38	.003
Delayed overall growth	students with special needs	20	2.1000	3.193	28.0	.003
	Normal	20	1.3500	3.241	38	.002
Unspecified intellectual disability	students with special needs	20	2.3500	3.241	29.1	.003
	Normal	20	1.2500	6.681	38	.000
Communication disorders	students with special needs	20	2.1500	6.681	35.3	.000
	Normal	20	1.3000	3.474	38	.001
Language disorder, Speech sound disorder	students with special needs	20	1.4500	3.474	31.4	.002
	Normal	20	1.3500	.531	38	.599
Infantile onset of stuttering fluency disorder, Practical social communication disorder	students with special needs	20	1.5000	.531	34.3	.599
	Normal	20	1.3000	.890	38	.379
Unspecified Communication Disorder, Autism spectrum disorder	students with special needs	20	1.7500	.890	37.8	.379
	Normal	20	1.2500	2.330	38	.025
Attention Deficit/Hyperactivity Disorder, Other Specific Attention Deficit /Hyperactivity Disorder, Unspecified Attention Deficit/Hyperactivity Disorder	students with special needs	20	1.7000	2.330	28.6	.027
	Normal	20	1.2000	2.337	38	.025
Specific learning disorder	students with special needs	20	1.9000	2.337	27.1	.027
	Normal	20	1.2500	3.025	38	.004

Movement disorders Developmental coordination disorder, stereotyped movement disorder	students with special needs	20	2.3000	3.025	28.6	.005
	Normal	20	1.4000	3.828	38	.000

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. It is clarify that the smallest mean was 1.2 for the normal group, but the greatest mean was 2.35 for students with special needs group, this means that the impact of drugs was strong on group two.

Scale of Bipolar and related disorders: The statistical analysis results of this dimension was as follow: Frequency and Chi-square tests: The results of descriptive tests show in table (6)

Table 6: Descriptive Analysis for D2

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
Exaggerated or grandiose self-esteem.	mild disease middle disease strong disease deep disease Total	24 13 2 1 40	10.0 10.0 10.0 10.0	35.000[a]	3	.000
Decreased need for sleep (for example, feeling rested after sleeping only 3 hours).	mild disease middle disease strong disease deep disease Total	26 10 3 1 40	10.0 10.0 10.0 10.0	38.600[a]	3	.000
More chatter than usual or pressure to keep talking.	mild disease middle disease strong disease deep disease Total	22 13 3 2 40	10.0 10.0 10.0 10.0	26.600[a]	3	.000
Flying ideas or a personal experience of racing ideas.	mild disease middle disease strong disease deep disease Total	22 13 4 1 40	10.0 10.0 10.0 10.0	27.000[a]	3	.000
Distraction (easily diverting attention to unimportant or irrelevant external stimuli). As reported or observed.	mild disease middle disease strong disease deep disease Total	25 10 3 2 40	10.0 10.0 10.0 10.0	33.800[a]	3	.000

From the previous table, the results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (7).

Table 7: T-Test Results for D2

	Study Groups	N	Mean	T-Test for Equality of Means		
				T	Df	Sig. (2-Tailed)
Exaggerated or grandiose self-esteem.	students with special needs	20	1.750	2.33	38	.025
	Normal	20	1.250	2.33	28.64	.027
Decreased need for sleep	students with special needs	20	1.800	3.00	38	.005

	Normal	20	1.150	3.00	25.20	.006
More chatter than usual or pressure to keep talking.	students with special needs	20	1.900	2.17	38	.036
	Normal	20	1.350	2.17	27.29	.039
Flying ideas or a personal experience of racing ideas.	students with special needs	20	2.000	3.76	38	.001
	Normal	20	1.200	3.76	27.25	.001
Distraction (easily diverting attention to unimportant or irrelevant external stimuli).	students with special needs	20	1.900	2.84	38	.007
	Normal	20	1.200	2.84	24.98	.009

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. We can show that the less mean was 1.2 for the normal group, but the greater mean was 2.00 for students with special needs group, this means that the impact of drugs was strong on group two.

Anxiety Disorders scale: The statistical analysis results of this dimension was as follow: Frequency and Chi-square tests: The results of descriptive tests show in table (8).

Table 8: Descriptive Analysis for D3

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
Repeated excessive discomfort) of this view strongly.	mild disease middle disease strong disease deep disease Total	24 13 3 40	13.3 13.3 13.3	16.550[a]	2	.000
A separation that forces separation from someone who is very attached to his occurs	mild disease middle disease strong disease deep disease Total	23 11 2 4 40	10.0 10.0 10.0 10.0	27.000[b]	3	.000
(Continuous and interval, middle, interval, foul) as disease, ratio, catastrophe, or the death.	mild disease middle disease strong disease deep disease Total	22 12 4 2 40	10.0 10.0 10.0 10.0	24.800[b]	3	.000
Continuous and excessive fear that an unfortunate event will occur) such as being lost, being kidnapped, having an accident,	mild disease middle disease strong disease deep disease Total	23 10 3 4 40	10.0 10.0 10.0 10.0	25.400[b]	3	.000
Illness (will cause separation from a person with whom he is related)	mild disease middle disease strong disease deep disease Total	22 12 3 3 40	10.0 10.0 10.0 10.0	24.600[b]	3	.000
Continuous objection or refusal of an outsider to an outsider such as school, work or other places because of Fear of separation.	mild disease middle disease strong disease deep disease Total	21 12 4 3 40	10.0 10.0 10.0 10.0	21.000[b]	3	.000

Excessive persistent fear or reluctance, because we are alone or open at home or other places.	mild disease middle disease strong disease deep disease Total	16 14 6 4 40	10.0 10.0 10.0 10.0	33.800[b]	3	.000

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (9)

Table 9: T-Test Results for D3

	Study Groups	N	Mean	T-Test for Equality of Means		
				T	Df	Sig. (2-Tailed)
Repeated excessive discomfort) of this view strongly.	students with special needs	20	1.7000	2.349	38	.024
	Normal	20	1.2500	2.349	31.307	.025
A separation that forces separation from someone who is very attached to his occurs	students with special needs	20	2.1000	3.048	38	.004
	Normal	20	1.2500	3.048	24.409	.005
(Continuous and interval, middle, interval, foul) as disease, ratio, catastrophe, or the death.	students with special needs	20	2.0000	2.774	38	.009
	Normal	20	1.3000	2.774	30.701	.009
Continuous and excessive fear that an unfortunate event will occur) such as being lost.	students with special needs	20	2.1500	3.187	38	.003
	Normal	20	1.2500	3.187	24.262	.004
Illness (will cause separation from a person with whom he is related)	students with special needs	20	2.0500	2.806	38	.008
	Normal	20	1.3000	2.806	25.729	.009
Continuous objection or refusal of an outsider to an outsider such as school, work or other places.	students with special needs	20	2.1500	3.204	38	.003
	Normal	20	1.3000	3.204	25.840	.004
Excessive persistent fear or reluctance, because we are alone or open At home or other places.	students with special needs	20	1.7000	1.125	38	.267
	Normal	20	1.4000	1.125	30.490	.269

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. We can show that the less mean was 1.30 for the normal group, but the greater mean was 2.45 for students with special needs group, this means that the impact of drugs was strong on group two.

Scale of Trauma and stressor- Related disorders: The statistical analysis results of this dimension was as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (10).

Table 10: Descriptive Analysis for D4

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
Feeling unusually restless.	mild disease middle disease strong disease deep disease Total	21 12 4 3 40	10.0 10.0 10.0 10.0	21.000[a]	3	.000

Difficulty concentrating due to anxiety.	mild disease middle disease strong disease deep disease Total	23 11 5 1 40	10.0 10.0 10.0 10.0	27.600[a]	3	.000
Fear of something awful that might happen.	mild disease middle disease strong disease deep disease Total	16 16 5 3 40	10.0 10.0 10.0 10.0	14.600[a]	3	.002
Feeling that the individual may lose control of himself	mild disease middle disease strong disease deep disease Total	14 17 6 3 40	10.0 10.0 10.0 10.0	13.000[a]	3	.005

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (11)

Table 11: T-Test Results for D4

	Study Groups	N	Mean	Std. Deviation	T-Test for Equality of Means		
					T	Df	Sig. (2-Tailed)
Feeling unusually restless.	students with special needs	20	2.1000	1.11921	2.746	38	.009
	Normal	20	1.3500	.48936	2.746	26.009	.011
Difficulty concentrating due to anxiety.	students with special needs	20	1.9500	.94451	2.999	38	.005
	Normal	20	1.2500	.44426	2.999	27.015	.006
Fear of something awful that might happen.	students with special needs	20	2.4000	.94032	4.430	38	.000
	Normal	20	1.3500	.48936	4.430	28.588	.000
Feeling that the individual may lose control of himself	students with special needs	20	2.5500	.82558	5.592	38	.000
	Normal	20	1.3500	.48936	5.592	30.884	.000

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. We can show that the less mean was 1.30 for the normal group, but the greater mean was 2.45 for students with special needs group, this means that the impact of drugs was strong on group two.

Dissociative Disorders: The statistical analysis results of this dimension were as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (12).

Table 12: Descriptive Analysis for D5

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
See the avatar in some avatars in some avatar examples.	mild disease middle disease strong disease deep disease Total	22 13 3 2 40	10.0 10.0 10.0 10.0	26.600	3	.000
Knowing about the desire to feel sexualits farewell, memory, awareness, cognition, readiness, and Arabic.	mild disease middle disease strong disease deep disease Total	22 10 6 2 40	10.0 10.0 10.0 10.0	22.400	3	.000
These signs and symptoms may be noticed by others .	mild disease middle disease strong disease deep disease Total	19 15 4 2 40	10.0 10.0 10.0 10.0	20.600	3	.000
Frequent loopholes in recalling events of daily life, important personal information.	mild disease middle disease strong disease deep disease Total	20 14 5 1 40	10.0 10.0 10.0 10.0	22.200	3	.000
Symptoms are inferior or consequential. Good market. Children who show their symptoms in symptoms.	mild disease middle disease strong disease deep disease Total	17 15 4 4 40	10.0 10.0 10.0 10.0	14.600	3	.002

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (13)

Table 13: T-Test Results for D5

		T-Test for Equality of Means		
		T	Df	Sig. (2-Tailed)
See the avatar in some avatars in some avatar examples.	Equal variances assumed	2.633	38	.012
	Equal variances not assumed	2.633	27.028	.014
Knowing about the desire to feel sexual, its farewell, memory, awareness, cognition, readiness, Arabic, and Arabic.	Equal variances assumed	4.759	38	.000
	Equal variances not assumed	4.759	24.349	.000
These signs and symptoms may be noticed by others .	Equal variances assumed	3.637	38	.001
	Equal variances not assumed	3.637	28.060	.001
Frequent loopholes in recalling events of daily life, important personal information, and/or traumatic events that--contrary to normal forgetfulness.	Equal variances assumed	2.795	38	.008
	Equal variances not assumed	2.795	28.998	.009

Symptoms are inferior or consequential. Good market. Children who show their symptoms. Other medical condition complex partial seizures	Equal variances assumed	4.065	38	.000
	Equal variances not assumed	4.065	26.933	.000

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups.

The scale of problem-solving disabilities: The statistical analysis results of this dimension was as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (14).

Table 14: Descriptive Analysis for D6

		Observed N	Expected N	Chi-Square	Df	Asymp. Sig.
Difficulties in mathematical thinking,.	mild disease middle disease strong disease deep disease Total	23 13 3 1 40	10.0 10.0 10.0 10.0	30.800[a]	3	.000
Poor ability to use feedback to infer rules and solve problems.	mild disease middle disease strong disease deep disease Total	21 14 5 40	13.3 13.3 13.3	9.650[b]	2	.008
Controversy that may escalate into the threat of physical violence, avoiding problem solving.	mild disease middle disease strong disease deep disease Total	18 17 3 2 40	10.0 10.0 10.0 10.0	22.600[a]	3	.000

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (15)

Table 15: T-Test Results For D6

	Study Groups	N	Mean	T-Test for Equality of Means		
				T	Df	Sig. (2-Tailed)
Difficulties in mathematical thinking.	students with special needs	20	1.8000	2.213	38	.033
	Normal	20	1.3000	2.213	28.755	.035
Poor ability to use feedback to infer rules and solve problems.	students with special needs	20	1.9000	2.924	38	.006
	Normal	20	1.3000	2.924	31.005	.006
Controversy that may escalate into the threat of physical violence, avoiding problem solving.	students with special needs	20	2.1500	3.827	38	.000
	Normal	20	1.3000	3.827	29.125	.001

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. We can show that the less mean was 1.30 for the

normal group, but the greater mean was 2.15 for students with special needs group, this means that the impact of drugs was strong on group two.

Scale of Feeding and eating disorders: The statistical analysis results of this dimension was as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (16).

Table 16: Descriptive analysis for D7

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
Atypical anorexia nervosa: All criteria for anorexia nervosa are met, except that despite significant weight loss, the individual's weight is within or above the normal limit.	mild disease middle disease strong disease deep disease Total	24 11 4 1 40	10.0 10.0 10.0 10.0	31.400[a]	3	.000
Bulimia nervosa (of low frequency and/or limited duration): All criteria for bulimia nervosa are met, except that binge eating as well as inappropriate compensatory behaviors occur, on average less than once per week and/or for less than 3 months.	mild disease middle disease strong disease deep disease Total	18 12 6 4 40	10.0 10.0 10.0 10.0	12.000[a]	3	.007
Binge eating (of low frequency and/or limited duration): All criteria are met for binge-eating disorder, except that binge eating occurs on average less than once per week and/or for less than 3 months.	mild disease middle disease strong disease deep disease Total	15 18 7 40	13.3 13.3 13.3	4.850[b]	2	.088
Laxative Disorder: Recurrent diarrhea behavior to effect Nocturnal eating syndrome: recurrent episodes of nighttime eating as demonstrated by eating, after waking up - from sleep or overconsumption of food after the evening meal there is awareness and rec	mild disease middle disease strong disease deep disease Total	21 11 8 40	13.3 13.3 13.3	6.950[b]	2	.031

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (17)

Table 17: T-Test Results for D7

		T-Test for Equality of Means		
		T	Df	Sig. (2-Tailed)
Atypical anorexia nervosa: All criteria for anorexia nervosa are met, except that despite significant weight loss, the individual's weight is within or above the normal limit.	students with special needs	1.219	38	.230
	Normal	1.219	32.561	.231
Bulimia nervosa (of low frequency and/or limited duration): All criteria for bulimia nervosa are met, except that binge eating as well as inappropriate compensatory behaviors occur, on average less than once per week and/or for less than 3 months.	students with special needs	3.126	38	.003
	Normal	3.126	25.847	.004

Binge eating (of low frequency and/or limited duration): All criteria are met for binge-eating disorder, except that binge eating occurs on average less than once per week and/or for less than 3 months.	students with special needs	4.168	38	.000
	Normal	4.168	37.969	.000
Laxative Disorder: Recurrent diarrhea behavior to effect Nocturnal eating syndrome: recurrent episodes of nighttime eating as demonstrated by eating, after waking up - from sleep or overconsumption of food after the evening meal there is awareness and rec	students with special needs	3.955	38	.000
	Normal	3.955	28.616	.000

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups.

Scale Sleep –Wake Disorders: The statistical analysis results of this dimension was as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (18)

Table 18: Descriptive Analysis for D8

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
This classification applies to cases in which the characteristic symptoms of a wakeful sleep disorder that cause.	mild disease middle disease strong disease deep disease Total	22 10 5 3 40	10.0 10.0 10.0 10.0	21.800[a]	3	.000
Clinically significant distress or impairment in social, occupational, or other areas, but not meeting the criteria.	mild disease middle disease strong disease deep disease Total	19 11 6 4 40	10.0 10.0 10.0 10.0	13.400[a]	3	.004
A full diagnosis of any of the disorders in the wake-sleep disorder category that do not qualify for a diagnosis of insomnia disorder.	mild disease middle disease strong disease deep disease Total	19 12 6 3 40	10.0 10.0 10.0 10.0	15.000[a]	3	.002
Other specified or other specified hyperactive somnolence disorder.	mild disease middle disease strong disease deep disease Total	20 10 7 3 40	10.0 10.0 10.0 10.0	15.800[a]	3	.001
The unspecified wakefulness disorder category is used in cases where the clinician chooses not to communicate a specific reason that.	mild disease middle disease strong disease deep disease Total	16 16 8 40	13.3 13.3 13.3	3.200[b]	2	.202
The present presentations do not meet the criteria for a diagnosis of any of the disorders in wake-sleep disorder category.	mild disease middle disease strong disease deep disease Total	19 12 7 2 40	10.0 10.0 10.0 10.0	15.800[a]	3	.001

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (19)

Table 19: T-Test Results for D8

	Study Groups	T-Test for Equality of Means			N	Mean
		t	df	Sig. (2-tailed)		
This classification applies to cases in which the characteristic symptoms of a wakeful sleep disorder that cause.	students with special needs	3.567	38	.001	20	2.2000
	Normal	3.567	24.986	.001	20	1.2500
Clinically significant distress or impairment in social, occupational, or other areas, but not meeting the criteria.	students with special needs	3.778	38	.001	20	2.4000
	Normal	3.778	25.745	.001	20	1.3500
A full diagnosis of any of the disorders in the wake-sleep disorder category that do not qualify for a diagnosis of insomnia disorder.	students with special needs	4.114	38	.000	20	2.3500
	Normal	4.114	26.455	.000	20	1.3000
Other specified or other specified hyperactive somnolence disorder.	students with special needs	4.524	38	.000	20	2.4000
	Normal	4.524	25.635	.000	20	1.2500
The unspecified wakefulness disorder category is used in cases where the clinician chooses not to communicate a specific reason that.	students with special needs	8.270	38	.000	20	2.4000
	Normal	8.270	36.538	.000	20	1.2000
The present presentations do not meet the criteria for a diagnosis of any of the disorders in wake-sleep disorder category.	students with special needs	1.405	38	.168	20	2.0000
	Normal	1.405	37.942	.168	20	1.6000

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. We can show that the less mean was 1.2 for the normal group, but the greater mean was 2.4 for students with special needs group, this means that the impact of drugs was strong on group two.

Scale of Disruptive Impulsive- Control and Conduct Disorders: The statistical analysis results of this dimension were as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (20)

Table 20: Descriptive Analysis for D9

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
This classification applies to cases in which symptoms characteristic of confessional and impulse-control disorder predominate	mild disease	22	10.0	20.600	3	.000
	middle disease	9	10.0			
	strong disease	5	10.0			
	deep disease	4	10.0			
	Total	40				
Behavior that cause clinically significant distress or impairment in social, occupational, or other areas.	mild disease	22	10.0	20.600	3	.000
	middle disease	9	10.0			
	strong disease	5	10.0			
	deep disease	4	10.0			
	Total	40				
But do not meet the full criteria for a diagnosis of any of the disorders in the confusion and impulse control disorders And the path.	mild disease	22	10.0	21.600	3	.000
	middle disease	10	10.0			
	strong disease	4	10.0			
	deep disease	4	10.0			
	Total	40				

The category Disorientation, Impulse Control, and Conduct Unspecified is used in situations in which the physician chooses.	mild disease middle disease strong disease deep disease Total	19 13 6 2 40	10.0 10.0 10.0 10.0	17.000	3	.001

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-test for two Groups: The T-test results shown in table (21)

Table 21: T-Test Results for D9

	Study Groups	N	Mean	T-Test for Equality of Means		
				T	Df	Sig. (2-Tailed)
This classification applies to cases in which symptoms characteristic of confessional and impulse-control disorder predominate	students with special needs	20	2.3000	3.740	38	.001
	Normal	20	1.2500	3.740	24.330	.001
Behavior that cause clinically significant distress or impairment in social, occupational, or other areas.	students with special needs	20	2.3000	3.740	38	.001
	Normal	20	1.2500	3.740	24.330	.001
But do not meet the full criteria for a diagnosis of any of the disorders in the confusion and impulse control disorders And the path.	students with special needs	20	2.2000	3.131	38	.003
	Normal	20	1.3000	3.131	24.731	.004
The category Disorientation, Impulse Control, and Conduct Unspecified is used in situations in which the physician chooses.	students with special needs	20	2.2000	3.400	38	.002
	Normal	20	1.3500	3.400	27.526	.002

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. We can show that the less mean was 1.250 for the normal group, but the greater mean was 2.30 for students with special needs group, this means that the impact of drugs was strong on group two.

Neurocognitive Disorders Scale: The statistical analysis results of this dimension was as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (22).

Table 22: Descriptive Analysis for D9

		Observed N	Expected N	Chi-Square	Df	Asymp. Sig.
This Classification Applies to Cases in Which Symptoms Characteristic of a Neurocognitive Disorder That Cause Clinically Significant Distress or Impairment in Social, Occupational, or Other Areas of Functioning Predominate, but Do Not Satisfy	Mild Disease Middle Disease Strong Disease Deep Disease Total	21 11 5 3 40	10.0 10.0 10.0 10.0	19.600[a]	3	.000
The full criteria for diagnosing any of the disorders from the category of neurocognitive disorders.	mild disease middle disease strong disease deep disease Total	22 11 5 2	10.0 10.0 10.0 10.0	23.400[a]	3	.000

The Unspecified Neurocognitive Disorder category is used in cases in which an exact etiology cannot be determined to make a firm diagnosis.	mild disease middle disease strong disease deep disease Total	22 11 5 2 40	10.0 10.0 10.0 10.0	23.400[a]	3	.000

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-Test for Two Groups: The T-test results shown in table (23)

Table 23: T-tEst Results for D10

	Study Groups	N	Mean	T-Test for Equality of Means		
				T	Df	Sig. (2-Tailed)
This classification applies to cases in which symptoms characteristic of a neurocognitive disorder that cause clinically significant distress or impairment in social, occupational, or other areas of functioning predominate, but do not satisfy	students with special needs	20	2.1500	2.891	38	.006
	Normal	20	1.3500	2.891	25.809	.008
The full criteria for diagnosing any of the disorders from the category of neurocognitive disorders.	students with special needs	20	2.0500	2.915	38	.006
	Normal	20	1.3000	2.915	26.324	.007
The Unspecified Neurocognitive Disorder category is used in cases in which an exact etiology cannot be determined to make a firm diagnosis.	students with special needs	20	2.1000	3.414	38	.002
	Normal	20	1.2500	3.414	25.948	.002

The previous table shows that most elements have a significant level less than 5%, this means that there are significant shown between Study Groups. We can show that the less mean was 1.250 for the normal group, but the greater mean was 2.30 for students with special needs group, this means that the impact of drugs was strong on group two.

Personality Disorders Scale: The statistical analysis results of this dimension were as follow: Frequency and Chi-square tests. The results of descriptive tests show in table (24).

Table 24: Descriptive analysis for D11

		Observed N	Expected N	Chi-Square	df	Asymp. Sig.
Ignite an intentional and purposeful fire on more than one occasion or opportunity.	mild disease middle disease strong disease deep disease Total	22 9 5 2 40	9.5 9.5 9.5 9.5	24.52	3	.000
B Emotional tension or excitement before the action	mild disease middle disease strong disease deep disease Total	23 8 5 4 40	10.0 10.0 10.0 10.0	23.400	3	.000

An increased sense of tension just before the theft was committed.	mild disease middle disease strong disease deep disease Total	22 11 5 2 40	10.0 10.0 10.0 10.0	23.400	3	.000
The feeling of pleasure, satisfaction, or relief (relaxation) at the time of the theft.	mild disease middle disease strong disease deep disease Total	18 15 6 1 40	10.0 10.0 10.0 10.0	18.600	3	.000

From the previous table results show that most elements have a lot of observation at mild disease level, but there are cases at middle and strong level, the chai square was at the level less than 5%, this means that there are significant differences between Study Groups.

T-Test for Two Groups: The T-test results shown in table (25).

Table 25: T-Test Results for D11

	Study Groups	N	Mean	T-Test for Equality of Means		
				T	Df	Sig. (2-Tailed)
Ignite an intentional and purposeful fire on more than one occasion or opportunity.	students with special needs	20	2.0500	3.116	36	.004
	Normal	20	1.2222	3.239	25.678	.003
B Emotional tension or excitement before the action	students with special needs	20	2.3000	3.955	38	.000
	Normal	20	1.2000	3.955	23.573	.001
An increased sense of tension just before the theft was committed.	students with special needs	20	2.1500	3.971	38	.000
	Normal	20	1.2000	3.971	25.366	.001
The feeling of pleasure, satisfaction, or relief (relaxation) at the time of the theft.	students with special needs	20	2.3000	5.858	38	.000
	Normal	20	1.2000	5.858	29.853	.000

The previous table shows that most elements have a significant level less than 5%, this means that there are significant differences between Study Groups. We can show that the less mean was 1.20 for the normal group, but the greater mean was 2.30 for students with special needs group, this means that the impact of drugs was strong on group two.

IV. CONCLUSION

It is clear from the results of the statistical analysis that the scale that was formulated during the study enjoys validity and stability, as the results of the Alpha Cronbach test indicate the reliability and validity of the scale, and the results of the correlation test indicate the validity and reliability of the scale and therefore it can be relied upon in completing the study and using it in diagnosis.

The results of the all dimensions of the scale indicate that the sample of students who suffer from disorders were more affected and vulnerable to problems resulting from drug abuse of various kinds,

but the ordinary students were less affected and their problems did not worsen to the same degree, as the diagnosis was mostly at the level of mild disease.

The results of the chi-squared test also indicate that there are significant differences in the diagnosis of the control group from the test group, where the statistical significance of the test was less than 5%.

A T-test was conducted and the results for all dimensions of the scale indicated that there are fundamental differences between the diagnosis of each of the study groups, in favor of the first group, where the levels of problems and psychological and neurological disorders were higher in the experimental sample than the control sample, at a level of significance of 5%.

Conflict of Interest

The researchers have no conflict of interest.

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Consent the Scientific Research Ethics Committee

The Scientific Research Ethics Committee at Taif University recently reviewed the request submitted by you to obtain the committee's approval of the research proposal shown below, knowing that the committee was approved by the National Bioethics Committee No. (O H A- O 2 - T - 1 0 5). The proposal meets the requirements of Altaf University, and the ethical approval has been granted from the date (July 2022 - July 2023)

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