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TOOLS FOR TRACKING ANTIBIOTIC RESISTANCE

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Abstract:

Objective: *Antibiotic resistance is amongst leading problems in pharmaceutical and medicinal science. The resistive genes are imposed a pressure by antibiotics which cause excessive genetic material exchange by resulting malfunctioning. Microbial population has also been terminated by undue antibiotic uses. Therefore, the problem needs a solution to introduce new tools to measure accurate resistance level. Bioinformatic and pharmaceutical technologies can revolutionize the industry.*

Patients and Methods: *The molecular study was conducted to determine protein natures, structures and functioning in subjected individuals. The biological modeling of living cell system and proteins enables to discover effective drug strategies. This helped to contest the expanding antibiotic resistance problem.*

Results: *The present study analyzed several types of data that included nucleotide and protein structures and sequences.*

Conclusion: *The results of protein analysis indicated that the accurate drug treatment is much effective and computational modeling can help to determine antibiotic resistance levels.*

Keywords: *Antibiotic resistance, microbial population, bioinformatics, pharmaceuticals, biological modeling, drug, proteins*

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INTRODUCTION:

Medical science is on a serious threat to deal with antibiotic resistance. The selective pressure caused by antibodies is major factor by which the genetic material of bacterial isolates is exchanged. Certain media i.e. water, soil and human micro biota has remarkably shown the change in microbial populations due to additive and excessive antibacterial uses. The scientists need to discover new classes of drugs so that to tackle with excessive antibiotic resistance [1]. The factor behind antibiotic resistance development is misuse of antibiotics. The educational campaigns were aimed to enhance clinicians' skills for using antibiotics. The main resistance was developed due to excessive use of antibiotics for livestock growth promotion. This practice was common after World War II [2]. The World Health Organization (WHO) used the term antibiotic resistance on April 2011 and started promoting this theme globally. This initiative also aimed to discover strategies to develop an antibiotic which does not become obsolete [3]. The fundamental studies based on *in silico* have provided the modeling methods for biosystems. Now a day, certain measurements have been discovered to combat the antibiotic resistance [4]. During first decade of twenties, the European Union and Swedish government forced measures against antibiotic resistance.

PATIENTS AND METHODS:

This research was carried out using random method by dividing the subjects into two groups. After conducting experiments, the results were compared to evaluate the relative impression of treatments. The data recording duration was between 2016 and 2018 [5]. Tools from bioinformatics were used to accurately measure the resistance. The global health is on an edge of facing antibiotic resistance. The subjected individuals selected were victims of diabetic retinopathy (i.e. non-proliferative and proliferative). The victims were tested against other eye diseases which were negative. Three different models were used to observed and compere the efficacy of the tools.

First method was used as wild travelling. In this method the antibiotic hot spot was observed. The main downstream of the drug flow was investigated in this case. The samples were collected from manufacturers at distinct locations of wastewater treatment units. The multidrug resistance bacterium Escherichia coli were used as control measure. The DNA samples were taken and kept under observation for the duration of 1 week, 2 week and 3 weeks from three different host patients. Before taking samples, the three patients were vaccinated with best recommended antibiotic available in market. The DNA samples were stored at 20oC in an incubation chamber. Swiss model was applied to model the results. The model is used for both comparative modeling and homology method. This model help to study protein structure and modeling the results in different dimensions. The subsequent studies resulted that swiss-model works on PROCHECK system. This model has following sequence in case of homology modeling. All the relating structures having maximum homology to our desired structures are sorted in this and is termed as fold assignment. The desired (primary) sequence in whose structure is to be formed is termed as target.

The second method included investigation of the suitable pharmaceutical product (i.e. antibodies). As, drug development is most critical phenomena faced by pharmaceutical and medical sciences. The pharma industry is not discovering new antibiotics, so the solution remains in investigating the best available antibiotic which has not developed the resistance. This also included to study the new microbe pathways, the proteins responsible for antibiotic production and favorable environment at which resistance is minimum. The individuals were vaccinated with triamcinolone acetonide @ 20mg (in 0.5 ml volume) using local anesthesia including xylocaine. The treatment was done with one week, two weeks and three-weeks duration to initial RESISTANCE sessions in group 1, 2 and 3 respectively. The laser spot range was fixed to 200-300 pm with a power of 150-200 MW for duration of 0.2s. The end session gave total 1600 burns approximately. All the patients were treated with xylocaine during anesthesia. The termination of study was based on visual activity of subjected bacteria. Autodock model was used to govern the molecular aspects of molecules which form modeled structures. This method includes the better drug management practices being adopted by the physicians. In this study, the most trended surveillance practices were taken and compared for the lowest resistance evolved. This practice also aimed to investigate the resistance bacteria. Hence, most phenomenal health system was investigated. Interdisciplinary measurements were also evaluated against minimum antibiotic resistance.

RESULTS:

Amongst three case categories, total 100 cases were observed with 64 male and 36 females. The age limit was restricted between 35 to 80 years. The mean age value was calculated as 75 years. The random selection of 30 individuals was made in both groups.

The grouping was done based on same baseline characteristics. The baseline studies indicated no significant different in method 1 of each group. The protein modeling was done before one day of RESISTANCE treatment and during 1st and 8th week of RESISTANCE. Pre-modeling tests are shown in Table 1. Post modeling protein acuity was statistically significant ($p < 0.05$). Twenty subjects from group 1 expressed improved resistance acuity. The resistance acuity number for second group was quite low i.e. 2.1. After vaccination, 68% of the subjects from group 1 resulted improved resistance. While only 5% from the group two shown improved antibiotic resistance. The individuals from group 1 were all having good pretreatment resistance. Whereas 39.3 % of group 2 individuals showed poor pretreatment resistance. Eight individuals of group 1 were vaccinated during anesthesia disorders. The condition was normal after three weeks without external influence.

Table I: Baseline resistance acuity in all patients (n=100)

Baseline resistance efficacy in control group	Group 1 (n=64)	Group 2 (n=36)
20%	0	0
30%	0	0
40%	0	0
50%	0	1
60%	10	11
70%	16	10
80%	4	7
90%	0	1
100%	0	0
Total	30	30

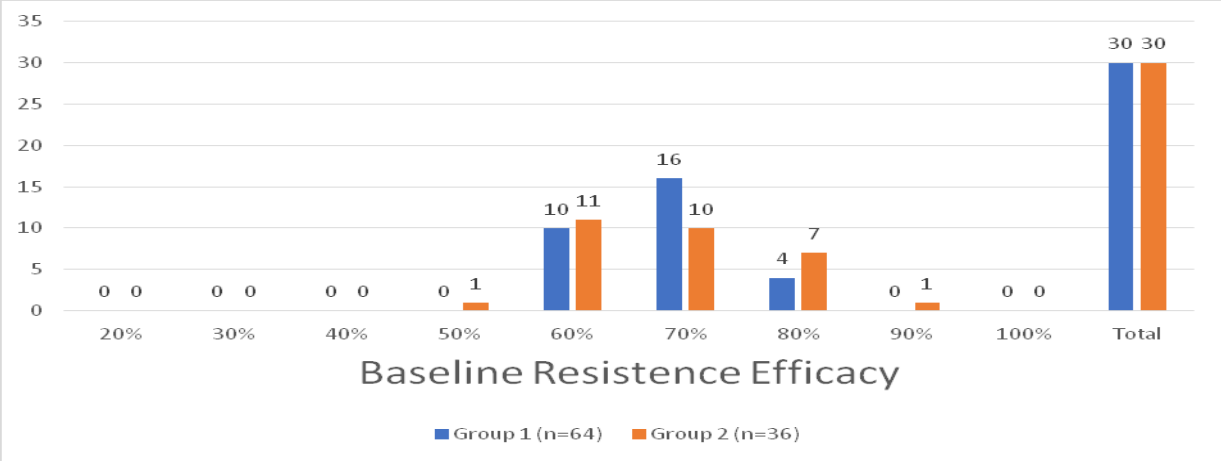
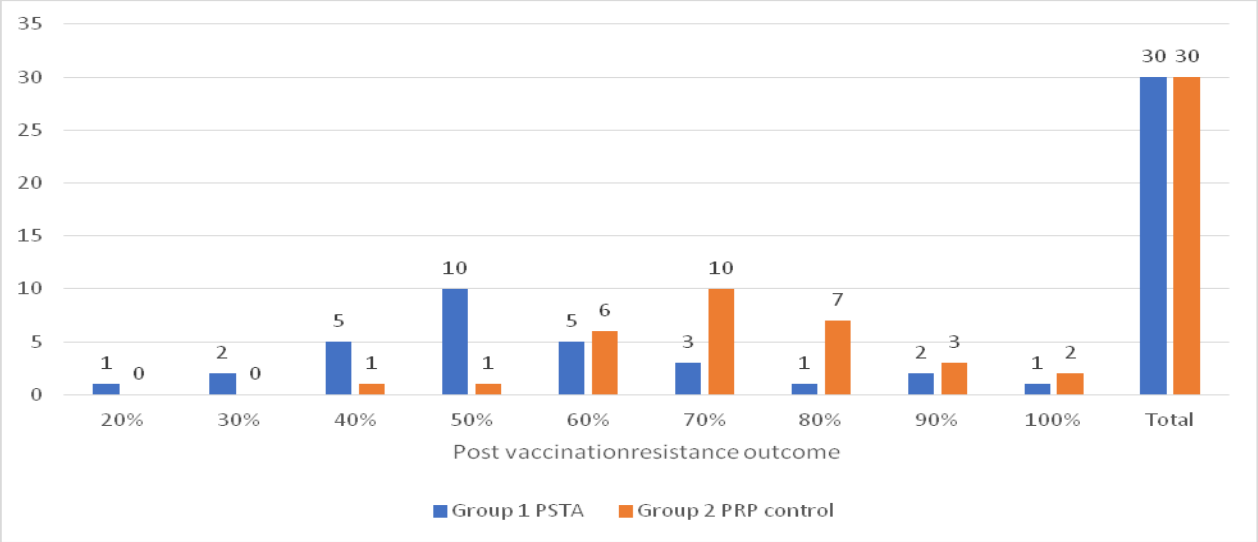


Table II: Post vaccination outcome **in Group 1 (posterior sub tenon triamcinolone acetonide + pan retinal photocoagulation) and Group 2 (pan retinal photocoagulation alone) n=64**

Baseline resistance efficacy in control group	Group 1 PSTA	Group 2 RESISTANCE control	Total
20%	1	0	1
30%	2	0	2
40%	5	1	6
50%	10	1	11
60%	5	6	11
70%	3	10	13
80%	1	7	8
90%	2	3	5
100%	1	2	3
Total	30	30	60



DISCUSSION:

The antibiotic resistance harms the immune system and human health. The patients when vaccinated with triamcinolone acetonide along with antibiotic vaccine produces remarkable results. Some scientists conclude that this effect may be temporary or permanent [6,7]. While this study reveals that after two months the measured value of antibiotic resistance in group 1 were statistically grater than the control individuals of group 2. The deviation in values were random after successive months and observation was quite difficult [8,9]. Hence vaccination of the suitable antibiotic in individuals can produce featured results. The results also indicate that the molecular weight of inhibitors is low and form biomolecule complexes. This causes conformational variations in biomolecule complexes [10]. This information provides base to pharmaceutical industry for the accurate drug formation. This applied work provides dimensions to regulate the process of antibiotic development.

CONCLUSION:

The antibiotic resistance problem is worldwide challenge. The limitations still exist to study and explore the phenomena properly. The synergetic impact of biological and bioinformatic tools along with molecular research can play role in establishing accurate protective measures. This study enables us to corelate different models used in measuring antibiotic resistance.

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