

# Investigation of acinetobacter baumannii isolates health essay

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T. Lewis et al, Journal of Hospital Infection 75(2010)37-41

## **Critical Review;**

### **Introduction:**

A multidrug resistant bacteria *A. baumannii* (MDR-Aci) strains are often colonized in military persons. Whenever they went to hospital for treatment during any injury, they transmit these bacterial strains in the civilian patients and health care members as well. Previous old techniques such as pulse field gel electrophoresis and VNTR analysis have been useful to identify the clonal outbreaks. However, they are unlikely to provide chain of transmission within apparently clonal outbreaks or nor be identified the pattern of spread such as 'super shedders'. Several new studies and research has been revealed the advent of whole genome sequence to investigate different bacterial disease outbreaks, genomic changes and variable loci by polymorphism. Similarly in this study, researcher has aimed to investigate whether (MDR-Aci) lineages are associated with individual patients while using 454 pyrosequencing to obtain more epidemiological information.

### **Method:**

In order to investigate the aimed of study, scientist has gone through with following procedures; Microbiology: They first investigate the *A. baumannii* isolates through antibiotics susceptibility testing. They took different sputum samples from civilian C1 and C2 patients and from military M1, M2, M3 and M4 patients they took wound swab samples and then colonized the samples. They use > 3 class of antibiotics e. g. quinolones,  $\beta$ -lactam/  $\beta$ -lactamase

etc). Molecular Typing: For further study, purified MDR-Aci samples sent to molecules department to isolate DNA of these samples and then later these samples gone for 454 pyrosequencing. The resulting sequenced data of all MDR-isolates combined to create consensus outbreaks assembly. They discard many false positive and negative variants and sequencing error. Finally, after getting well trusted SNPs, they did PCR and Sanger sequencing.

## **Results:**

After filtering and complete agreement with 454-pyrosequencing data, here they find the comparison of first SNP of M1 isolates. Which revealed that it's a ancestral genotype at three SNP loci. Second SNP has separated C1 patient's isolates from all other patients' isolates. The third SNP differentiate the M3 isolates from all other isolates. There is no detection found between patients isolates of C2, M2 and M4. The unusual interesting fact was that the patient's M2 and M4 were injured in the same accident and had treated with same clinical care. However, it is also fact that patients M4 did not come in contact with patient M2 and c2 in other hospital. They conclude that M1 is unlikely to transmit MDR-Aci to civilians, transmission from C1 or M3 to C2 is rule out by very low probability with ancestral state for SNPs 2 and 3. So interpretatively the patient C2 acquired MDR-Aci from patients M2.

## **Discussion and Conclusion:**

Whole genome sequencing has been provided a more close relatedness to MDR-Aci lineages, which contain SNPs and it can be useful to identify the route cause of transmission. So the potential of pyrosequencing has worth to investigate the hospital outbreaks. In addition they conclude that this

technology has different biological key illumination between isolates which can be useful to identify genetic determinants associated with virulence or antibiotic resistance. It is replacing the gel bas methods by their accuracy, low cost and high efficiency.

### **Critical Review:**

The aims of the study are clearly stated and the background is adequately set to understand the objective. However, the author failed to describe more about A. baumannii bacteria. The central message was clear about the impact of genome sequencing to investigate transmission of MDR-Aci isolates. Good methodological approach is made through processing with microbiology, DNA isolation and then using 454 pyrosequencing. They clearly differentiate the results in each labeled and selected patient. The study is valuable to identify the role of sequencer in hospital outbreaks. All the references given by author are appropriate and relevant.

### **Paper2:**

#### **Whole Genome Sequencing to characterize Mycobacterium tuberculosis outbreaks; a retrospective observational study**

Timothy M walker et al, lancet infectious Diseases (2013) 13: 137-46

### **Introduction:**

From the last decade, the ratio of Mycobacterium tuberculosis is gradually increasing in UK and has been identified 50-70 cases per 100, 000

individually. The guideline for the detection of M. TB is mycobacterial interspread repetitive unit variable number tandem- repeats (MIRU-VNTR)

genotyping. However, epidemiological data are necessary to confirm the

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diseases outbreaks. The data collection is quite difficult as patients are unwilling to give volunteer information. MIRU-VNTR genotyping is now replacing by whole genome sequencing strategies, which can detect microevolution within M. TB lineages as this can transmit between hosts. The researcher of this paper has aimed to evaluate the genetic diversity of mycobacterium tuberculosis strains in UK.

### **Method:**

In order to investigate the infectious diseases outbreaks, researchers use illumine technology to sequence M. TB genome of frozen culture samples which were archived. They divide the isolates into four groups; first cross sectional diversity, in which they select random pairs for culture and genome sequence. Second they measured longitudinal diversity and select 100 longitudinal from the same patients who were separated by at least 6 month. Third they evaluate host diversity and they select all isolates form household outbreaks. Fourth they measured community based MIRU-VNTR clusters for the evaluation of whole genome sequencing to gain additional benefits comparatively MIRU-VNTR. Finally they measured and estimate the nucleotide sequence and rate of change in DNA sequence with host and between hosts in household outbreaks. MIRU-VNTR cluster data of 11 communities were used to interpret the network diagram.

### **Result:**

The researcher sequenced 390 separated isolates of 254 patients along with five major global lineages (most frequently European-American and central Asian) of mycobacterium tuberculosis. In the longitudinal isolates they found

the rate of change in DNA sequenced is 0.5 SNP from 30 individual and in 25 separated families. The alteration rate of SNPs is quite higher from last three years. They estimate that 96 % of paired isolates from household and individual are contradicted with five or fewer SNPs. They compared in three ways; the separated isolated from none of 69 epidemiologically linked patients have more than 5 SNPs, the epidemiological unlinked patients has 17 % and 15 % SNPs in possible linked patients. The p-value of the data was  $<0.0001$ . The finding data revealed that super spreaders were present only in two community's clusters.

### **Conclusion:**

The characterization of tuberculosis outbreaks can be detected through whole genome sequencing and it reveals the direction of transmission of these isolates between different tuberculosis cases. The impact of whole genome sequencing in clinical setup shows that it's contributing to prevent and control infection and will also be helpful for early diagnosis of diseases by detecting super spreaders of tuberculosis.

### **Critical Review:**

The aims of the study are clearly stated and the background is adequately set to understand the objective. This is the quality and recent research which defines the potency of genome sequencing which leads to early treatment and diagnosis of an individual M. TB infected. Good methodological approach is made along with four divisional categories of isolates. Results are presented with diagrams and data illustrations. All the references given by the author are

appropriate and relevant. In the limitation of the study they cleared about all arguments relate to study for the viewers.

### **Paper 3:**

#### **MRSA outbreaks analysis through whole genome sequences**

Simon R Harris et al, lancet infectious Diseases (2013) 13: 130-36

#### **Introduction:**

Mostly MRSA infections were mainly occur due to a small number of health care associated lineages that were poorly modified for persistence in the community. Community based MRSA infections are now relocating previously dominant health care MRSA lineages. The implementation is undergone for the prevention of health and community based MRSA, in which the basics understanding are to reveal the transmission dynamics of MRSA. One of the basic approaches to track the transmission route is to obtain genotype, MRSA isolates and their genetic relatedness. The old techniques were enough to discernment and were not suitable for this purpose but recently whole genome sequencing has revolutionized to detect these outbreaks. This hindrance has been beaten by whole genome sequence, in which researcher can easily identify the MRSA transmission outbreaks between the situation of health care associated and community related MRSA infection.

#### **Method:**

In order to investigate these MRSA outbreaks, researcher took samples from the neonatal ward of well known Cambridge University Hospital NHS, UK in 2011. The following steps for the procedure they have done; They took clinical samples for swab culture. By using latex agglutination kit, they <https://assignbuster.com/investigation-of-acinetobacter-baumanniii-isolates-health-essay/>

identified bacteria. Antimicrobial testing done by disk diffusion method by using different number of antibiotics. Proceed for DNA extraction and amplification done and after the PCR they run whole genome sequencer for all amplified samples by using illumine. They aligned sequence for the chromosome accession number and plasmid of reference isolates to detect SNP or insertion and deletions.

### **Result:**

The researcher's team of this project has been identified that 12 infants is colonized with MRSA on period of 6 months who were extremely suspected but still the outbreaks of the diseases were not identified. However, whole genome sequencing has been detected 26 related cases of MRSA carrier patients and also found the transmission route in the neonatal ward, between postnatal ward and also on the community. They detect new genotype of MRSA outbreak i. e. (ST) 2371 which is closing similar to ST22, although it carries Panton valentine leucocidine, an encoding gene. It revealed by whole genome sequence that MRSA outbreaks are transmitted by staff member during periods without unknown infection in the neonatal ward.

### **Conclusion:**

Conclusively, whole genome sequencing is playing a significant role to stop or prevent the infection either in hospital or in a community. It provides rapid, accurate and critical identification of bacterial transmission route along with low cost and high morbidity.



## **Critical Analysis:**

The aims of the study are clearly stated and the background is adequately set to understand the objective. This is also a quality and recent research which defines potency of genome sequencing, in order to investigate the outbreaks of MRSA infection transmission. Good and easy methodological techniques are made for approaching result. Results are clear and revealed new sequence type. However, author fails to describe detail about gene encode Panton valentine leucocidine. All the references given by author are appropriate and relevant. Author also cited his own publication; Harris SR et al, (2010) which is also relevant.

## **Paper4:**

### **To investigate the transmission of Clostridium difficile genome through Next generation Sequencer, Micro evolutionary Analysis**

Xavier didelot et al, genomic Biology (2012), 13: R11

## **Introduction:**

Over the last decade, Clostridium difficile infection has been more common in health care clinical facilities. It is believed that that transmission occurs in hospital between symptomatic patients was reinforced during enhancement of infection control. It is important to identify the transmission lineages of c. difficile to control the infection and prevention. Previous technique such as MLST (multi locus sequence type) and single PCR ribotype are unlikely to distinguish the isolates of c. difficile on a fine scale. The researcher of this paper already did work on this c. difficile investigation through using comprehensive epidemiological information. They did this research and <https://assignbuster.com/investigation-of-acinetobacter-baumanniii-isolates-health-essay/>

collect data during new patient admission and ward movement to identify the route of nosocomial transmission between symptomatic cases. Indeed, this research was failed as it required high quality patient's record with accuracies and omission but fail due to it was difficult task. Further more, the patient's pathways were not directly informative about transmission. Therefore they decide for new strategy for the analysis of transmission, which does not just require epidemiological data and they used whole genome sequencing. It will give direct information about transmission through fine scale patterns. In addition they compare the result of sequencing analysis of plausible transmission with the designated patient, who were determined during admission and movements.

## **Method:**

In order to find the method they used some important general information are mentioned below;

### **1. Sample Collection.**

A total of 1290 Sample contains isolates of c. difficile were sent to Oxford University Hospital, UK for testing. They made the subset of samples

### **2. Sample Treatment.**

For the sample treatment they took stool sample because it was identified as EIA positive They done the culture of feacal sample and incubate at 37C for 7 days. Using Colombia blood agar,(CBB)plates, sub culture was also done for each colonies. After culture and fluorescent of UV illumination, they obtain underwent MLST. Then isolated were stored at -80 C

### **3. DNA preparation:**

The previously stored frozen isolate were transferred in a new CBA plates and incubate at 37C anaerobically for further 48 hours. The DNA extraction was then prepared for these samples.

### **4. DNA sequencing**

DNA was sequenced by synthesis technology, illumineThey produce multiplexed paired end librarian of sequence DNA with an average size of 200bp reads. Twelve plex pooled libaray produce 51 or 100 bp reads. 96 - plex pool libraries produce 99 or 100 bp reads.

### **5. Assembly and variants**

The mapped all the isolates against single chromosome of C. diffecile strains CD630 having length 4, 290, 252 bp

### **6. Molecular Clock estimate**

To check the estimate, the fully sequenced the genome of C. diffecile colonies, which were taken from different samples.

### **7. Comparative Analysis of Genomic from distinct cases**

They did compute phylogenic UPGMA on single genome from each of 486 CD cases. Further more clonal frame was used for both mutation and recombination.

### **8. Epidemiological link with Patients result**

They also compared the genome data with previous epidemiological study for the validity of the results.

## **Results:**

In order to understand the results and findings of paper, here are some important points are mentioned below; They find that plausible transmission is highly interlinked with patients sharing time and space in hospitals. On the other hand, those patients' pairs who were genome matched in the study, they are too distantly related for the direction transmission of this infection. They find that molecular clock rate represents 1.4 mutations per genome on average per year. They found that lineages of *C. difficile* are substantially varied by the effect of recombination.

## **Conclusion:**

Whole genome sequencing is providing the fine resolution of microevolution to reconstruct for the identification of transmission. In conclusion, the microevolution analysis based on whole genome sequence which increases the rate of rapid identification of any bacterial outbreaks. It controls and prevents the associated infection spreading among patients and in between health care members.

## **Critical Review:**

The aims of the study are clearly stated but quite difficult to understand the epidemiology of this paper and the background is inadequately set to understand the rationale of paper. It is also a quality and recent research which defines the potency of genome sequencing, in order to investigate the nosocomial transmission of *C. difficile*. Sensitive methodological techniques are made for approaching results. Results are clear and reflect back to aim. All the references given by author are appropriate and relevant.

## **Paper5:**

### **Critical Review:**

The aims of the study are clearly stated and the background is adequately set to understand the objective. Among with other studies this paper also revealed the importance of genome sequencing by denoting new pathotype of e. coli stains.. Sensitive methodological techniques are made for approaching result. Results are clear and reflect back to aim. All the references given by author are appropriate and relevant.