The discovery of antibiotics

Science, Biology

Introduction

The discovery and introduction of antibiotics in the 1940’s revolutionized the medical field, drugs such as penicillin and streptomycin lead the way into helping save millions of lives, including curing tuberculosis (Ling et al., 2015). As of today, antibiotics fall into one of two categories, they are either bactericidal or bacteriostatic. A bactericidal kill off bacteria with a 99. 9% efficiency and bacteriostatic only inhibit the further growth of bacteria. The mechanism by which these drugs work differs for both groups. However, it is understood that these drugs target DNA replication, protein synthesis and cell wall inhibition (Kohanski et al., 2007). The most common way to discover antibiotics is for researchers to sample random soil, and to test if the microorganisms in the soil are capable of killing or inhibiting the growth of bacteria (Ling et al., 2015).

Antibiotics proved to be a great resource for treating disease across the world. However, it was soon realized that such drugs will not always work. A number of different bacteria begun to develop resistance to antibiotics. A bacterium is identified as antibiotic-resistant if it can grow with that drug present. Resistance occurs when a bacteria acquire novel proteins that help offset the drugs ability to kill or inhibit that bacteria. For example, disease-causing bacteria can pick up proteins that help pump the drugs out of the cell, and remove any harmful compound (Okusu et al., 1996). Other ways that bacteria become resistance include mutation of the bacterial genome and by obtaining plasmids via horizontal gene transfer. Just as the discovery of antibiotics was great for medicine, the discovery of resistance has been

detrimental for the field. It has become more difficult to find cures with so many of the bacteria now being resistant and all the natural resources for antibiotics being exhausted (Ling et al., 2015).

The development of drug-resistant strains of bacteria has motivated the scientific community to look for new antibiotics. The best method to do this is to examine random samples of soil from around the world and look for microorganisms that are capable of killing or inhibiting bacteria. If the soil contained bacteria that inhibit the growth of the bacteria its plated against, then that soil contains an antibiotic-producing bacteria (Bizuye et al., 2013).

In this study, an anal sample was isolated and tested for resistance against twelve different antibiotics, with the utilization of the Kirby Bauer experiment (Table 2). The ABA DABA tests were then applied to determine the identity of the bacterial isolate. Subsequently, based on the identity of the anal isolate, we predicted which antibiotics it will be resistant to. We hypothesized that the anal isolate will be resistant to Azithromycin, Penicillin G, Rifampin and Vancomycin because the spectrum of activity of these drugs does not fit the morphology of the isolated sample.

Results:

I. ABA DABA

The ABA DABA tests include various ways of examining an unknown bacterium in order to obtain the characteristics and the identity of that unidentified isolate. This process included gram staining, in order to determine if an outer cell wall exists for the bacteria. In addition, tests were conducted to examine if the enzyme catalase was present and also if

cytochrome c oxidase was evident. The oxidative and catalase tests were important to determine if the bacterium is capable of aerobic respiration. Furthermore, the phenol red test was to examine if the isolate can ferment sugars, and as a result, can live anaerobically. The minimal media test was to observe if the bacterium needed extra vitamins for growth. Lastly, the fluorescent pigment test and the motility of the bacterium are to help provide more information to identify the isolate.

II. Kirby Bauer Experiment

The anal isolate was tested against twelve different antibiotics to determine which of the antibiotics the isolate was susceptible too. The diameter of the zone of inhibition was critical to determining whether the bacterium was susceptible, resistant or intermediate to the antibiotic. The expected results were obtained by identifying the Genus the isolate belonged too. Based on that, each antibiotic spectrum of activity was examined to determine whether it has the ability to target the isolate anal sample. Based on Table 3, it is evident that nearly all the expected and actual results matched. The isolate A was inhibited by antibiotics capable of targeting gram-negative bacteria. The only contradiction is with the Azithromycin, an antibiotic which targets gram-positive bacteria.

III. Test Subject History

The anal sample was collected from a healthy male adult. The adult maintains a normal eating habit, 2-3 meals a day and uses the bathroom regularly. No serious medical conditions were reported, however, the test subject did complain about reoccurring stomach pains. Then after testing positive for Helicobacter Pylori the subject was assigned to take Amoxicillin.

The subject reports he was administered a two-week dosage and completed it accordingly. Nevertheless, the subject still encounters the same stomach pains even after completing the full Amoxicillin dosage.

Discussion

After numerous ABA DABA tests, the anal isolate was identified as being a part of the Enterobacteriaceae family and more specifically the Citrobacter organism. Based on the characteristics of this family of microorganisms, predictions about the resistance to each of the antibiotics were made. Enterobacteriaceae are gram-negative bacteria, and therefore they should be resistant to Azithromycin, Penicillin G, Rifampin, and Vancomycin because these antibiotics target gram-positive bacteria. The predictions contained only one contradiction, for Azithromycin, which the isolate A showed susceptibility too.

However, this contradiction is explained in an article published in the Journal of Antimicrobial Agent and Chemotherapy. In the study, they examined the activity of Azithromycin and its improved performance against gram-negative organisms. The study revealed that Azithromycin was much more effective against gram-negative organism in the Enterobacteriaceae family (Retsema et al., 1987). Although Azithromycin primarily targets gram-positive bacteria, it can also affect a number of gram-negative bacteria.