Disadvantages of phenotypic methodologies

To start with, phenotype is defined as the visible characteristics of an organism resulting from the interaction between its genetic makeup and theenvironment(Encarta 2008). Phenotypic methodology has many advantages and disadvantages and this essay talks about the dis advantages . The fact that most laboratories can do an automatic DNA makes genotyping testing more available than phenotyping. First and foremost the test is not usually readily available and accessible making the time for the outcome of the result to be prolonged and inevitably long.

Phenotypic methods for most drugs does not have clinically significant cut off to differentiate sensitive and resistant isolates and this has not been delineated for most of the drugs. From the first principle, genotyping is less complex, faster, and less expensive than phenotyping. Another disadvantage is that certain changes in resistance mutation detected by genotyping are not sometimes detected by phenotyping. Such changes might be the prime step in the path to high-level resistance, and detection of these mutations might stimulate a change in therapy in a patient with detectable plasma viremia.

Therefore phenotypic methodologies may not be able to determine a minute shifts in the susceptibility that follows the existence of only one or more mutation which may lead to decreased drug effect. A good example is the 74V and 90M mutation in the sequinavir and didanosine respectively. Phenotypic method is applied to differentiate isolates based on the phenotypic appearances which are a corollary of genetic composition.

The method has a low discriminating range within same species and therefore has been applied only within same variety of organisms. Numerous

phenotypic methodologies have been suggested for use in discriminating among various groups of bacteria. These include biochemical tests (Olsen etal 1992)), phage susceptibility (Zierdlt etal 1980)), outer membrane protein profiles (Barekam etal 1981), antibody reactivity (Valsalovic etal 1994), fimbriation (Latham and Stamm1984), bacteriocin production and susceptibility, and other methods.

However, these systems have serious disadvantages, including unstable phenotypes, low sensitivity at the intraspecies level, and limited specificity. However, a few phenotypic methods have been used successfully as bacterial source tracking (BST) methodologies. Phenotyping that is dependent on the biochemical properties could be expensive and waste a lot of time . In this method the basal metabolic rate of the organism is greatly affected by the growth parameters and conditions.

Some variables used in the biochemical approach can also give rise to falsediscrimination. A good example is the L monocytogen which did not provide a coherent and reliable outcome making the use of antimicrobial susceptibility not to be encouraged while dealing with these bacteria. Phenotypic characteristics are not usually reproducible as they are manifestation of genetic expression and this is affected largely by the prevailing growth parameters.

Phenotypic methodology despite advantages is not without its own limitation and setbacks as it is difficult under this method to determine and establish clinically remarkable value for the prediction of the virology response. It also has a notable problem of handling making it limited. It solely depends on the specific specimen storage, conveyance method and preparation. When

specimen are improperly handled this may lead to false positive and negative data interpretation results.

The DNA from virus while using the method can be desecrated from unprofessional handling in the laboratory. It must be noted that both the genotypic and phenotypic approaches study and examine the most important viral quasispecies. Another disadvantage of phenotypic methodology is that in case of a virus that the proof of its resistance to drug has been established and that has been selected by previous treatments with drugs or has been acquired by initial transmission , if another resistant strain of such virus develop again, it may not be detected by this method.

Furthermore, when dealing with the Human immunodeficiency virus for example, any collected sample with copy of the virus less than 500 RNA more often than not will not generate results. In other words, the method is not sensitive to a minor variant case. The phenotype method also relies on the replication of the amplified gene sequences using the polymerase chain reaction and as such the possibility of cross contamination is highly plausible and this may occur with or without appropriate technique and carefulness.

It is therefore advised for this reason that an outcome that does not tally with the present clinical state or previous treatment of patient is an indication for repeating the resistance test. In conclusion, phenotypic method has several disadvantages in that it is highly variable, due to environmental factors that lead to variation in gene expression, it has poor reproducibility and the discriminatory power is unsatisfactory. It may also falsely associate unrelated isolates and conversely when only a tiny and narrow framework of biochemical tests are used.