Extended Abstract
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Constructing Kinetic Mathematical Models to Predict Cancer Behavior: A New Mirror Image as a New Medical Hypothesis

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Abstract

Biological behaviour is still dilemma irrespective to highly advancements in tumor knowledge due to diverse and interacting underlying mechanisms, an issue that stimulates researchers, practitioners, and scientist to explore more and more thoughts, ideas, and mechanisms.

Based on my experience in the cancer research, I have constructed the mirror image model that predicts cancer behaviour. The expression of biomarkers is a very important feature of biological cancer behaviour. In this model, the expression of two biomarkers using immunohistochemistry was implemented. We have previously published an article about the use of digital imaging techniques for better understanding of cellular reactivity, in which we showed how can the expression of biomarkers be changed from qualitative to quantitative through the use of imaging analysis properties provided by adobe Photoshop software. The idea depends in calculating the total pixels per image, then an option to select a color of the image to compute its distribution as pixels. The obtained number is divided by the total pixels in slide. The resulting number is recorded. Using these options gave us the possibility to shift our knowledge in following the biological behaviour of cancer (Al-Jarrah et al., 2010; Bani-Ahmad et al., 2018). However, we have previously conducted several studies to follow the biological activities of several diseases including diabetes and neurological diseases (Al-Jarrah et al., 2013; Alkhatib et al., 2013; 2014;Amawi et al., 2019;Ali Alsarhan et al., 2020).

The mirror –image model: We constructed our model by creating the idea that if we compute the expression of two biomarkers in relation with a certain tumor, here we studied acute myeloid leukemia (AML). For studying this particular haematological malignancy, we selected both of p53 and WT1 due to their importance and controversial roles. Using immunohistochemistry, we studied the expression of these two biomarkers on samples of control patients and patients with AML. We have got 4 groups of patients as seen in figure (1): control group (1), AML (2), relapsing group (3), and non-relapsing group (4). In this model the expression of biomarkers was identified for all groups, then for each group, we divided the expression of p53 by that of WT1, and WT1 by p53 to construct the model as seen in figure (1). Using this approach enabled us to construct our model with the following features:

1- We derived mathematical formulations that can be applied to predict the biological behaviour of AML. In control group, the expression ratio of WT1/p53> 3.7. This implies that at this ratio, WT1 will control the biological reactivity of p53 within physiological limits. In AML group, we have observed that the expression of both biomarkers have increased within the ratio WT1/p53≈1, this implies that WT1 is not able to control the biological reactivity, and AML has developed.

2- We think that this model has given the chance to identify the area for intervention. By modifying techniques to calculate the expression of these biomarkers, it is possible to identify populations at risk to develop AML and to develop strategies to restore the original ratio. We plotted a triangle between groups 1 and 2. At the base of this triangle, no AML on the other hand, the head of the triangle represents the area of well- developed AML.

3- In group (3), non-relapsing group, the ratio of WT1 is slightly higher than that of p53. This means that as the disease did not witness more development, the expression of both p53 and WT1 is still under control.

4- In relapsing group, it is observed that the oncogenic properties of p53 exceeded the ability of WT1 to control AML. We observe the expression of p53 in its highest level, and WT1 in its lowest level.

5- This is a preliminary study that paved the road for more studies on other cancers using different biomarkers.

6- As a mathematical idea, the possibility to study other diseases that have variations in their nature and impacts different systems and organs such as COVID-19 may be studied to reach better understanding with better therapeutic options.

7- We recommend that such great techniques such as Micro array to be designed to include such type of analysis.

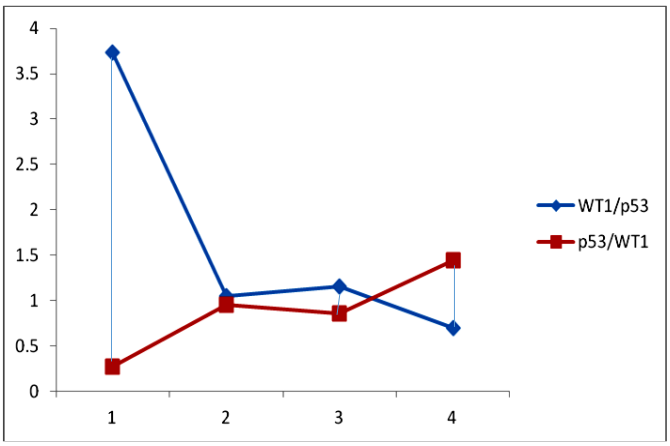

Figure 1: The ratio of expression of Wt1/p53 (red line) and p53/WT1 (blue line). From the points 1-2, the control group showed that the expression of WT1 predominates the expression of p53 then p53 starts increasing to reach similar level of WT1 and then at point 2, AML has developed. Between points 3 and 4, the expression of WT1 predominates again in non-relapsing patients where p53 predominates over WT1 in relapsing patients (Bani-Ahmad et al., 2018).

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