REANALYSIS OF THE STUDY RESULTS OF AN ARTICLE IN ACTA MEDICA MEDITERRANEA REPORTED IN 2011

JIAN-WEII ZHOU[1], CUI KONG[2]
[1]Medical Laboratory, Affiliated Hospital of Jining Medical College, Shandong Province, Jining - [2]Nursing Department, Affiliated Hospital of Jining Medical College, Shandong Province, Jining, PR China

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I carefully read the article in your journal entitled "Primary exploration of the third complementarity determining region 3 spectratyping and molecular features of T cell receptor alpha chain (TRAV) in the peripheral blood mononuclear cell (PBMCs) and tissue of patients with colorectal carcinoma"[(1)], which reported the features of the skewed TRAV complementarity determining region 3 (CDR3) of colorectal carcinoma.

Not long ago, I looked through another paper issued in the journal Cancer Epidemiology which introduces the molecular features of T cell receptor beta chain (TRBV)[(2)]. We put together the results of the predominant gene families in the two articles and analyzed the data simultaneously, and found that, not only in TRAV but also in TRBV of PBMC, there were different skewness frequencies in the different gene families. As shown in Table 1, the number of the predominant proliferative TRAV6 was 6 and the frequency was 85.7%, while the according data for TRAV2 were 2 and 28.6%; TRBV20 and TRBV21 were the highest gene families with the frequency of 42.9%, while there was no predominant proliferation found in some gene families, such as TRBV5.1, TRBV10, TRBV12, and so on.

According to the frequency of the each gene family of TRAV and TRBV, we draw the histograms respectively. Moreover, the two grams were put together back to back, and a figure like a big key formed (Figure 1).

The prominent columns like the kits of the key, and the higher the frequency of the TRAV or TRBV gene family, the higher the kit of the key. Therefore, to some extent, the key presents the total characterization of the skewness of TRAV and TRBV of the seven patients with colorectal carcinoma. As we known, the skewness of T cell receptor (TCR, which includes TRAV and TRBV) specific to the associated antigen of colorectal carcinoma, so the key formed with the skewed genes could be taken as the summary clonal changes of TRAV and TRBV, namely, it is a specific key to colorectal carcinoma. There is a proverb in China says that 'Open different locks with different keys', and then, there should be a key specific to each of other diseases, such as hepatitis B, tuberculosis, breast cancer and so on.

Through the again analysis of the data in the two articles, we hope to pose a new idea or a novel angle on analyzing the skewness of TCR for the researchers. In near future, there probably are many reports focus on the keys specific to the different infectious disease, tumor or autoimmune diseases.

According to the reports in ACTA Medica Mediterranea and Cancer Epidemiology, the features of complementarity determining region 3 (CDR3) of T cell receptor alpha chain (TRAV) and beta chain (TRBV) were reanalyzed with two histograms. If the two grams together, it is easy to see that the merged gram likes a big key, which is due to the different the frequency of the each gene family of T cell receptor (TCR). A and B side respectively represents the predominant skewed TRAV and TRBV gene families. The prominent columns like the kits of the key, and the higher the frequency of the TRAV or TRBV gene family, the higher the kit of the key.

Predominant usage TRAV	Times for each predominant gene	Skewness frequency of the every predominant gene family (%)	Predominant usage TRBV	Times for each predominant gene	Skewness prequency of the every predominant gene family (%)
1.1	3	42.9	1	2	28.6
1.2	2	28.6	2	1	14.3
2	2	28.6	3	2	28.6
3	5	71.4	4	1	14.3
4.1	4	57.1	5.1	0	0
4.2	3	42.9	5.2	2	28.6
5	2	28.6	6	2	28.6
6	0	0	7	1	14.3
7	1	14.3	8	0	0
8	2	28.6	9	2	28.6
9	6	85.7	10	0	0
10	4	57.1	11	2	28.6
11	0	0	12	0	0
12	1	14.3	13.1	2	28.6
13	0	0	13.2	2	28.6
14	2	28.6	14	2	28.6
15	1	14.3	15	0	0
16	3	42.9		0	0
17	5	71.4	17	2	28.6
18	1	14.3	18	2	28.6
19	1	14.3	19	0	0
20	2	28.6	20	3	42.9
21	2	28.6	21	3	42.9
22	1	14.3	22	2	28.6
23	4	57.1	23	0	0
24	2	28.6	24	0	0
25	1	14.3			
26	4	57.1			
27	1	14.3			
28	3	42.9			
29	1	14.3			
30	0	0			
31	2	28.6			
32	5	71.4			

Table 1: The skewness frequency of each of TRAV and TRBV gene families in PBMC of colorectal carcinoma patients

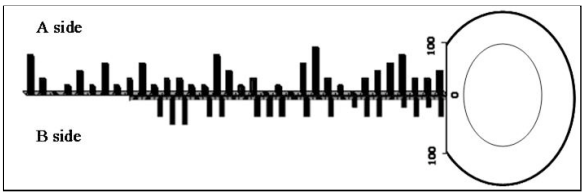

Figure 1: The key formed with the predominant TRAV and TRBV in PBMC of seven patients with colorectal carcinoma.

To some extent, the key presents the total characterization of the skewness of TRAV and TRBV of the seven patients with colorectal carcinoma.

References

1) Jian-wei Zhou, Rui Ma, Wen-tai Tang, Rong Luo, Xin-sheng Yao: *Primary exploration of the third complementarity determining region spectratyping and molecular features of T cell receptor alpha chain in the peripheral blood and tissue of patients with colorectal carcinoma*. ACTA Medica Mediterranea (2011) 27: *97-104*.
2) Zhou J, Ma R, Luo R, Sun Y, He X, Sun W, Tang W, Yao X: *Primary exploration of molecular and spectratyping features of CDR3 of TCR β chain in the peripheral blood and tissue of patients with colorectal carcinoma*. Cancer Epidemiol. (2010) 34(6): *733-740*.

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Correspoding author
Dr. JIANWEI ZHOU
E-mail: immunolife@126.com
(China)