CLINICAL SIGNIFICANCE OF SERUM $\beta_2$-MICROGLOBULIN IN VARIOUS LIVER DISEASES. S. Fujiyama, Y. Takahashi, and T. Sakai.

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Using the Phadebas $\beta_2$-micro Test, serial determinations of serum $\beta_2$-microglobulin ($\beta_2$-m) levels were carried out in 460 patients with various liver diseases including 49 cases of hepatocellular carcinoma (HCC) and its clinical usefulness was evaluated. It considered that normal upper limit of serum $\beta_2$-m level was 2.4 mg/l. High serum $\beta_2$-m levels were found in patients with acute hepatitis (62.5%), chronic hepatitis (30.0%) and liver cirrhosis (56.6%). In general, serum $\beta_2$-m levels in chronic liver diseases tended to increase with degree of impaired liver function, but in individual cases it fluctuated with the clinical course. To compared with benign diseases, the incidence and serum levels of $\beta_2$-m were considerably high in HCC (75.8%) and hepatocellular cancer (66.7%). The serum $\beta_2$-m was not closely related to tumor growth or clinical evolution, and there was no significant correlation between serum $\beta_2$-m and other tumor markers (AFP, CEA and ferritin) in these liver cancers. The ascitic/serum ratio of $\beta_2$-m in the patients with HCC was significantly higher than that in liver cirrhosis. From these results, the presence of hepatic diseases must be considered in evaluating $\beta_2$-m levels, and measurements of serum $\beta_2$-m alone seem to be of limited values in the diagnosis and monitoring of liver cancer.


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Response-error-relationship (RER) can be used for reasonable weighting in regression of RIA standard curve and quality control. However, some investigators have claimed that there is no constant relationship between errors and response, such as counts, B/Y or B/Bo. The purpose of this presentation is to investigate relationship between response and error, and to find the most suitable models for RER, if any relationship is present. In this study, counts were used for response and standard deviation or variance was used for representing errors. Data from unknown samples were binned into 20 groups which were made by dividing the difference between the maximum and minimum counts in a certain assay with 20. Models used here for RER analysis were as follows:

1. $Y = b_0 + b_1X$ (2) $Y = a + bX$ (3) $Y = bX + cX^2$ (4) $Y = a + bX + cX^2$ (5) $Y = \log(a + bX + cX^2)$ (6) $Y = a + bX + cX + dX^2$ (7) $Y = a + bX + cX + dX^2 + eX^3$ (8) $Y = a + bX + cX + dX^2 + eX^3 + fX^4$ (9) $Y = a + bX + cX + dX^2 + eX^3 + fX^4 + gX^5$ (10) $Y = a + bX + cX + dX^2 + eX^3 + fX^4 + gX^5 + hX^6$ (11) $Y = a + bX + cX + dX^2 + eX^3 + fX^4 + gX^5 + hX^6 + iX^7$ (12) $Y = a + bX + cX + dX^2 + eX^3 + fX^4 + gX^5 + hX^6 + iX^7 + jX^8$ (13).

The stability of distributions of patients' test values and performances of statistical parameters derived from these RIA was performed in our laboratory for the past one year. The parameters studied were Hoffmann's "average of normals" (NM), the "number plus" (NP) and a median of values that fall within the "normal" reference range (NMe). In Tt, TSH and GH RIA, the patterns are constant and NMe showed close correlations with values of "normal" quality-control sera. The degree of the correlations depended upon the extents of the reference ranges employed. In Tt, cortisol, IRI, LH and FSH RIA, the patterns were not consistent and NMe and NMe rarely correlated with values of control sera. NP showed close correlations with values of control sera in only Tt RIA and appeared affected by a disturbance in the distributions. In general, NMe may be useful adjuncts to conventional quality-control of RIA for the substances satisfying the following conditions: (1) the patterns of their distributions are almost constant, (2) the inter- and/or intra-individual variations are less prominent and (3) number of their test values that fall within the reference range in a run of assay are preferably more than 50, though frequency of abnormal data appears not to be critical.