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Stochastic Model to Find the Prognostic Value of CD97 and CD55 in Primary Gallbladder Carcinoma Using Gamma Distribution

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ABSTRACT:

CD97 is a member of the epidermal growth factor (EGF) seven span transmembrane (TM7) families with adhesive properties. This family includes EMR1, EMR2, EMR3, ETL and the mouse microglia marker F4/80, which are characterized by an extended extracellular region with a variable number of EGF domains. So far, CD97 is the only EGF-TM7 family member of which a ligand has been identified.

CD97 as a member of the EGF-TM7 family with adhesive properties plays an important role in tumor aggressiveness by binding its cellular ligand CD55, which is a complement regulatory protein expressed by cells to protect them from bystander complement attack. Previous studies have shown that CD97 and CD55 both play important roles in tumor dedifferentiation, migration, invasiveness and metastasis. The aim of this study was to investigate CD97 and CD55 expression in primary gallbladder carcinoma (GBC) and their prognostic significance with the help of sojourn time distribution in a Markovian G-Queue by using Gamma distribution.

Key Words: Gallbladder Carcinoma, Epidermal Growth Factor, Seven Span Transmembrane, Sojourn Times, First Passage Times, Gamma Distribution.

2010 Mathematics Subject Classification: 60H99, 60G99

I. INTRODUCTION:

Primary gallbladder carcinoma (GBC) is the sixth most common gastrointestinal cancer in Asian and Western countries. This carcinoma has extremely poor prognosis and increasing incidence worldwide because of its inherent biology and often advanced stage at diagnosis, despite the recent advances in diagnostic modalities. GBC has the great propensity to directly invade the liver, and it also frequently metastasizes to the liver and pericholedochal lymph nodes. There are no adjuvant chemotherapeutic combinations widely accepted for GBC due to their toxicity, drug resistance and limited efficacy.

Curative surgical approaches are still the principal treatment, but the prognosis of GBC remains poor with respect to postsurgical 5 year survival rates. Thus, the search for new prognostic markers for GBC patients is important to allow the assessment of metastasis and to provide the opportunity for adequate postoperative treatment in high risk patients [7].

CD97 is a member of the epidermal growth factor (EGF) seven span transmembrane (TM7) families with adhesive properties [8]. This family includes EMR1, EMR2, EMR3, ETL and the mouse microglia marker F4/80, which are characterized by an extended extracellular region with a variable number of EGF domains. So far, CD97 is the only EGF-TM7 family member of which a ligand has been identified [9]. In the case of many glycosylphosphatidylinositol anchored proteins, CD55 is either bound to the cell membrane or released from the membrane into the microenvironment. The expression and clinical impact of CD97 and its ligand CD55 in GBC have not been previously investigated. Herein, we found that the expressions of CD97 and CD55 are both upregulated in human GBC. Their expression levels in GBC were both associated with the severity of the tumor. Furthermore, CD97 and CD55 expressions were independent poor prognostic factors for overall survival in patients with GBC [16].

We consider a single server Markovian queue with two types of customers; positive and negative, where positive customers arrive in batches and arrivals of negative customers remove positive customers in batches. Only positive customers form a queue and negative customers just reduce the system congestion by removing positive ones upon their arrivals. We derive the LSTs (Laplace Stieltjes Transform) of sojourn time distributions for a single server Markovian queue with positive customers and negative customers by using the first passage time arguments for Markov chains. The minimal non negative solution $H^*(s) = \frac{1}{2\lambda_2}\left[(\lambda_1+\lambda_2+s) - \sqrt{(\lambda_1+\lambda_2+s)^2 - 4\lambda_1\lambda_2}\right]$ of the $m \times m$ matrix equation is used to find the effect of CD97 and its ligand CD55 in primary gallbladder carcinoma.

1.1. Notations:

GBC	-	Gallbladder Carcinoma
LST	-	Laplace Stieltjes Transform
EGF	-	Epidermal Growth Factor
$TM7$	-	Seven Span Transmembrane
λ^+	-	Positive Customers
λ^-	-	Negative Customers
OS	-	Overall Survival
λ_1	-	Shape Parameter
λ_2	-	Scale Parameter
s	-	Assuming Time

II. G - QUEUE:

We consider a queue with two types of customers; positive and negative. Positive customers are ordinary ones who, upon arrival, join the queue with the intention of being served. In contrast to the positive

customers, the arrival of negative customers removes some of the positive customers from the system, if any available, and then disappears; otherwise the negative customer is lost. Only positive customers can from a queue and negative customers just reduce system congestion. Such queues have been called G-queue [3].

Since [1] introduced the notion of negative customers to represent the inhibitator signal in neural networks and commands to delete some transactions in distributed computer systems or databases, there has been a growing interest not only in networks of queues [1] [3] & [5] but also in single node queues with negative customers [4] & [6]. Interest in time delays in the G-queue has increased recently. From [2] derived the LSTs of the sojourn time distributions for the M/M/1 G-queue under the combinations of various queueing disciplines and removal strategies. From [3] investigated the end to end delay in an open tandem pair of a G-queue with FCFS discipline and RCE removal strategy. Most papers assume that upon arrival to a queue, a negative customer removes an ordinary customer from the queue. Recently, several authors have generalized this concept, allowing a negative arrival to remove a batch of customers [5], a random amount of workload, or even all work in the system [6].

However, the results about sojourn time distribution even for single node G-queues with batch arrival or batch removal are few to the author's best knowledge. In this paper, we use the first passage time arguments of Markov chains to derive the LST of the sojourn time distribution in single server Markovian G-queues with a batch arrival of positive customers and/or batch removal by a negative arrival. The mathematical accessibility of our model compared with that of [2] represents a part of the motivation for the study of batch arrivals/removals. Furthermore, our model is related to the inventory systems with perishable products such as fruit, vegetables and meat, in which arrival and removal occur in batches and instantaneous removal of inventory usually depends on the length of time that the products spent it the system.

2.1. Queue Length distribution:

In this section, we describe the mathematical model in detail and derive the queue length distribution in equilibrium at the arrival instants of positive customers. We consider a single server queue in which positive customers arrive in batches according to a Poisson process with rate λ^-, which is independent of the arrival process of positive customers. We assume that each arrival of a negative customer removes a random number B of positive customers in the system. This is, upon a negative arrival, if there are k positive customers in the system, $min(B,k)$ positive customers are removed and the negative customer disappears. The service time distribution of all customers is exponential with mean $\frac{1}{\mu}$. For the notational simplicity, we let $\tilde{\mu} = \lambda^- + \mu$ and $\lambda = \lambda^+ + \lambda^-$. We assume that the batch size A of positive customers and the quota B of a negative customer take finite values to avoid calculations of infinite matrices. However, this assumption is not a strong restriction, since the supports of A and B may be arbitrarily large and one can apply our model to A and B taking infinite values by truncating the tail pats of the state spaces with sufficiently small tail probabilities. Let $P(A = n) = a_n$ and $P(B = n) = b_n, n = 1, 2, \ldots$ with $a_n = 0, n \geq l + 1$ and $ba_n = 0, n \geq m + 1$ for some $1 \leq l, m < \infty$. We denote the means $\bar{a} = E(A)$ and $\bar{b} = E(B)$ and generating functions $A(z) = \sum_{n=1}^{l} a_n z^n$ and $B(z) = \sum_{n=1}^{m} b_n z^n$.

Note that the stationary distribution of the queue length in this system is invariant under the service discipline and removal strategies and concern only positive customers. This model is equivalent to the $M^A/M^B/1$ queue where customers arrive in batches with batch size A according to a Poisson process with rate λ^+ and the customers are served in batches of maximum size $\tilde{B}$ with $\tilde{b}_k = P(\tilde{B} = k), 1 \leq k \leq m,$

Where, $$\tilde{b}_k = \begin{cases} \frac{\lambda^- b_1 + \mu}{\tilde{\mu}} & k = 1 \\ \frac{\lambda^- b_n}{\tilde{\mu}} & 2 \leq k \leq m \end{cases}$$

and the service time distribution is exponential with parameter $\tilde{\mu}$. The necessary and sufficient condition for this system to be positive recurrent is given (e.g [10]) by

$$\rho = \frac{\lambda^+ a}{\mu + \lambda^- b} < 1$$

We assume that $\rho < 1$ throughout.

Now we turn our attention to the queue length distribution at the epochs of positive customers, which will be imperative in the upcoming sections. Let $\{N_n\}$ be the number of positive customers in the system at the epoch immediately before the arrival of the nth batch of positive customers. Let A_n be the batch size of the nth arrival of positive customers with the same distributions as A and D_{n+1}, where D_{n+1} is the number of positive customers departed from the system during the $(n+1)^{th}$ inter arrival period of the batch of positive customers. Then it a be seen that

$$N_{n+1} = \max(N_n + A_n - D_{n+1}, 0)$$

The probability d_n that n positive customers potentially leave the system during the inter arrival time of a batch of positive customers is given by

$$d_n = \begin{cases} p & n = 0 \\ \sum_{j=1}^{n} 1^b(j,n) p q^j & n \geq 1 \end{cases}$$

Where $p = \frac{\lambda^+}{\lambda^+ + \tilde{\mu}}, q = 1 - p$ and $b(j,n)$ is the j-fold convolution of the probability mass function $\{\tilde{b}_k, 0 \leq k \leq m\}$. Simple calculations yield

$$\tilde{B}(z) = \sum_{n=1}^{m} \tilde{b}_n z^n = \frac{1}{\tilde{\mu}}(\mu z + \lambda^- B(z))$$

and hence the probability generating function $d(z) = \sum_{n=0}^{\infty} d_n z^n$ is given by

$$d(z) = \frac{\lambda^+}{\lambda^+ + \mu(1-z) + \lambda^-(1 - B(z))}$$

Denoting $d_n = 0$ for $n \leq -1$ and $\bar{d}_n = \sum_{k=n}^{\infty} d_k, n \geq 0$, we deduce that the transition probability matrix $P = (p_{ij})$ of $\{N_n\}$ is given by $p_{ij} = \begin{cases} \sum_{k=1}^{l} a_k \bar{d}_{i+k} & j = 0 \\ \sum_{k=1}^{l} a_k \bar{d}_{k+i-j} & 1 \leq j \leq i+l \\ 0 & j \geq i \geq l+1 \end{cases}$

Following similar procedures as those in [10], the stationary distribution $\pi = \{\pi_i, i = 0, 1, \ldots\}$ of $\{N_n\}$ is given by

$$\pi_k = C \sum_{i=1}^{K} \sum_{j=0}^{n_i - 1} c_{ij} \left(\frac{d^j}{dx^j} x^k \mid x = \alpha_i \right), k \geq 0$$

where $\alpha_i, 1 \leq i \leq K$ is the solution of the equation

$$\alpha^l = d(\alpha)\left(\alpha_1 \alpha^{l-1} + \alpha_2 \alpha^{l-2} + \cdots + \alpha_l\right) \tag{1}$$

with n_i being the multiplicity of α_i $(1 \leq i \leq K)$, such that $1 \leq n_i \leq l$ and $\sum_{i=1}^{K} n_i = l$ $c_{ij}, 0 \leq j \leq n_{i-1} - 1, 1 \leq i \leq K$ are arbitrary constants, which are can be determined by the $l - 1$ simultaneous equations:

$$\pi_j = \sum_{i=0}^{\infty} \pi_i p_{ij}, j = 1, 2, \ldots, l-1 \tag{2}$$

under the constraint

$$\sum_{i=1}^{K} \sum_{j=0}^{n_i - 1} c_{ij} = 1$$

(3)

and C, the normalizing constant (in $\sum_{i=0}^{\infty} \pi_i = 1$) is given by

$$C = \left[\sum_{i=1}^{K} \frac{c_{i0}}{1 - \alpha_i} + \sum_{i=1}^{K} \sum_{j=1}^{n_i - 1} c_{ij} \frac{j!}{(1-\alpha_i) j+1} \right]^{-1}$$

After simple but tedious algebra, we have from (2) and (3) the following linear system of equations for $\{c_{ij}, 0 \leq j \leq n_{i-1} - 1, 1 \leq i \leq K\}$:

$$Hc = e_l$$

where $c = (c_{10}, c_{11}, \ldots, c_{1,n_1-1}, c_{2,0}, c_{2,1}, \ldots, c_{2,n_2-1}, \ldots, c_{K,n_K-1})^t$ and $e_l = (0, 0, \ldots, 0, 1)^t$ is the l unit vector and H is the $l \times l$ matirsx with its kth $(1 \leq K \leq l-1)$ row

$$h_k = h_{10}(k), h_{11}(k), \ldots, h_{1,n_1-1}(k), h_{2,0}(k), \ldots, h_{2,n_2-1}(k), \ldots, h_{K,n_K-1}(k)$$

and l^{th} row $h_l = (1, 1, \ldots, 1)$ and for $1 \leq k \leq l-1, 1 \leq i \leq K, 0 = j \leq n_i - 1$

$$h_{ij}(k) = \sum_{r=k+1}^{l} \alpha_r \sum_{n=0}^{r-k-1} (k - r + n)(k - r + n - 1) \ldots (k - r + n - j + 1) \alpha_i^{k-r+n-j}$$

2.2. Special Cases:

(i) Let $l = 1$ that is $A \equiv 1$. In this case, (1) becomes

$$\tilde{\mu} \alpha \tilde{B}(\alpha) - (\lambda^+ - \tilde{\mu})\alpha + \lambda^+ = 0$$

and is has a unique solution $0 < \alpha < 1$, say α_0, and the stationary distribution is given by

$\pi_n = (1-\alpha_0)\alpha_0^n, n \geq 0$

(ii) Let $l = 1$ & $m = 1$ that is $A \equiv 1$ & $B \equiv 1$. In this case, (1) becomes

$$\alpha^2 - (1+\rho)\alpha + \rho = 0$$

and the stationary distribution is given by

$\pi_n = (1-\rho)\rho^n, n \geq 0$

2.3. The First Passage Times:

The sojourn times, which will be treated in the upcoming sections, can be considered as the first passage times of the corresponding Markov chains. So we need to investigate the first passage times for some Markov chains related to compound Poisson processes.

First, we consider the compound Poisson process

$$X(t) = \sum_{i=1}^{N(t)} X_i$$

where $\{N(t), t \geq 0\}$ is a Poisson process with rate v and $\{X_i\}$ is a sequence of independent and identically distributed (IID) random variables, which are independent of $\{N(t), t \geq 0\}$ and have probability mass function $x_k = P(X_1 = k), k = 1, 2, \ldots$ and probability generating function $\Xi(z) = \sum_{n=1}^{\infty} x_n z^n, |z| \leq 1$. Let $U_X(n)$ be the first passage of time of $X(t)$ to the state n, that is

$$U_X(n) = \inf\{t \geq 0 : X(t) \geq n$$

and let $U_X(n,t) = P(U_X(n) \leq t)$ be the probability distribution function of $U_X(N)$. By conditioning the first transition of the process $\{X(t)\}$, we have the following proposition.

2.4. Proposition:

The LST $U_X^*(n,s)$of $U_X(n,t)$ is given recursively by

$$U_X^*(1,s) = \frac{v}{v+s},$$

$$U_X^*(n,s) = \frac{v}{v+s}\left(\bar{x}_n + \sum_{i=1}^{n-1} x_i U_X^*(n-i,s)\right), n \geq 2$$

where $x_i = \sum_{k=i}^{\infty} x_k, i \geq 1$. The double transform $\tilde{U}_X^*(z,s) = \sum_{n=1}^{\infty} z^n U_X^*(n,s)$ is given by

$$\tilde{U}_X^*(z,s) = \left(\frac{z}{1-z}\right)\left(\frac{v(1-\Xi(z))}{s+v(1-\Xi(z))}\right)$$

Now we consider the difference of two independent compound Poisson processes

$$X_1(t) = \sum_{i=1}^{N_1(t)} X_{1,i} \text{ and } X_2(t) = \sum_{i=1}^{N_2(t)} X_{2,i}$$

where $\{N_1(t)\}$ and $\{N_1(t)\}$ are independent Poisson processes with rates λ_1 and λ_2 respectively, and $\{X_{1,i}\}$ and $\{X_{2,i}\}$ are independent sequences of IID random variables with $P(X_{1,i} = k) = x_{1,k}, k \geq 1$ and $P(X_{2,i} = k) = x_{2,k}, 1 \leq k \leq m$. We assume that the random variable $X_{2,i}$ is bound by m. Define a Markov chain

$$Z(t) = X_1(t) - X_2(t), t \geq 0$$

with $Z(0) = 0$. Let Z_n be the state at the instant immediately after the n[th] transition of the process $\{Z(t), t \geq 0\}$ and τ_n the time interval between the n[th] and n+1[th] transitions. Then $\{(Z_n, \tau_n), n \geq 0\}$ is a Markov renewal process with the transition probability matrix $Q_Z(t)$ of the form

$$Q_Z(t) = \begin{matrix} \vdots \\ -2 \\ -1 \\ 0 \\ 1 \\ 2 \\ \vdots \\ \vdots \end{matrix} \begin{pmatrix} \cdots & -2 & -1 & 0 & 1 & 2 & \cdots & \cdots & \cdots \\ & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \cdots & C_1 & C_2 & C_3 & C_4 & C_5 & \cdots & \cdots & \cdots \\ \cdots & C_0 & C_1 & C_2 & C_3 & C_4 & \cdots & \cdots & \cdots \\ & & C_0 & C_1 & C_2 & C_3 & \cdots & \cdots & \cdots \\ & & & C_0 & C_1 & C_2 & \cdots & \cdots & \cdots \\ & & & & C_0 & C_1 & \cdots & \cdots & \cdots \\ & & & & \vdots & \vdots & \vdots & \vdots & \vdots \\ 0 & & & & \vdots & \vdots & \vdots & \vdots & \vdots \end{pmatrix} \left(1 - e^{-(\lambda_1+\lambda_2)t}\right)$$

where each level $i = \{(i,1),(i,2),\ldots,(i,m)\}, i = 0, \pm 1, \pm 2, \ldots$ is the set of m states, the state (i,k) in level i means the state $(i,k) = mi + k - 1$, C_i is the upper triangular matrix

$$C_0 = \begin{pmatrix} c_{-m} & c_{-m+1} & c_{-m+2} & \cdots & c_{-1} \\ & c_{-m} & c_{-m+1} & \cdots & c_{-2} \\ & & c_{-m} & \cdots & c_{-3} \\ & & & \ddots & \vdots \\ 0 & & & & c_{-m} \end{pmatrix}$$

and

$$C_{n+1} = \begin{pmatrix} c_{mn} & c_{mn+1} & \cdots & c_{mn-m+1} \\ c_{mn-1} & c_{mn} & \cdots & c_{mn-m+2} \\ \vdots & \vdots & & \vdots \\ c_{mn-m+1} & c_{mn-m+2} & \cdots & c_{mn} \end{pmatrix}$$

where

$$c_i = \begin{cases} \frac{\lambda_1}{\lambda_1+\lambda_2} x_{1,i} & i \geq 1 \\ \frac{\lambda_2}{\lambda_1+\lambda_2} x_{2,-i} & -m \leq i \leq -1 \\ 0 & i = 0 \end{cases}$$

Define the first passage time as

$$G_Z(n) = \inf\{t \geq 0 : Z(t) \leq n\}$$

and denote its distribution function $G_Z(n,t) = P(G_Z(n) \leq t)$. Now we derive the LST $G_Z^*(-n,s)$ of $G_Z(-n,t), n \geq 1$.

2.5. Proposition:

The LSTs $G_Z^*(-n,s)$ for $1 \le k \le m$ are recursively given by

$$G_Z^*(-1,s) = \sum_{j=1}^{m}[H^*(s)]_{ij} \tag{4}$$

$$G_Z^*(-k,s) = \sum_{j=1}^{m-k+1}[H^*(s)]_{ij} + \sum_{j=m-k+2}^{m}[H^*(s)]_{ij}\, G_Z^*(m-k+1-j,s)$$

and for $n \ge 2$ and $k = m, m-1, \dots, 1$ by

$$G_Z^*(-mn+k-1,s) = \sum_{j=1}^{m}\left[\left(H^*(s)\right)^n\right]_{ij} + \sum_{j=k+1}^{m}\left[\left(H^*(s)\right)^n\right]_{ij} G_Z^*(k-j,s) \tag{5}$$

where $H^*(s)$ is an $m \times m$ matrix, which is the minimal non negative solution of the matrix equation.

$$H^*(s) = \left(\frac{\lambda_1+\lambda_2}{\lambda_1+\lambda_2+s}\right)\sum_{n=0}^{\infty} C_n [H^*(s)]^n \tag{6}$$

While $[H^*(s)]_{ij}$ denotes the (i,j) entry of the matrix $H^*(s)$.

Let $T(i+r,j;i,j')$ be the first hitting time of $\{Z(t), t \ge 0\}$ from state $(i+r,j) = m(i+r)+j-1, r \ge 1, 1 \le j \le m$, to state $(i,j') = mi+j'-1, 1 \le j' \le m$, with the additional requirement that (i,j') is the first state at level i to be visited and $\tau_i(j,k)$ is the first passage time from state (i,j) to state $(i,k), 1 \le j,k \le m, j-k > 0$. When the process $\{Z_n\}$, starting at $(0,1)$, that is, $Z_0 = 0$, hits the level $-n$, and visits state $(-n,j) \in \{(-n,1),\dots,(-n,k)\}$, then $G_Z(-mn+k-1) = T(0,1;-n,j)$; and if the state visited is $(-n,j) \in \{(-n,k+1),\dots,(-n,m)\}$ then $G_Z(-mn+k-1)$ is the sum of $T(0,1;-n,j)$ and $\tau_{-n}(j,k)$. Thus we have for $n \ge 1, 1 \le k \le m$

$$P(G_Z(mn-k+1) \le t) = \sum_{j=1}^{k} P(T(0,1;-n,j) \le t) + \sum_{j=k+1}^{k} P(T(0,1;-n,j) + \tau_{-n}(j,k) \le t) \tag{7}$$

Let $H_{jj'}^{[r]}(t) = P(T(i+r,j;i,j') \le t)$ be the distribution function of $T(i+r,j;i,j')$ and $H_{jj'}^{[r]*}(s)$ be the LST of $H_{jj'}^{[r]}(t), 1 \le j,j' \le m$. Let $H^{[r]}(t)$ and $H^{[r]*}(s)$ denote the $m \times m$ matrices with (j,j') entry $H_{jj'}^{[r]}(t)$ and $H_{jj'}^{[r]*}(s)$ respectively. By the spatial homogeneity for levels of $Q_Z(t)$ the distribution of $T(i+r,j;i,j')$ does not depend on level i but only on r and (j,j') and hence we get

$$H^{[r]*}(s) = [H^*(s)]^r, r \ge 1$$

From the spatial homogeneity of the transition probability $Q_Z(t)$ for states $\tau_i(j,k), j > k$, depends only on the difference of the states $j-k$ and its distribution function is the same as that the $G_Z(k-j)$. Note that, by the Markovian property, $T(0,1;-n,j)$ and $\tau_{-n}(j,k), n \ge 1$ are independent. By taking LST in (7), we have (4) & (5). By using the same arguments as in [11] we have that $H^*(s)$ is the minimal non negative solution of

$$H^*(s) = \left(\frac{\lambda_1+\lambda_2}{\lambda_1+\lambda_2+s}\right)\sum_{n=0}^{\infty} C_n [H^*(s)]^n$$

2.6. Special Cases:

1. If $m > 1$ and $l \leq m-1$, then $C_n = 0, n \geq 2$ and hence we have

$$H^*(s) = \left(\frac{\lambda_1+\lambda_2+s}{\lambda_2+\lambda_2} I - C_1\right)^{-1} C_0$$

where I is the $m \times m$ identity matrix.

2. If $m = 1$, that is, $X_{2,i} \equiv 1$ then $G_Z^*(n,s)$ is obtained from (4) and (6) as

$$G_Z^*(-n,s) = [H^*(s)]^n, n \geq 1$$

and $H^*(s)$ is the solution of the equation

$$z = \frac{1}{\lambda_1+\lambda_2+s}(\lambda_2 + \lambda_1 z \Xi_1(z))$$

(8)

with $|z| < 1$ where $\Xi_1(z) = \sum_{i=1}^{\infty} x_{1,i} z^i$

3. If $l = m = 1$, that is $X_{1,i} \equiv 1$ and $X_{2,i} \equiv 1$, then letting $\Xi_1(z) = z$ in (8) and solving equation (8), we have

$$H^*(s) = \frac{1}{2\lambda_1}\left((\lambda_1+\lambda_2+s) - \sqrt{(\lambda_1+\lambda_2+s)^2 - 4\lambda_1\lambda_2}\right) \quad (9)$$

III. EXAMPLE:

To further investigate the clinical usefulness of CD97 and CD55 expression in GBC, we compared overall survival (OS) according to various clinicopathologic factors including expression levels of CD97 and CD55. Age and sex did not influence the OS. However, patients with high histologic grade, advanced pathologic T stage, clinical stage, nodal metastasis, positive venous/lymphatic invasion, CD97 and CD55 expression were significantly correlated with short survival. The median survival time of patients with GBC was 38 months (range, 1-119 months). The survival curves according to CD97 and CD55 expression are shown in figure (1) and (2). The OS rates of CD97 negative and CD97 positive were 42.9% and 12.5% respectively {figure (1) & $P = 0.02$} and the OS rates of CD55 negative and CD55 positive were 45.8% and 17.8% respectively {figure (2) & $P = 0.02$}. These analyses with Kaplan Meier method clearly showed the significant impact of CD97 and CD55 expression on clinical outcome [12-15] & [17-20].

Figure 1: Correlation of CD97 expression with overall survival rates in 138 patients with GBC (Compared with Log Rank test)

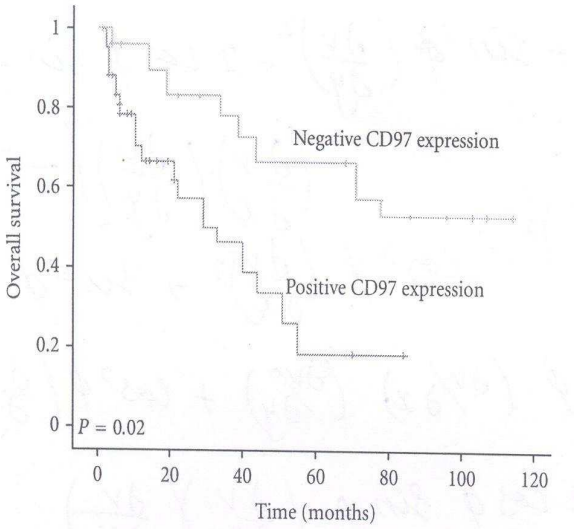
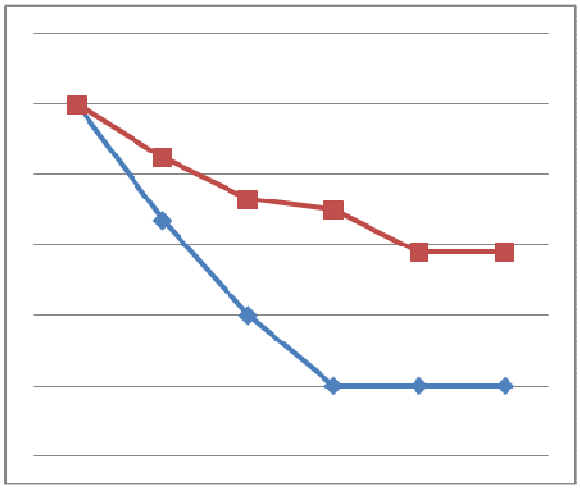


Figure 2: Correlation of CD55 expression with overall survival rates in 138 patients with GBC (Compared with Log Rank test)



Red Line: Negative CD97 Expression
Blue Line: Positive CD97 Expression

Figure 4: Correlation of CD55 expression with overall survival rates in 138 patients with GBC using Gamma Distribution

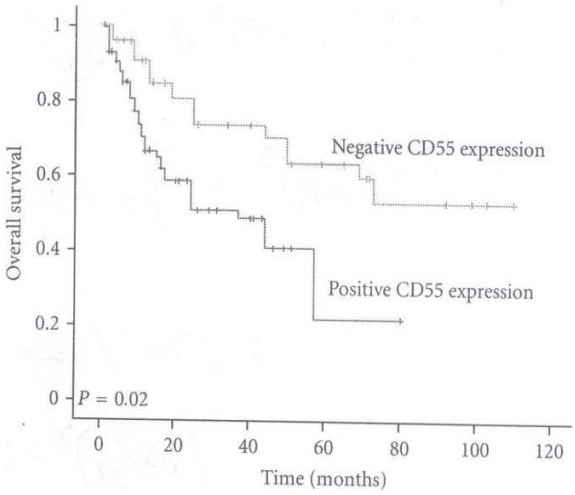
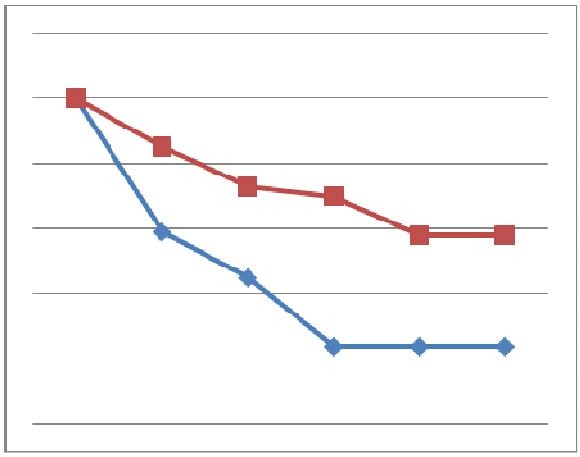


Figure 3: Correlation of CD97 expression with overall survival rates in 138 patients with GBC using Gamma Distribution



Red Line: Negative CD55 Expression
Blue Line: Positive CD55 Expression

IV. CONCLUSION:

Our results provide convincing evidence for the first time that the expressions of CD97 and CD55 are both upregulated in human GBC. The expression levels of CD97 and CD55 in GBC were associated with the severity of the tumor. Furthermore, CD97 and CD55 expressions were independent poor prognostic factors for overall survival in patients with GBC. The minimal non negative solution of the $m \times m$ matrix equation in the Markovian G-Queue by using gamma distribution gives the same results as the medical report mentioned above. The medical reports {Figure (1) & (2)} are beautifully fitted with the mathematical model {Figure (3) & (4)}; $(i.e)$ the results coincide with the mathematical and medical report.

REFERENCES:

1. Gelenbe E, "Product from Network with Negative and Positive Customers", Journal of Applied Probability, 28 (1991), Page Number 656-663.
2. Harrison P G and Pitel E, "Sojourn times in Single Server Queues with Negative Customers", Journal of Applied Probability, 30 (1993), Page Number 943-963.
3. Harrison P G and Pitel E, "Response Time Distribution in tandem G-networks", Journal of Applied Probability, 32 (1995), Page Number 224-246.
4. Harrison P G and Pitel E, "The M/G/1 Queue with Negative customers", Advanced Applied Probability, 28 (1996), Page Number 540-556.
5. Henderson W, Northcote B S & Taylor P G, "Geometric Equilibrium distribution for Queue with Interactive Batch Departures", Annual Operations Research, 48 (1994), Page Number 493-511.
6. Jain G & Sigman K A, "Pollaczek Khinchine Formulation for M/G/1 Queues with Disasters", Journal of Applied Probability, 33 (1996), Page Number 1191-1200.
7. Mustafa T, Eckert A & Klonisch T, "Expression of the Epidermal Growth Factor Seven Transmembrane Member CD97 Correlates with Grading and Staging in Human Oral Squamous Cell Carcinomas", Cancer Epidemiology Biomarkers and Prevention, Volume 14, Number 1, Page Number 108–119, 2005.
8. Kwakkenbos M J, Kop E N & Stacey M, "The EGF-TM7 Family: a Post Genomic View", Immunogenetics, Volume 55, Number 10, Page Number 656-666, 2004.
9. Lea S, "Interactions of CD55 with Non Complement Ligands", Biochemical Society Transactions, Volume 30, Number 6, Page Number 1014-1019, 2002.
10. Miller R G, "A Contribution to the Theory of Bulk Queues", Journal of Royal Statistics Society Service, b21 (1959), Page Number 320-337.
11. Netus M F, "Structured Stochastic Matrices of M/G/1 Type and their Applications", Marcel Dekker, New York 1989.
12. P. Senthil Kumar, A. Dinesh Kumar & M. Vasuki, "Stochastic Model to Find the Diagnostic Reliability of Gallbladder Ejection Fraction Using Normal Distribution", International Journal of Computational Engineering Research (IJCER), Volume 4, Issue 8, August 2014, Page Number 36-41.
13. P. Senthil Kumar, A. Dinesh Kumar & M. Vasuki, "Stochastic Model to find the Gallbladder Motility in Acromegaly Using Exponential Distribution", International Journal of Engineering Research and Applications (IJERA), Volume 4, Issue 8 (Version 2), August 2014, Page Number 29-33.
14. P. Senthil Kumar, A. Dinesh Kumar & M. Vasuki, "Stochastic Model to Find the Gallbladder Dynamics with Gallstones Results Using Exponential Distribution", IFRSA's International Journal of Computing (IIJC), Volume 4, Issue 3, July 2014, Page Number 619-622.
15. P. Senthil Kumar, A. Dinesh Kumar & M. Vasuki, "Stochastic Stochastic Model to Find the Multidrug Resistance in Human Gallbladder Carcinoma Results Using Uniform Distribution", International Journal Emerging Engineering Research and Technology (IJEERT), Volume 2, Issue 4, July 2014, Page Number 416-421.
16. Kwakkenbos M J & Pouwels M Matmati, "Expression of the largest CD97 and EMR2 isoforms on leukocytes facilitates a specific interaction with chondroitin sulfate on B cells", Journal of Leukocyte Biology, Volume 77, Number 1, Page Number 112–119, 2005.
17. Wobus M, Vogel B, Schm Ucking E, Hamann J & Aust G, "N-Glycosylation of CD97 within the EGF Domains is Crucial for Epitope Accessibility in Normal and Malignant Cells as well as CD55 Ligand Binding", International Journal of Cancer, Volume 112, Number 5, Page Number 815–822, 2004.
18. Liu D, Trojanowicz B & Radestock Y, "Role of CD97 Isoforms in Gastric Carcinoma", International Journal of Oncology, Volume 36, Number 6, Page Number 1401–1408, 2010.

19. Wobus M, Huber O, Hamann J, & Aust G, “CD97 Over Expression in Tumor Cells at the Invasion Front in Colorectal Cancer (CC) is Independently Regulated of the Canonical Wnt Pathway”, Molecular Carcinogenesis, Volume 45, Number 11, Page Number 881– 886, 2006.
20. Mustafa T, Klonisch T & Hombach-Klonisch S, “Expression of CD97 and CD55 in Human Medullary Thyroid Carcinomas,” International Journal of Oncology, Volume 24, Number 2, Page Number 285–294, 2004.