



UNIVERSITI PUTRA MALAYSIA

**IDENTIFICATION OF DEREGULATION IN PROTEIN EXPRESSION
LEVEL OF ERLOTINIB-RESISTANT H1299 CELL LINES**

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PENGESAHAN

Dengan ini adalah disahkan bahawa projek yang bertajuk “**Identification of deregulation in protein expression level of erlotinib-resistant H1299 cell lines**” telah disiapkan serta dikemukakan kepada Jabatan Mikrobiologi oleh **Syukriyah Binti Mat Daud (162549)** sebagai syarat untuk kursus BMY 4999 projek.

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ABSTRACT

Erlotinib, a small-molecule epidermal growth factor receptor (EGFR) tyrosine kinase inhibitor, has been shown to be an effective solution in treating non-small cell lung cancer (NSCLC). However, most patients who initially show a good response to erlotinib treatment eventually develop resistant and experience progressive disease. There is no absolute answer on how the cells can develop resistance against the erlotinib. It was suggested that changes in the cell cycle could contribute to the acquired resistance of NSCLC. In this study, untreated H1299 and erlotinib-resistant H1299 (H1299-R) were used to compare proteins expression levels involved in cell cycle. The main cell cycle players that were investigated included Cyclin A and E, Cyclin-dependent kinases (CDK) 2, 4, and 6, p21, NF κ B, and β -actin. A calorimetric method, alkaline phosphatase, was used to detect the amount of proteins present in the sample. Although the concentration of the protein loaded into the gel was increased from 75 μ g to 85 μ g, the results obtained were similar. Both cell lines possessed β -actin and Cyclin A proteins only.

ABSTRAK

Erlotinib, molekul kecil sebagai perencat epidermal growth factor receptor (EGFR) tyrosine kinase, telah terbukti menunjukkan penyelesaian yang berkesan untuk merawat non-small cell lung cancer (NSCLC). Walaubagaimanapun, kebanyakan pesakit yang pada asalnya bertindak balas dengan erlotinib akhirnya menjadi tahan dan mengalami penyakit yang berterusan. Tiada jawapan yang pasti bagaimana sel-sel tersebut boleh menimbulkan tahan terhadap erlotinib. Ada yang mencadangkan bahawa perubahan dalam kitaran sel mungkin yang menyumbang kepada mendapat tahan pada NSCLC. Untreated H1299 dan erlotinib-resistant H1299 (H1299-R) telah digunakan untuk membandingkan paras ekspresi protin yang terlibat dalam kitaran sel. Pemain utama dalam kitaran sel yang dikaji termasuk cyclin A dan E, cyclin-dependent kinases (CDK) 2, 4, dan 6, p21, NF κ B dan Beta actin. Kaedah kalorimetrik, alkaline phosphatase telah digunakan untuk menentukan jumlah protin dalam sel. Walaupun kepekatan protin yang dimasukkan ke dalam gel telah dinaikkan dari 75 μ g kepada 85 μ g, keputusan yang diperolehi adalah sama. Kedua-dua sel mempunyai β -actin dan Cyclin A.

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CHAPTER 1

INTRODUCTION

The lungs are a pair of spongy, air-filled organs located on either side of the chest. Their principal function is to perform gaseous exchange between the body and the surroundings. They are used to supply oxygen, and to release carbon dioxide from the bloodstream.

Cancer is now believed to result from perturbations in the cell cycle that result in unlimited proliferation and an inability of a cell to undergo differentiation and/or apoptosis (Malumbres and Barbacid, 2009). However, the exact mechanism of the cancer is not yet known, and different cancers seem to have different triggers.

Lung cancers have been classified into two major types, which are small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). However, NSCLC is the most frequently diagnosed type of lung cancer and is the leading cause of cancer-related mortality worldwide (Travis et al., 1995; Gridelli et al., 2007).

According to the American Cancer Society, most lung cancer statistics include both small cell and non-small cell lung cancers (NSCLC). Lung cancer is the second most common cancer in both men and women (not counting skin cancer). Lung cancer accounts for about 27% of all cancer deaths and is by far the leading cause of cancer death among both men and women. The mortality rate of lung cancer is much higher than that of colon, breast, and prostate cancers combined.

Studies show that mutations in the tyrosine kinase (TK) domain of the epidermal growth factor receptor (EGFR) gene of NSCLC are the one of the causes of the tuour occurence. The over expression of EGFR has been reported and implicated in the progression of many human maglinant tumours, including NSCLC (Inamura et al., 2010).

Surgical resection, one of the treatments for NSCLC case, is not the best solution as it is only viable for certain types of early stage cancer. As the majority of lung cancer cases are diagnosed in the late stages, it is not always an option. Standard treatment such as chemotherapy, radiotherapy, and surgery has reached a plateau in this disease (Gridelli et al., 2007). Chemotherapy with active agents recognized as a better treatment. Because of that, more research has been conducted on targeting the EGFR as a treatment.

Increased EGFR expression is known to correlate with poor clinical outcome in patients with NSCLC. The EGFR has been considered a potential therapeutic target because of this. In recent years, several compounds that have been develop to target the EGFR signaling pathway have demonstrated significant anticancer activity (Noonberg and Benz, 2000; Herbst and Bunn, 2003).

The two reversible EGFR tyrosine kinase inhibitors approved for the treatment of advanced NSCLC are elotinib and gefitinib. Of these, treatment using erlotinib has shown a significant improvement in median survival, quality of life, and related symptoms in an unselected population of advanced NSCLC patients (Gridelli et al., 2007).

Erlotinib (Tarceva; Genentech, South San Francisco, CA), is a synthetic anilinoquinazoline compound that acts by competitive inhibition. It competes with adenosine triphosphate (ATP) at the TK domain of the receptor, resulting in an inhibition of the EGFR signaling pathway (Machetti et al., 2005). Other than that, erlotinib also has significant anti tumour activity as a first-line treatment (Gridelli et al., 2007).

Although erlotinib has been approved as a therapy for advanced and chemoresistant NSCLC, however the development of resistance against this drug can reduce the drug's efficacy in treatment. Most of the patients who initially respond to erlotinib eventually become resistant and experience progressive disease within a year or two (Gazdar, 2009).

Development of resistance against erlotinib limits the chances of surviving the cancer, which already has a poor overall survival rate. Hence, other treatments that involve the manipulation of the cellular mechanisms may serve as an alternative to help to solve this problem. One of the alternatives is to study the deregulation of protein expression in the erlotinib-resistant NSCLC cell-lines. The objectives of the study are:

1. To optimize the amount of total lysate required to detect selected proteins in H1299 cell lines.
2. To evaluate the level of proteins expression of main cell cycle players in H1299 cell lines.
3. To compare between protein expression level of the selected cell cycle players in H1299 and H1299R cell lines.

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