Review Article

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Review on Personalised Medicine for Cancer Treatment

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Abstract

Personalized medicine is individual medical care that is based on one's own genes and disease conditions. That comes from studies of human genes and the genes in different cancers. Cancer is one of the dangerous leading diseases. In 2020 alone, India will have 1.32 million new cancer cases which will lead to 3 patients per minute. Numbers of cancer deaths 851678 were reported during 2020 in India alone. Recently, personalized medicine has mainly involved the systemic use of genetic or other data about individual patients to enhance that patients' prophylactic and therapeutic care. Information about a patient's proteinaceous genetic and metabolic profile could be used to make personalized medical care. This spot of recent advances in treatment that have resulted in improved patient outcomes progresses is still poor for many patients with certain cancer with a high death rate associated with late diagnosis. where molecular assays that help to measure the level of protein and genes or specific mutation are used to provide a specific therapy for an individual condition by satisfying disease condition and helps in choosing a proper drug therapy to that patient's specific needs additionally this method used to estimate a patient risk factor and. In this review we discussed, recent advances, challenges and future perspective of personalized medicine in cancer.

Keywords: Personalized medicine; Cancer; Advanced treatment

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Introduction

Personalized medicine is an emergency approach to patient treatment in which based on individual's characteristics, including the genetic profile; guide the clinical decisions, aiming for the right treatment for right person at right time [1]. It is based on Pharmacogenetic and Pharmacogenomic and Pharmacoproteomic information but consideration for individual patients. A cell with normal DNA developed into cancerous cell through the genetic changes. The growth of cancer complicate progress difference in the levels of DNA, RNA, Proteins and metabolic between cancer patients and healthy person could be called Biomarkers [2]. The last few years cancer patient's treatment has been revolutionized as several molecular alterations have been identified as diverse of cancer development and progression. The Biomarker based approach process basic science to cancer treatment. The first molecular based medicine for the patients was used Endocrine therapy in breast cancer [3] [**Figure 1**].

History of Personalized Medicine

On April 16, 1999, a short article entitled "New Era of Personalized Medicine: Targeting Drugs for Each Unique Genetic Profile," appeared in The Wall Street Journal and here, the public was introduced to the term "personalized medicine" for the first time [4]. Two staff reporters, Robert Langreth and Michael Waldholz, wrote that described the formation of the Single Nucleotide Polymorphisms (SNP) Consortium. This consortium was established as collaboration between a number of pharmaceutical companies and academic research institutions in the U.S. and U.K. with the support from the Welcome Trust Foundation. The goal to provide a public resource on SNPs in the human genome, and the plan was to identify at least 300,000 [5]. The pharmaceutical companies join the consortium to develop drugs designed to target the individual patient's molecular and

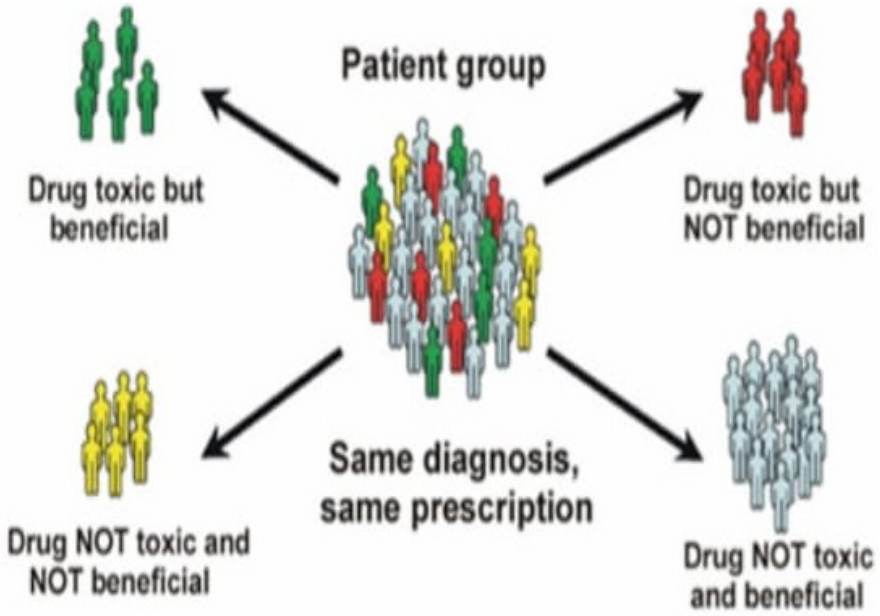

Figure 1 Different types of effects on patients based on Traditional model.

genetic makeups and thereby individualize pharmacotherapy. A few months after the article first appeared in The Wall Street Journal, it reappeared in "The Oncologist" [6]. Republishing The Wall Street Journal article 20 years ago, The Oncologist became the first journal to introduce the idea of personalized medicine to the medical community.

The article by Langreth and Waldholz contained several of the arguments for individualizing pharmacotherapy, as we know them, from the past 20 years of discussions [7]. They stated that the current pharmacotherapy was a “one-size-fits-all” approach in which even the best drugs work in only 50%–70% of the patients. This aspect was also addressed a couple of years later by Spear et al. in an article published in Trends in Molecular Medicine in 2001, which has been quoted frequently in relation to the discussion about efficacy of pharmacotherapy and personalized medicine. Langreth and Waldholz also mentioned disease heterogeneity and the genetic variability as a factor that may impact the treatment outcome negatively. Furthermore, it was emphasized that an understanding of this variability might be able to improve the treatment outcome for the single patient [**Figure 2**].

The concept of companion diagnostics was also described but not mentioned in general terms as such; however, the authors discussed a simple diagnostic test that could inform the treating physicians of who would benefit from certain drugs and who was at risk of developing serious side effects. The description given in the article is very close to the definitions of companion diagnostics, recently defined in different guidance documents issued by the regulators in the U.S., the European Union (EU), and other countries worldwide. The article gave several examples of when a diagnostic test could be potentially useful as a treatment decision tool. One example was in relation to treatment of women with breast cancer. Just a few months before the article was published in The Wall Street Journal, the first treatment based on a monoclonal antibody guided by a diagnostic test was approved by the Food and Drug Administration (FDA). At the end of September 1998, trastuzumab (Herceptin; Genentech, South San Francisco, CA) obtained regulatory approval for treatment of patients with metastatic breast cancer whose tumors overexpress the HER2 protein [8]. An immunohistochemical assay (HercepTest; Dako, Glostrup, Denmark) for detecting HER2 overexpression in the tumor tissue was approved simultaneously with the drug[9].This assay aimed at selecting patients likely to respond to treatment with trastuzumab. The development of trastuzumab was the first drug to use the drug-diagnostic codevelopment model, in which a companion diagnostic assay is developed in parallel to the drug based on a thorough molecular understanding of the pathophysiology and the mechanism of action of the drug. Since the turn of the century this model has proven successful numerous times, especially within oncology and hematology [10].

Although trastuzumab was the first targeted cancer drug to use the drug-diagnostic codevelopment model successfully, the first steps to combine drugs and diagnostics were taken 2 decades earlier. Here, the selective estrogen receptor modulator tamoxifen (Nolvadex; AstraZeneca, Cambridge, U.K.) was developed for treatment of metastatic breast cancer, and data on the estrogen receptor (ER) status was correlated with treatment outcome. Based on the results from a phase II trial, published in 1976, the investigators concluded that “the high degree of correlation between response and positive ER suggests the value of this test as a means to select patients for tamoxifen treatment” [11]. However, in this phase II trial, testing for ER status was only performed in 17 out of 76 enrolled patients, and the test result was not used as a selection criterion as we know it from today’s enrichment trial design.

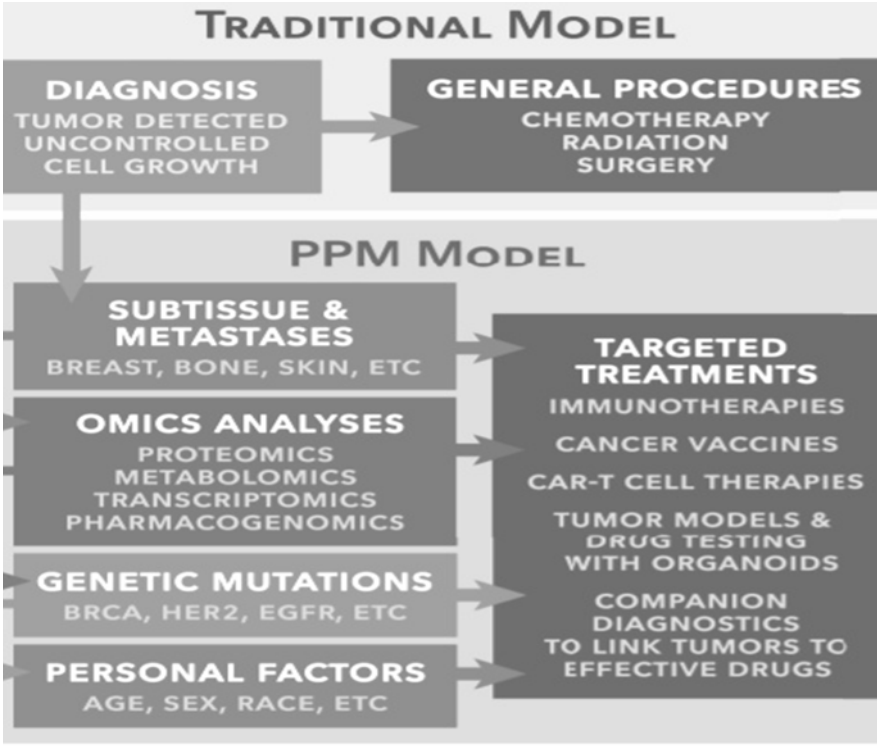

Figure 2 Traditional model VS PPM model.

Just after the turn of the century, another important milestone for targeted therapy was passed, namely the development and regulatory approval of the small molecule tyrosine kinase inhibitor imatinib (Gleevec; Novartis, Basel, Switzerland) [12]. This drug inhibits the BCR-ABL protein tyrosine kinase, a constitutively activated tyrosine kinase, which is present in virtually all patients with chronic myeloid leukemia (CML). The cause of CML is the translocation of regions of the BCR and ABL genes to form a BCR-ABL fusion gene, and the product of this gene is the BCR-ABL protein. Clinical studies with imatinib induced impressive high rates of both cytogenetic and hematologic responses in patients with CML [13,14].

Why We Go For Personalized Medicines

The different cells have the same DNA, genes coding in one organ and their cells behave differently than genes in other organs. In cancer, the gene's expression pattern is different but different tumors may have the same DNA. Some technologies used for gene expression micro assay allow us to examine the gene expression profile of 100s of genes at a time and differentiate a cancer associated gene expression profile normal profiling [15]. The personalized medicines are treatment generated before the reference to the patient's disease history then make the individual's genetic makeup to decide the proper regimen for treatment. Care taken based on patients family history, environment, social circumstances and lifestyle. Bladder cancer, brain cancer, cervical cancer, Gastrointestinal stomach tumor (GIST), lungs cancer intracellular agent (vemurafenib and Olaparib) and ovarian, breast and prostate cancer. Additionally such a method can be used to assess a patient's risk factor for the number of conditions and to tailor individually preventative treatment [16].

Some examples for personalized medicine in treatment of cancer

Metastatic malignant melanoma

Metastatic malignant is a disease with a very poor prognosis median survival at diagnosis is only 18 months in 4 stages. However, recent advanced in personalized therapy have resulted in a significant change in outlook for a large subset of metastatic malignant melanoma patients, 66% of malignant melanoma have a BRAF oncogene mutations, resulting in single amino acid substitution V600E, which determine increased diseased condition and decreasing response to existing cytotoxic chemotherapy vemurafenib is a potent and selective RAF inhibitor reduce the risk of mortality by 63% and the risk of death or disease progression by 74% in the patients with un selectable , previously on treated stage lllC/IV BRAF V600E mutation positive malignant melanoma compared with standard treatment [17,18].

Breast cancer

Breast cancer is the leading cancer in females. The factors that are involved in breast cancer are genetic, environmental, and behaviour based on diet, exercise, and lifestyle. Preventative approaches are mammogram screening has been adapted by the large population. Screening for two types of BRCA1 and BRCA2 mutations are also common practices in clinics for women in parity status at different age groups [19]. The current and future personalized approaches in breast cancer song et al are discussed.

Trastuzumab is the well-known example for the breast cancer a humanized IgGi monoclonal antibodies in the breast cancer patients whose tumors overexpressed the oncogene HER2.HER2 is responsible for the cell proliferation and over expressed in 20-25% of patients with breast cancer. HER2 positive status confesses a poor prognosis but it is also a stronger predictor its response to trastuzumab [20]. A coheane systematic review of 8 controlled trials involving 11,991 patients. Patients showed the breast cancer range reduced by one-third. Trastuzumab was added to standard chemotherapy regimen for longer than 6 months in the subset of patients who over expressed the HER2 growth factors. The recurrent rate of breast cancer reduced 40%.

Colon Cancer

Cetuximab in CRC (Colonrectal Cancer),the epidermal growth factor receptor (EGFR) is overexpressed in many epithelial cancers, resulting in dysregulated cell proliferation and an aggressive phenotype [21]. EGFR inhibition is therefore a promising therapeutic strategy in personalized medicine research. Cetuximab, a monoclonal antibody directed against EGFR, has proven utility in patients with CRC expressing wild-type KRAS, which encodes a downstream effector of EGFR involved in intracellular signalling. A randomized trial of 572 patients with CRC unresponsive to standard chemotherapy demonstrated that wild-type KRAS status predicted response to cetuximab, with improved quality of life and almost doubled overall and progression-free survival, when compared to patients with wild-type KRAS treated with supportive care only. Patients with mutated KRAS did not benefit from cetuximab treatment [22]. Cetuximab is therefore licensed for use in the 60% of CRC tumours expressing the wild-type KRAS gene [23].

The use of KRAS status as a predictor of response to EGFR inhibitors in CRC is being extended to other cancers, such as non-small cell lung cancer (NSCLC). Predicting response to therapies based on gene mutation status allows individualized therapy and has potential health economic benefits by reducing prohibitive treatment costs [22]. Targeted therapies are expensive, and the cost of providing personalized medicine must not be underestimated, particularly in an era of public fiscal austerity. Personalized medicine provides the prospect of health-economic gains, on a population basis, by limiting expenditure to where it is most cost effective by ensuring drugs are targeted where they are going to be most effective and least toxic, costs of treatment and complications can be reduced.

Lung Cancer

There are two main types of lung cancer: non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC). Small cell lung cancer makes up about 20% of all lung cancer cases. Cancer made up of both types is called mixed small cell/large cell cancer. If the cancer started somewhere else in the body and spread to the lungs, it is called metastatic cancer to the lung. Because of the heterogeneity of cells, it is extremely difficult to treat lung cancer. Regular treatment techniques, mainly surgical and chemotherapy have been used to treat lung cancer. Based on recent data and understanding of the genetic basis of lung cancer, EGFR, K-ras, ALK, MET, CBL, and COX2 are being used as therapeutic targets [24]. Curran recently demonstrated utilization of crizotinib in the treatment of NSCLC [25]. Crizotinib is and inhibitor of anaplastic lymphoma kinase (ALK) and showed promising results. Other investigators have also observed benefits of using crizotinib for lung cancer treatment [26,27]. Erlotinib and EGFR mutated lung cancer has also provided significant clinical results. FLEX trial has also demonstrated promising results [28]. Data from histopathological examination and the patient's history also is considered in evaluating the state of the disease and its aggressiveness. Nyberg et al. [29] studied association between SNPs and acute interstitial lung disease in Japanese population undergoing treatment with gefitinib. This research provided basis for further research. In Chinese population, ABCC1 polymorphism was found to be associated with lung cancer susceptibility in patients undergoing chemotherapy [30]. Genomic variations in EGFR and ERCC1 have also been correlated with drug response in small cell lung cancer patients [31,32].

Challenge and Future Prospective Of Personalised Medicine in Cancer

As personalized medicine gains more popular and more commonplace, for those the treatment for affected. When personalized treatment is used, there should be a greater number of tests used to diagnose a disease. For the greater number of tests, healthcare is expensive to provide for the insurance companies for the long haul, the usage of personalized medication will be advantageous because it will provide the ability to respond to various interventions and treatments will help in the development of disease preventive strategies. Only 5% of commercial health insurance providers offer genetic testing coverage. This question the whether customized medicine can be successfully implemented in the United States under the current system for delivering healthcare.

Doctors and primary care physicians should do their jobs better by gaining an educational background and hands-on experience in genomic and proteomic tests and their interpretation, developing the decision-making tools, and creating service lines around prevention and wellness to replace revenues lost by traditional medical practice. When deciding the treatment, an oncologist needs to weigh not just the genes and biology of the cancer but the age, medical condition, lifestyle, and goals of each patient. Government should play an active role in approving personalized medicine tests quickly and provide incentives for using them. The Genomics and Personalized Medicine Act were introduced in the U.S. Congress and covers scientific barriers, adverse market pressures, and regulatory obstacles. Public education and communication about personalized medicine should be part of the outreach to the population at large. Furthermore, consumers should be protected from possible harm resulting from the premature translation of research findings, and the innovative and cost-effective application of discoveries that improve personalized medical care should be encouraged [33].

Insurance companies base their premium calculations on costs for huge populations, whereas the price of tailored medicine is determined for considerably fewer people need to be updated

for customized therapy Large-population models to be successful. By avoiding needless and ineffective treatments, preventing side effects, and delivering more effective targeted medicines, a precise diagnosis will save the payer money over time. Additionally, this will support the "pay for performance" idea and lower health care expenditures. In order to adopt customized treatment, it is also important to consider ethical concerns and genetic testing; data on these topics should be gathered and studied. Health care providers must create instruments to retain sophisticated patient data and tools to aid in making decisions [33].

The incidence of cancer increased year by year, and more and more people die of cancer. Because there is a huge difference in the 5-year survival rate of early treatment and late treatment, so early diagnosis is particularly necessary. We can use the gene pattern derived from high-risk group to perform risk assessment, and improve cancer screening, early diagnosis, and treatment.

Due to the tumor heterogeneity, different patients have different gene mutations, which lead to different sensitivity to the drug. Thus, identity of differentially expressed genes was needed for precise treatment. Some effective cancer biomarkers have been discovered and used in clinic. For example, CEA and AFP are the most common tumor markers that are derived from abnormal protein products of tumor cells. However, due to low specificity of these proteins, it only plays a supporting role, but not a determing factor in clinic diagnosis. With further studies, more and more differentially expressed proteins or peptides will be found; these proteins or peptides combined to form a pattern, increase specificity of the tumor diagnosis, and reduce the false positive rate.

The patter that mentioned above could be composed by different types of biomarkers from genome, transcriptome, proteome, metabolome, and radiome. Not only the same kind of molecular markers can be composed of pattern, different kinds of molecular markers can also be combined together to form an integrative pattern, for example, mass spectrometry imaging data and gene expression microarray data are composed into an integrative pattern. Analysis results show that a pattern that combined MSI data and biological data is able to provide a meaningful discrimination between samples. It might be a useful tool to identify potential in large-scale biological, especially to identify cancer patient and health people.

However, there are still some problems regarding pattern recognition. First, it perhaps has different variations of genes or proteins in the different stages of tumor development. How to identify these genes and their proteins remains a challenge. Second, the recurrence of tumor is not only a simple change of gene or protein, but also is closely related to the patient's living environment and eating habits. Only focus on one aspect is not enough. In the future, one has to combine these laboratory parameters with the patients' daily habits together to create a pattern model, in order to achieve a more accurate prediction of tumor and individualized treatment. Combined with other factors, such as age, sex, family history, obesity, lifestyle, etc. The model one expects to establish is a series of data from patients which can predict the probability of occurrence of a tumor, and is able to change specific medications according to key sites. It is necessary to establish a model for prediction, prognosis and the best choice of drug use for cancer [34] [**Figure 3**].

Application of Personalized Medicines

- Personalized medicines will create a more unified treatment approach specific to the individual and their genome [35].

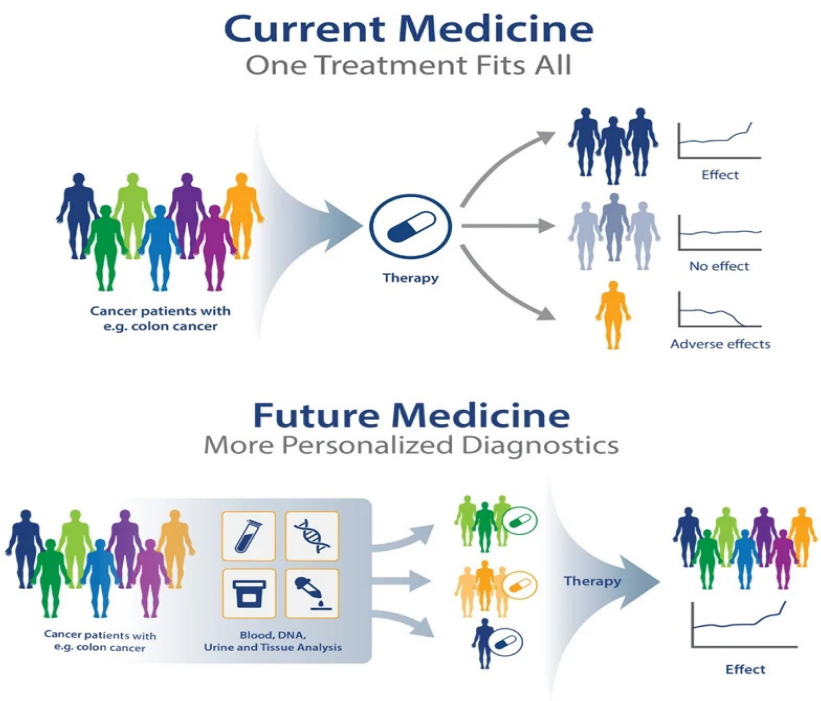

Figure 3 Future of personalized medicine.

- Personalized medicines are about tailoring a treatment as individualized as the disease. Customize disease-prevention strategies. Prescribe more effective drugs avoid prescribing, side effect and failure rate of pharmaceutical clinical trials [35].
- Having an individual's genomic information can be significant in the process of drug development. Having a detailed account of an individual's genetic play a major role in deciding if a patient can be chosen for inclusion or exclusion in the final stages of a clinical trial. In addition, drugs that are deemed ineffective for the larger population can gain approval by using personal genetics data to qualify the effectiveness and need for that specific drug or therapy even though it may only be needed by a small percentage of the population [35].
- Physicians commonly use a trial and error strategy until they find the correct drug therapy that is more effective for their patient. With personalized medicine, these drug therapy can be more specifically tailored by predicting how an individual's body will respond and if the therapy will work based on their genome. This has been summarized as "therapy with the right drug at the right dose in the right patient." This approach is most accurate [35].
- Gene profiling for the heart transplant patients has enabled the prediction of acute cellular rejection that was before detected by an operative procedure after damage had occurred [36].
- DNA-based gene profiles for cancer susceptibility, gene expression profiling has been used to generate risk of being cancer patients and determine origin of cancer [36].
- Genetic screening begins at birth with newborn screening tests for a suitable of conditions. Whole genome sequencing has been useful in establishing a diagnosis for newborns affected with severe congenital malformations or other undiagnosed health issues requires intensive care unit [36].

Conclusion

We are entering a future era in which it is possible to provide rational therapy to patients on the basis of personalized data. This may provide the greatest opportunity in history to take big steps forward in improving patient healthcare. However, as we attempt to move personalized cancer therapy into standard of care, there are many challenges that need to be overcome. A continuous effort by major cancer centers acting as committees and sharing information will lead to the incredible promise of personalized medicine in a rapid and efficient manner.

References

1 Jackson SE, Chester JD (2015) Personalised cancer medicine. Int j cancer 137(2): 262-266.

2 Gambardella V, Tarazona N, Cejalvo JM, Lombardi P, Huerta M et al. (2020) Personalized medicine: recent progress in cancer therapy. Cancers 12(4): 1009.

3 Cheng T, Zhan X (2017) Pattern recognition for predictive, preventive, and personalized medicine in cancer. EPMA J 8(1): 51-60.

4 Langreth R, Waldholz M (1999) New era of personalized medicine: Targeting drugs for each unique genetic profile. The Oncologist 4: 426-427.

5 Sachidanandam R, Weissman D, Schmidt SC (2001) A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. Nature 409: 928-933.

6 Spear BB, Heath, Chiozzi M, Huff J (2001) Clinical application of pharmacogenetics. Trends Mol Med 7: 201-204.

7 Jorgensen JT (2015) Clinical application of companion diagnostics. Trends Mol Med 21: 405-407.

8 Slamon DJ, Leyland, Jones B, Shak S (2001) Use of chemotherapy plus a monoclonal antibody against HER2 for metastatic breast cancer that overexpresses HER2. N Engl J Med 344: 783-792.

9 https://www.taylorfrancis.com/chapters/edit/10.1201/9780429066504-3/development-herceptest%E2%84%A2-bench-bedside-jan-tr%C3%B8st-j%C3%B8rgensen-henrik-winther

10 Jørgensen JT Hersom M (2016) Companion diagnostics-a tool to improve pharmacotherapy. Ann Transl Med 4: 482.

11 Lerner HJ, Band PR, Israel L (1976) Phase II study of tamoxifen: Report of 74 patients with stage IV breast cancer. Cancer Treat Rep 60: 1431-1435.

12 Chabner BA (2001) The oncologic four minute mile. The Oncologist 6: 230-232.

13 Druker BJ, Talpaz M, Resta DJ (2001) Efficacy and safety of a specific inhibitor of the BCR-ABL tyrosine kinase in chronic myeloid leukemia. N Engl J Med 344: 1031-1037.

14 Kantarjian H, Sawyers C, Hochhaus A (2002) Hematologic and cytogenetic responses to imatinib mesylate in chronic myelogenous leukemia. N Engl J Med 346: 645-652.

15 Offit K (2011) Personalized medicine: new genomics, old lessons. Hum Genet 130: 3-14.

16 Baehner FL, Lee M, Demeure MJ (2011) Genomic Signatures of cancer: basis for individualized risk assessment, selective staging and therapy. J Surg Oncol 103: 563-573.

17 Chapman PB, Hauschild A, Robert C (2011) Improved survival with vemurafenib in melaNoma with BRAF V600E mutation. N Engl J Med 364: 2507-2516.

18 Tsai J, Lee JT, Wang W (2008) Discovery of a Selective inhibitor of oncogenic B-Raf kinase with potent antimelanoma activity. Proc Natl Acad Sci USA 105: 3041-3046.

19 Song M, Lee KM, Kang D (2011) Breast cancer prevention based on gene-environment interaction. Mol Carcinog 50: 280-290.

20 Goldenberg MM (1999) Trastuzumab, a recombinant DNA-derived humanized monoclonal antibody, a Novel agent for the treatment of metastatic breast Cancer. Clin Ther 21: 309-318.

21 Wheeler DL, Dunn EF, Harari PM (2010) Understanding resistance to EGFR inhibitors-impact on future treatment strategies. Nat Rev Clin Oncol 7: 493-507.

22 Karapetis CS, Khambata Ford S, Jonker DJ (2008) K-ras mutations and benefit from cetuximab in advanced colorectal cancer. N Engl J Med 359: 1757-1765.

23 Fearon ER (2011) Molecular genetics of colorectal cancer. Annu Rev Pathol 6: 479-507.

24 Salgia R, Hensing T, Campbell N, Salama AK, Maitland M et al. (2011) Personalized treatment of lung cancer. Semin Oncol 38: 74-83.

25 Curran M P (2012) Crizotinib: in locally advanced or metastatic non-small cell lung cancer. Drugs 72(1): 99-107.

26 Ou, SH (2011) Crizotinib: a novel and first-in-class multitargeting tyrosine kinase inhibitor for the treatment of anaplastic lymphoma kinase rearranged non-small cell lung cancer and beyond. Drug Des Devel Ther 5: 471-485.

27 Shaw AT, Solomon B, Kenudson MM (2011) Crizotinib and testing for ALK. J Natl Compr Netw 9: 1335-1341.

28 O'Byrne K J, Gatzemeir U, Bondarenko I, Barrios C, Eschbach C et al. (2011) Molecular biomarkers in non-small cell lung cancer: a retrospective analysis of data from the phase III FLEX study. Lancet Oncol 12: 795-805.

29 Nyberg F, Barratt BJ, Mushiroda T, Takahashi A, Jawaid A et al. (2011) Interstitial lung disease in gefitinib treated Japanese patients with non-small cell lung cancer: genome-wide analysis of genetic data. Pharmacogenomics 12: 965-977.

30 Yin J Y, Han LF, Huang Q, Xu XJ, Zhou HH et al. (2011) ABCC1 polymorphism Arg723Gln (2168G - A) is associated with lung cancer susceptibility in a Chinese population. Clin Exp Pharmaco Physiol 38: 632-637.

31 Wu JY, Shih JY, Chen KY, Yang CH, Yu CJ et al. (2011) Gefitinib therapy in patients with advanced non-small cell lung cancer with or without testing for epidermal growth factor receptor (EGFR) mutations. Medicine 90: 159-167.

32 Osawa, K (2011) SNPs in ERCC1 and drug response to cisplatin in non-small cell lung cancer patients. Pharmacogenomics 12: 445-447.

33 Kaddi CD, Parry RM, Wang MD (2013) Multivariate hypergeometric similarity measure. IEEE/ACM Trans Comput Biol Bioinform 10: 1505-1516.

34 Mukesh Verma (2012) Review Personalized Medicine and Cancer. J Pers Med 2: 1-14.

35 Mancinelli L, Cronin M, Sadée W (2000) "Pharmacogenomics: the promise of personalized medicine". Personalized Medicine Coalition 5-8.

36 https://www.elsevier.com/books/emery-and-rimoin-s-principles-and-practice-of-medical-genetics-and-genomics/pyeritz/978-0-12-812537-3.