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Biomarkers: The Future of Medical Science to Detect Cancer

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Abstract

A biomarker, or biological marker, is in general a substance used as an indicator of a biological state. It is a characteristic that is objectively measured and evaluated as an indicator of normal biological processes, pathogenic processes, or pharmacologic responses to a therapeutic intervention. Biomarkers play an essential role in much disease detection. Much kind of biomarkers are available in the field of medical science with lots of positive as well as negative effect. Biomarkers will become one of the major driving forces of pharmaceutical research and drug development in the coming years. A specific and ideal biomarker for many unbeaten disease like cancer is still a big challenge.

Biomarker

The word biomarker in its medical context is a little over 30 years old, having first been used by Karpetsky, Humphrey, and Levy in the April 1977 edition of the *Journal of the National Cancer Institute*, where they reported that the "serum RNase level was not a biomarker either for the presence or extent of the plasma cell tumour. " Few new words can have proved so popular. A recent Pub-Med search lists more than 370,000 publications that use it! Part of this success can no doubt be attributed to the fact that the word gave a long -overdue name to a phenomenon that has been around at least since the seventh century B.C, when Sushustra, the " father of Ayurvedic surgery, "recorded that the urine of patients with diabetes attracted ants because of its sweetness. However, although the origins of biomarkers are indeed ancient, it is fair to point out that the pace of progress over the first 2500 years was somewhat less than frenetic [1]. More than 11 million people are diagnosed with cancer every year. It is estimated that there will be 16 million new cases every year by 2020 [2]. Cancer is a cluster of diseases involving alterations in the status and expression of multiple genes that confer a survival advantage and undiminished proliferative potential to somatic or germinal cells [3]. There is increasing evidence to suggest that cancer is also driven by 'epigenetic changes' like DNA methylation and altered patterns of histone modifications, leading to alterations in chromatin condensation status thereby regulating expression of certain set of specific genes [4]. Cancer cells display a broad spectrum of genetic alterations that include gene rearrangements, point mutations, and gene amplifications, leading to disturbances in molecular pathways regulating cell growth, survival, and metastasis. When such changes manifest in majority of patients with a specific type of tumour, these can be used as biomarkers for detection and developing targeted therapies, besides predicting responses to various treatments [5-7].

As biomarker identification for cancer need pathway related study which includes various pathways those are responsible for proper regulation of various cell functions. These pathways are very much complex and need specific attention to specific component of the pathway. In every pathway there are number of component playing role in regulation. Study of only one component is not an easy task what possible is a comparative study with two or more component. In the process of carcinogenesis there are number of chances where we can identify biomarkers (Figure 1) and track the event in early stage.

Time to time many experiment based on biomarkers have been performed and very interesting result will obtained as biomarkers are used widely in the development of oncology drugs. Cancer is recognized as a major cause of mortality the world over; accounting for 7.4 million (or 13%) of all deaths in 2004. The World Health Organization (WHO) estimates incidence of cancer to continue rising to reach an estimated 9.2 million deaths in 2015. The rising prevalence of the disease forms one of the major factors driving the growth of the use of cancer biomarkers in drug development and discovery. Biomarkers are chemical, physical, or biological parameters that can be used to indicate disease states. Cancer biomarkers facilitate high-speed, non-invasive cancer diagnosis; and enhance early cancer detection and screening. The demand for cancer biomarkers is also increasing because of their ability to trace the exact type of cancer and to target patient-specific molecular structure.

Biochemistry of biomarker

Biomarkers can be used to develop targeted therapies, predict risk for cancer, help screen for cancers, and forecast how well a person is likely to respond to a cancer treatment, or monitor the patient. For example, cholesterol, a fatty substance produced by the body, is a biomarker for heart disease. A doctor can take a blood sample and determine your cholesterol levels to predict your risk for having a heart attack. If your doctor puts you on an anticholesterol medication, your cholesterol can be measured in a follow-up appointment to determine whether the medication is working; that is, whether it has lowered your cholesterol and reduced your risk for having a heart attack. Biomarkers are used in the same way to manage cancers and for other kind of diseases [8]. Biomarkers are tests that can be used to follow body processes and diseases in humans and animals. They can be used to predict how a patient will respond to a medicine or whether they have, or are likely to develop, a certain disease. For example, the levels of chemicals in the fluid surrounding the brain may be able to predict the likelihood that a patient with mild memory problems will go on to develop dementia

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due to Alzheimer's disease [9]. Biomarker is a 'substance', analyte, or otherwise a 'thing'. Various assay methods are needed to measure the biomarker second important thing to be noticed is assay method is not the biomarker and one biomarker can have multiple assays that are capable of measuring the biomarker assay method performance characteristics are important. Biomarkers are qualified for a specific context of use a context of use is a comprehensive statement of the manner and purpose of use, including how to apply results to decision making [10]. New biomarkers of safety and efficacy are becoming powerful tools in drug development. Their application can be accelerated if a consensus can be reached about their qualification for regulatory applications [11]. Current practice in biomarker acceptance is closely associated with professional debate often initiated at the level about whether qualification for specific biomarkers should be discussed at all. While a biomarker must be defined both as a test measurement as well as a preclinical or clinical interpretation of the result from this measurement, professional debate often confounds measurement with interpretation. For example, the detection of a specific molecular species is often discussed in isolation from the interpretation of this detection in a specific preclinical or clinical context. The International Life Science Institute Health and Environmental Sciences Institute (ILSI/HESI) assembled a technical committee for the development and application of biomarkers of toxicity [12]. This committee has focused on data generated by its members to better under-stand the analytical and preclinical performance of biomarkers of toxicity, with an initial focus on troponins and biomarkers of nephrotoxicity [13].

Working of biomarkers can be understood with CA 125 which is biomarker for Ovarian Cancer). The investigators attached an antibody that binds to the cancer biomarker CA 125. When solutions with known concentrations of CA 125 were applied to the biosensor, the device accurately measured concentrations as low as 1 "enzymatic unit" per milliliter (U/mL) of solution to as high as 1,000 U/mL. The maximal normal blood level of CA 125 is considered to be 35 U/mL. The researchers obtained identical results when they tested human blood plasma for CA 125 levels [14]. Like CA 125 the working mechanism of biomarker C12 protein chip for multi-tumour marker detection system can be understood with the help of (Figure 2). Biomarker C12 is based on specific binding of antigens to antibodies; multiple antibodies are immobilized on solid matrix, to capture the specific tumour markers in serum samples. The concentrations of tumour markers are determined quantitively through a chemiluminescent mechanism [15]. Biochemistry or working of biomarkers are different and can vary

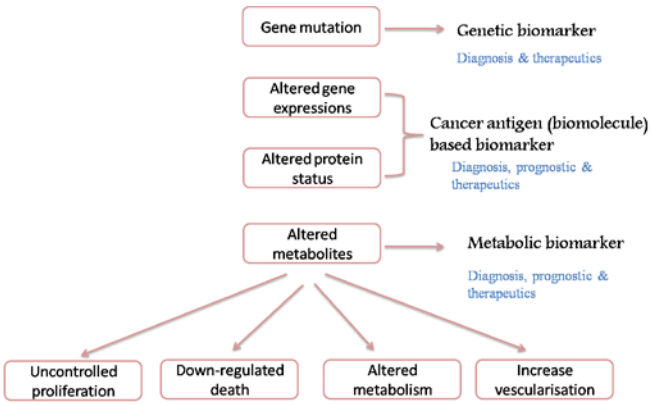

Figure 1: The process of carcinogenesis, showing opportunities of identifying biomarker.

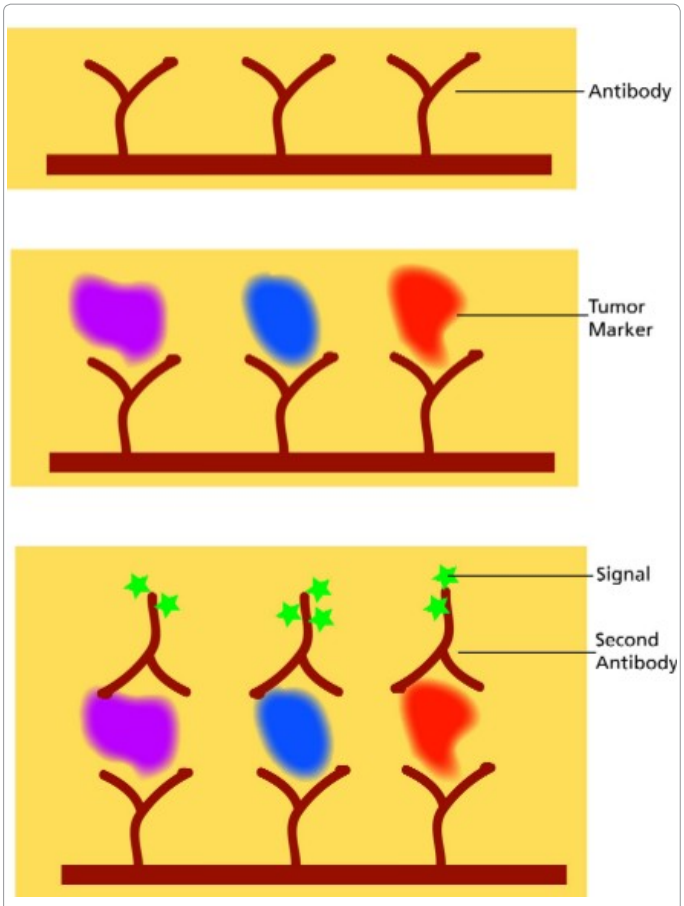

Figure 2: working mechanism of biomarker C12 protein chip for multi-tumour marker detection system.

case by case like in above situation where working based on antibody-antigen interaction.

Biomarker in drug development and bioinformatics

In drug discovery pipeline, one of the most important steps is the determination of three-dimensional structure of a target protein or nucleic acid. Bioinformatics software can use the three-dimensional structural information of the unliganded target to design entirely new lead compounds de-novo. This software allows rapidly and accurately docking large numbers of candidate molecules into the binding site of the target macromolecule prior to actual synthesis and biological studies [16]. Importance of bioinformatics and proteomics in identification of biomarker can be understood by (Figure 3) which define their role in detail.

Here is another term companion biomarker which means that a particular diagnostic test is specifically linked to a therapeutic drug either in drug development or in the clinic. Biomarkers of disease have long played an important role in diagnostic medicine as evidenced by the intense use of specific clinical laboratory tests in the diagnosis of disease. Biomarkers can be used in five very distinct ways in drug development:

- companion biomarkers can be correlated with biological events during drug development in order to validate drug targets or to predict drug response;
- biomarkers can be used as companion diagnostics in drug

development to characterize patient populations in order to better understand the extent to which new drugs reach intended therapeutic targets can alter proposed therapeutic pathways and achieve successful clinical outcomes;

- biomarkers can be used to stratify patient populations for drug response in primary prevention or disease-modification studies, particularly in specific clinical areas such as neuron degeneration and cancer;
- clinically useful biomarkers are becoming increasingly useful to make proper therapeutic decisions regarding candidate drugs; and
- Clinically useful biomarkers are becoming increasingly required by the FDA and other outside authorities to make proper regulatory decisions regarding candidate drugs.

This TriMark Publications report describes new biomarker technology platforms developed for the analyses of drug targets that are connected to the effectiveness of therapeutic agents in a clinical setting. The emphasis is on those companies that are actively developing and marketing new companion diagnostic tests for performing biomarker tests during drug development, as opposed to the more routine and clinically accepted companion markers that are manufactured and marketed by large diagnostic companies for routine clinical use [17]. Genomic biomarkers provide good opportunity to create TPP-Use Genomic Biomarker for Stratification to separate responders from non non-responders, Stratification to exclude patients at risk for AE, Enrichment of responder population and get increased chance of winning, In a shorter period of time, and At less cost (decreased size of trial) [18].

Biomarkers and tumour

Therapies for patients with cancer have changed gradually over the past decade, moving away from the administration of broadly acting cytotoxic drugs towards the use of more specific therapies that are targeted to each tumour. Several groups have attempted to generate such profiles through identifying genes or pathways that potentially affect how a cell responds to a drug, often by using models based on cell lines. A small number of human tumour samples can then be tested for the expression of these *in vitro*-generated sets of candidate genes. The approaches that have been explored so far are discussed in this section and illustrated in Figure 5a, Collections of tumour cell lines of known drug sensitivity can be used to build gene expression signatures that discriminate between sensitive and resistant cell lines. Such *in vitro*-generated drug-sensitivity signatures can be validated on tumour samples from patients treated with the same drugs. Figure 5b, Gene-expression signatures for signalling pathways can be constructed *in vitro* by introducing the gene of interest (a mutant *RAS* gene that is constitutively active in the example here) into tumour cell lines and studying the effect of the presence of the oncogene on genome-wide gene expression. Tumour samples for which the status of the RAS pathway is unknown can then be assessed by comparing their gene expression patterns with that of the 'activated RAS pathway' identified *in vitro*. If a drug that targets the RAS pathway is available, then similarity between the gene expression profile of the tumour and a RAS pathway signature could be used to guide the choice of therapy. Figure 5c, Functional genetic approaches can be used *in vitro* to uncover which genes can contribute to drug resistance in tumour cell lines.

More specifically, using these approaches genome scale gain-of-function screens or RNA-interference-based loss-of-function screens full-length complementary DNAs or small interfering RNAs are introduced to change the abundance of gene products, turning drug sensitive cell lines into drug-resistant cell lines. The predictive ability of the genes that are candidates for modifying drug responses can then be examined by assessing their expression levels in a relatively small number of clinical samples from patients treated with the same drug [19].

Biomarkers of disease

Over the past few years a significant amount of data pertaining to the diagnosis of human diseases has been generated with the help of mRNA (cDNA) microarrays and several other kinds of techniques. They have been responsible for identifying new disease subtypes that would not have been possible using conventional techniques. As a result, the need for new molecular based classifications of some types of cancers has to be identifies [20]. In cancers, one would expect an altered expression of proteins responsible for signal transduction processes in the cell. In fact, in many instances the protein products of protooncogenes are involved in signal transduction [21] and alterations in these genes result in uncontrolled cellular signalling. Over expression and post-translational modifications of several oncogene products have been detected in transformed liver cells [22].

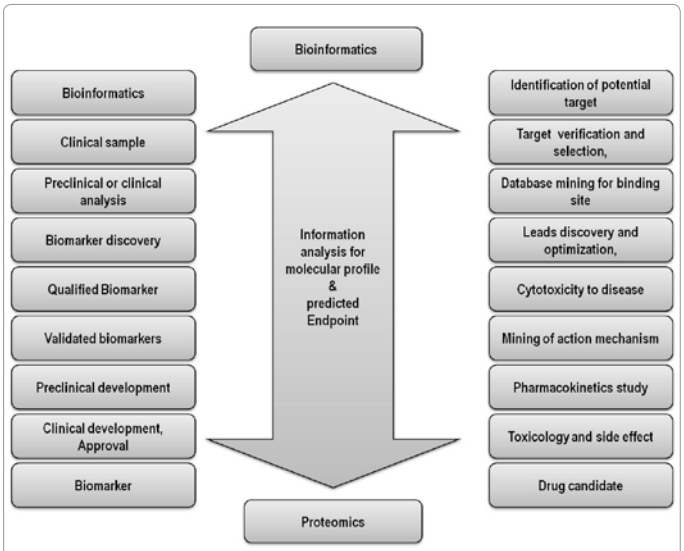

Figure 3: Schematic flow diagram of the applications of bioinformatics in proteomic research on biomarker discovery and drug development.

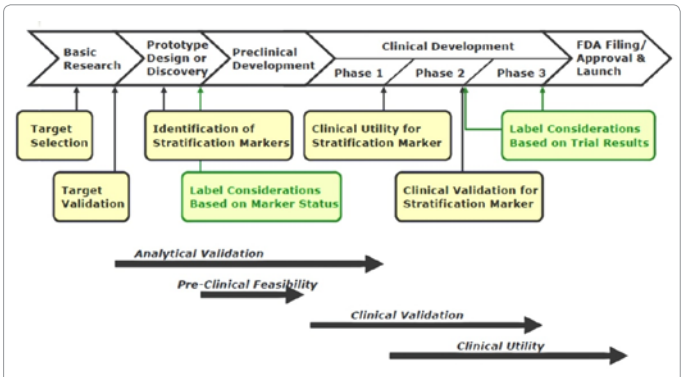

Figure 4: Biomarkers at clinical and preclinical level source-http://clinical-bioinformatics.com/wp-content/uploads/2011/03/Biomarrkers-and-the-Drug-PipelineFIG1.jpg

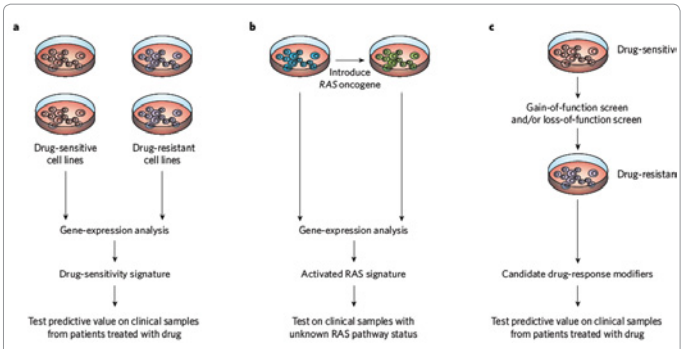

Figure 5:

Additionally, cancer has been associated with altered glycosylation of many proteins [23]. It is apparent that in most diseases, proteins are subjected to numerous changes including post-translational modifications and/or proteolytic cleavage. Furthermore, there is overexpression or under expression of a number of proteins in some diseases. These observations highlight the fact that mRNA expression profiling falls short of providing a complete solution to the tasks of biomarker discovery and diagnosis of disease. Microarrays that provide information on differential expression of mRNA will not provide information on post-translational modifications. Alternative splicing of the mRNA transcript can produce different protein forms, and at this time the only way to study the impact of these proteins is at the protein level. An additional concern is the lack of correlation between mRNA levels and protein concentrations [24]. Finally, an especially significant impediment to the discovery and use of clinically usable biomarkers with mRNA/cDNA techniques is their limited utility for the analysis of biological fluids [25].

The discovery of new disease biomarkers (signatures) and the ability to measure them rapidly preferably at the initial point of care will revolutionise disease diagnosis. Now a day's research focuses on finding such biomarkers (in human cells) that are linked with specific diseases, and developing assays or tests that can detect changes in these biomarkers at very low levels. Cell membrane associated phenomena particularly insulin-like growth factors and associated receptors, signaling systems, g-protein coupled receptors, disease biomarker identification and validation, particularly related to human colorectal cancer, proteomics, microarrays and biochips, mass spectrometry, nanotechnology etc are widely studied out in present and Future diagnostic and drug discovery will depend on the development of higher throughput, higher content, multiple information assay formats which will be integrated with panels of validated, novel biomarkers (or signatures) for early stage disease identification [26]. Biomarkers currently in use are mainly categories on the basis of disease and techniques. Biomarker identification for any disease can be categories under the heading of Discovery, Verification, Validation, and Application [27]. The discovery of such biomarkers, however, which must be plucked from tens of thousands of proteins that fill our cells, presents a challenge. If not identified with precision and validated in large patient groups, they could do more harm than good. validation include various experiment with the help of which we can say that whether our finding is correct protein of molecule and finally Application; Application means where it can be used and how it can be beneficial to fulfill our need of disease detection.

Cancer biomarker

There has been much interest in biomarkers of cancer risk in predicting future patterns of disease, especially as cancer treatment has made such positive strides in the last few years. Serum biomarkers are produced by body organs or tumours and measure antigens on cell surfaces. When detected in high amounts in blood, they can be suggestive of tumour activity. Serum biomarkers are nonspecific for cancer and can be produced by normal organs as well. One of these serum biomarkers in wide use is PSA. PSA is produced by normal prostate cells in small amounts, but the higher the PSA is in the serum, the higher the correlation is toward the existence of prostate cancer. PSA is probably the only serum biomarker currently used consistently in primary care. Cancer antigen 125 (CA-125) can be a biomarker of ovarian cancer risk or an indicator of malignancy, but it has low sensitivity and specificity. Levels of this marker can be high in people who have pancreatitis, kidney or liver disease, making its accuracy as a cancer diagnostic tool very limited. However, it can be used to follow the progress of treatment of cancer, and predict a treatment failure when levels rise despite the use of chemotherapeutic agents. Sometimes, a combination of several tumor markers can give risk predictions in someone whose family history for the disease is quite high. Carcinoembryonic antigen (CEA) is another biomarker that is elevated in patients with colorectal, breast, lung, or pancreatic cancer. As a screening test, it can be elevated by many other factors than cancer; smoking for instance raises CEA levels. Following CEA post-surgery for colon cancer however is an effective way of determining the adequacy of postoperative therapy. While PSA is used in insurance testing to assess the risk of underlying prostate cancer, other biomarkers are neither specific enough nor cost effective to use. There are even questions with PSA, as some prostate cancer may be so slow growing as to never affect eventual mortality or be unlikely to progress. Genetic testing is still not sophisticated not even accurate enough on which to forecast risk, and is not part of the testing required by insurers [28]. There is some example of Cancer Biomarkers in used currently Clinical Practice [29]. Alpha Fetoprotein/AFP

- CA125/MUC16
- ER alpha/NR3A1
- ER beta/NR3A2
- ErbB2/Her2
- Kallikrein 3/PSA
- Progesterone R/NR3C3
- Progesterone R B/NR3C3

Tumour markers are endogenous proteins or metabolites whose amounts or modifications are indicative of tumour state, progression characteristics, and response to therapies. They are present in tumour tissues or body fluids and encompass a wide variety of molecules, including transcription factors, cell surface receptors, and secreted proteins. Effective tumour markers are in great demand since they have the potential to reduce cancer mortality rates by facilitating diagnosis of cancers at early stages and by helping to individualize treatments.

Biomarker and genomic techniques

Proteomic research first came to the fore with the introduction of two-dimensional gel electrophoresis. At the turn of the century, proteomics has been increasingly applied to cancer research with the wide-spread introduction of mass spectrometry and proteinchip. There is an intense interest in applying proteomics to foster an improved understanding of cancer pathogenesis, develop new tumour

biomarkers for diagnosis, and early detection using proteomic portrait of samples. The early detection of cancer has a potential to dramatically reduce mortality. The thermostable fractions of serum samples from patients with ovarian, uterus, and breast cancers, as well as samples from benign ovarian tumor were analyzed using two-dimensional gel electrophoresis (2-DE) combined with matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF)/TOF MS. Of them, alpha-1-acid glycoprotein and clusterin were expressly down-regulated in breast cancer, whereas transthyretin was decreased specifically in ovarian cancer [30]. Conventional 2DE method will continue to contribute significantly in serum biomarker identification; the gel-free techniques such as LC-MS/MS and SELDI-TOF are expected to greatly facilitate the serum biomarker discovery process with increased sensitivity, high-throughput and automation.

Identifying genomic biomarkers for cancer prediction is of great practical value. Such effort can lead to better understanding of cancer genetics, more accurate prediction of tumour behaviours and rational treatment selection. Using gene expression data generated from microarrays for biomarker selection is very challenging due to the high dimensionality and gene cluster structure, where the clusters consist of correlated genes or genes in the same pathway. In this application, we will develop novel clustering penalized methods for genomic biomarker selection in cancer studies. Beyond developing general methodologies, we will thoroughly investigate their applications in cancer classification and survival studies. The specific aims of this study include: first to develop effective clustering penalized methodologies for biomarker selection at both the cluster level and the within-cluster gene level. Following approaches are useful: Supervised Adaptive Group Lasso-SAGLasso and Group Bridge Lasso-GBL. Properties of the proposed approaches, including computational algorithms and asymptotic, will be investigated; second one is Classification analysis using proposed penalized approaches, where the outcome of interest denotes cancer status or response to therapy. Logistic classification and ROC based classification will be considered; third Cancer survival analysis using proposed penalized approaches, where the outcome is censored event time such as time to collapse in cancer patients. Especially we will consider Cox and AFT models; and fourth Intensive empirical studies of the proposed approaches using various cancer genomic data. Extensive numerical studies will be used to evaluate the proposed approaches under different clustering schemes and compare with existing approaches. The proposed clustering penalized approaches are expected to produce parsimoneous predictive models and properly account for the gene cluster structure. They can reveal the associations of cancer outcomes with both gene groups and individual genes, and are expected to behave better than existing approaches in terms of biomarker selection and predictive model building [31].

The recent progress of proteomics has opened up novel avenues for cancer-related biomarker discovery. However, adopting high-throughput proteomic approaches to multiplexed set-ups, providing a minimally invasive screening procedure, targeting non-fractionated biological fluids, such as blood, has proven to be challenging. In recent years, the technology has made significant progress [32]. Assuming that the proteome is the global representative of all biological processes that take place in cancer cells, then the discovery of specific biomarkers in the midst of such biological complexity would seem difficult in the absence of ultra-high resolution analytical techniques for quantitative measurement of tens to hundreds of thousands of components, and robust data acquisition and analysis techniques to efficiently and reliably process these large datasets. Current progress in proteomics has been largely due to recent developments in mass spectrometry (MS)-based technologies [33]. Particularly, new techniques for the ionization of proteins and peptides, such as matrix-assisted laser desorption-ionization (MALDI) and electro spray ionization (ESI) combined with time-of-flight (TOF), as well as new hybrid mass spectrometers, are now becoming the tools of choice for protein characterization. These advances have been highly recognized by the scientific community to include two mass spectrometrists, Drs. John B. Fenn and Koichi Tanaka as co-recipients (with the developer of NMR Dr. Kurt Wüthrich) recipient of the 2002 Nobel Prize for chemistry. These techniques have also been accompanied, although with a significant lag, by dramatic improvements in bioinformatics tools for analysis of complex datasets. In addition, powerful multi-dimensional chromatographic and sample labelling techniques have been developed to further benefit from the improvements in mass spectrometry [34-36]. The standard proteomic approach for biomarker research consists of isolation of cell proteins from clinical specimens (tissue or biological fluids such as serum, ascites, saliva, etc.), digestion with proteases such as trypsin, and separation of the resulting mixture by two-dimensional (2D) electrophoresis or liquid chromatography (LC). The desired spots (2D) or protein fractions (LC) are isolated, digested, and peptides are separated by LC and depending on the sample complexity, the low-molecular weight fractions may be further fractionated by ion-exchange chromatography. The peptides are then subjected to electrospray or MALDI mass spectrometry (MS) or MS/MS analysis for qualitative and quantitative [37]. Current clinical and pathological markers poorly predict early disease development and response to treatment. Standard diagnostic methods, including tissue histopathology are now shifting rapidly toward molecular diagnosis due to the rapid progress in proteomic instrumentation. This powerful technology can identify all proteins and their posttranslational modifications in disease conditions, and hence will greatly accelerate progress toward novel diagnostic and predictive tools to track early disease and tailor treatments to specific patients.

Bioinformatics and biomarker discovery

The discovery of new biomarkers is often carried out by comparing physiological changes between normal and disease states. This could be understood with help of (Figure 5) which show some important elements in the discovery of new biomarkers. The disease state is often characterized by well-known structural changes in proteins and enzymes. For example, glycosylation, which is the addition of polysaccharides (sugars) to polypeptides (proteins), yields new forms of glycoproteins. An abnormal concentration of glycoprotein's can then act as a biomarker for various diseases, including muscular dystrophy, acute chronic inflammation and leukemia.

After identifying potential biomarkers, researchers must validate whether biochemical compounds or genetic patterns are useful, as one of the biomarkers described above. In the validation phase, researchers systematically modify putative biomarker compounds, and then check for phenotypic changes or alterations in biochemical and physiological profiles. Because of the diverse types of biomarkers, the many sources of new biomarkers and the various methods used to discover and validate them, there is an equally impressive set of bioinformatics tools available for biomarker analysis [38]. The availability of the complete human genome has paved the way for the systematic understanding of human diseases. Recent technological advances in functional genomics and proteomics have fueled interest in identifying the biomarkers of complex diseases such as cancer and neurodegenerative diseases enabling a systems level analysis. Functional genomics describes the use of large scale data produced by high throughput (HTP) technologies

to understand the function of genes and other parts of the genome. With the help of high-throughput gene expression technologies, it is possible to analyze the expression of a large number of sequences in diseased and in normal tissues. Recent advances in mass spectrometry and improved bioinformatics and statistical tools have revolutionized the biomarker discovery approach. In biomarker discovery, much of the efforts have been directed towards the development of strategies and platforms for quantitative protein profiling based upon the needs of different types of biological samples. The biomarker search can be performed on tissues, on body fluids, or on cultured cells. Body fluids may include urine, saliva, tears, sweat, and nipple aspirate fluid. The last may exhibit a lot of variation as compared to serum and cerebrospinal fluid (CSF). For most of the neurological disorders serum and CSF are used for proteomics or Metabolomics analysis. Techniques used in biomarker discovery include 2-D gel electrophoresis, gel free MS, and protein array technology. The more widely used approach, 2-D gel electrophoresis, which provides the capability to qualitatively and quantitatively resolve complex protein mixtures to unique spots, is a potential tool for biomarker discovery [39]. One of the major problems is that any given biomarker in a pool of biomarkers may have been derived by an experimental strategy that has over- or under-represented its relationship to the target outcome, be it a biological value or disease risk association. Thus, in the pool, its contribution to the significance of the larger pool may be distorted. The more hypotheses (that is, biomarker association with outcome) tested, the greater the risk of false-positive findings. These biases inflate the potential clinical validity and utility of published biomarkers while negative results often remain hidden [40].

Conclusion

When we try to look behind there are number of deaths only due to poor or detection of many kind of disease and after development of medical science early detection become more easy and so its treatment. One study shows that recent advances in arthritic medication can arrest the disease if the drugs are started at the onset of the disease. But early detection would allow many more people to avoid getting to the point of heavy medication [41]. Not only for arthritic for other disease early detection is going to become boon in the field of medical sciences. But still there are diseases for which early diagnosis is not possible because of lack of biomarker identification. Biomarkers are the need of today to detect many lethal diseases including cancer. Cancer treatment is possible if we can arrest tumour in primary stage. Tumour become cancer after it becomes metastasized and before this process if we can detect it we can remove completely from body and inhibit it to move to other body part. Genomic technologies offer the promise of a comprehensive understanding of cancer. These technologies are being used to characterize tumours at the molecular level, and several clinical successes have shown that such information can guide the design of drugs targeted to a relevant molecule. One of the main barriers to further progress is identifying the biological indicators or biomarkers, of cancer that predict who will benefit from a particular targeted therapy [42]. Prostate cancer is the most frequently diagnosed cancer in men. Screening for prostate-specific antigen (PSA) has led to earlier detection of prostate cancer, but elevated serum PSA levels may be present in non-malignant conditions such as benign prostatic hyperlasia (BPH) [43].

Today is the era of technology and every day is day of new invention. Expertise increases day by as our expectation too. We can hope for better tomorrow where early detection will be definitely possible not only for cancer but for other diseases also.

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