INTERNATIONAL JOURNAL OF MULTIDISCIPLINARY RESEARCH AND ANALYSIS

ISSN(print): 2643-9840, ISSN(online): 2643-9875

Volume 05 Issue 07 July 2022

DOI: 10.47191/ijmra/v5-i7-30, Impact Factor: 6.261

Page No. 1834-1836

Study Molecular Biology Clinically and Biologically Relevant in the Tumorigenesis and Progression of Cancer

Hayder Hatem Abdulwahhab

University of Çankırı Karatekin Department of Biology , Molecular biology

The paper aims to develop a new concept for stratifying cancer patients using their biomarker profiles. The study leading to HCC only assessed the diagnostic aspect of recurrent cancer. However, the next clinical evaluations will be geared towards predicting recurrence. Thus, the finalized platform should make it possible to determine marker profiles in a clinical context and to develop a set of rules for predicting the progression of the pathology, more particularly of recurrence. Such a predictive tool would be beneficial for the management of patients with bladder cancer. Indeed, the latter has a high rate of recurrence and improving the determination of the risk of recurrence would allow optimal and personalized care for each patient (Ahram M, 2008). Finally, this concept of personalized medicine thanks to the information obtained by the analysis of several parameters on our platform can be applied to other cancers or pathologies.Individual markers could play a role important diagnostic or predictive, and this clinical utility in the laboratories clinical automated manner. The arrays of CpG methylation islands have allowed the identification of new individual epigenetic profiles and candidates that are clinically and biologically relevant in the tumorigenesis and progression of cancer, with utility for the early detection of the disease (Burger M, 2013). The characterization of BDNF in tissue samples, urine and cell lines in an integrated way has allowed the identification of a new gene that is epigenetically silenced by methylation and that has clinical utility for the diagnosis and tumor stratification of patients with cancer. It is necessary to characterize other candidates identified both at the methylation and miRNA levels and to carry out complementary and independent validations to define markers that also allow early non-invasive detection (J.S. Ross, 2014).

The Polymerase Chain Reaction (PCR) has been the main diagnostic tool that has taken advantage of the benefits of molecular biology to the point of reaching great versatility as an analysis technique. The specificity, performance and fidelity of PCR are directly influenced due to the different components that make it up, such as the reaction mixture, cycling regimen and DNA polymerase; the technique allows the selective amplification of any DNA segment, knowing the flanking sequences, obtaining a specific DNA sequence without resorting to cloning in a host organism Its applications are variable and unlimited, an example of this is the possibility of carrying out genetic expression studies, direct sequencing of amplified sequences, detection of mutations, monitoring of the effectiveness of disease treatment, diagnosis of genetic and infectious diseases and in forensic science in the identification of remains biological, determination of paternity and forensic evidence in criminology (Edwards NJ, 2015).

The DNA sequence consists of determining the order of the bases A, C, G and T in a DNA fragment; This method was described by Sanger in 1977, and it makes it possible to obtain the sequence of a specific DNA fragment, a gene or part of it, and to be used today. This method has evolved over time and today implemented different types of sequences, highlighting the parallel, massive or new generation sequence (NGS), which allows the exploration of complete genomes of humans or other species; and the pyrosequence, with which it is possible to determine the sequence of a molecule of DNA, identifying individual bases, or short sequences of nucleic acids at specific positions. Hybridization is a method that is based on the union of two single strands of nucleic acids that produce double-stranded structures, which are DNA hybrids, RNA-RNA or DNA-RNA. The hybridization method is based on the development of two nucleic acid molecules: one homogeneous of sequence distinguished as a probe and the other heterogeneous of sequence known, which contains the target sequence to be analyzed. Single-stranded nucleic acids come from cloned DNA fragmented by restriction enzymes, or from synthetic oligonucleotides (Gogalic S, 2015).

This recently introduced methodology is a closed system combining the amplification of nucleic acids and the detection of the products in one step. This makes it faster, more efficient and reduces the risk of cross contamination with a mplicons as it eliminates post PCR manipulation. The detection system monitors the changes in fluorescence produced as it goes amplification taking place, thus allowing view product backlog in real time. It is a qualitative and quantitative test, since by quantifying the

fluorescence emission, we can know the microbial load or the number of copies originally present in the sample. With this methodology it is also possible perform mutation analysis and genotyping studies (Cancer Genome Atlas, 2014).

The results are summarized in Table 1. No result was obtained for U.P.K.3.A because its complete analysis could not be carried out due to a technical difficulty (the 96-well plate was damaged by the pipetting machine during the analysis). Calibration curves in urine could be obtained for all other markers, with the exception of F.B.L.N3.

Table 1. Biomarker assays from the second study (Biomarkers Definitions, 2001)

Marker pen	Calibration range in the diluent	Calibration range in urine	Detection limits (urine) **	Detection of marker in patient samples
BIRC5	+	+	1000 pg/mL	+
EN2	+	+	1.25 ng/mL	+
FBLN3	+	-	25 ng/mL (diluant)	+
FGFR3	+	+	1000 pg/mL	+
IL8	+	+	125 pg/mL	+
MMP9	+	+	666.7 pg/mL	+
MYC	+	+	1.25 ng/mL	-
p53	+	+	10 ng/mL	-
PTGS2	-	+	5 ng/mL	+
TMOD1	+	+	2.5 ng/mL	+
UPK3A	-	-	N/A	N/A
VIM	+	+	112.5 ng/mL	-

Table 2. Individual performance of parameters

Clinical parameter	Pr(>|z|)	AUC	Marker	Pr(>|z|)	AUC
diagnostic sample	0.42	0.5	DCN_{puce}	0.67	0.57
sex	0.89	0.51	$VEGF_{puce}$*	0.05	0.67
age.diagnosis	0.7	0.48	$IL8_{puce}$*	0.08	0.69
sample age	0.45	0.57	$CDH1_{puce}$	0.66	0.53
grade.diagnosis (G2 / G3)	0.32 / 0.48	0.57	$IL6_{puce}$	0.65	0.48
stage.diagnosis	0.52	0.55	$EN2_{puce}$*	0.09	0.65
number of previous recurrences *	0.08	0.63	$EGFR_{puce}$	0.86	0.53
therapy.BCG *	0.1	0.65	$ErbB2_{puce}$*	0.06	0.73
therapy.mitomycin	0.49	0.54	$MMP7_{puce}$	0.9	0.5
nr.RTUV. previous *	0.33	0.58	$MMP9_{puce}$	0.72	0.58
			$IL8_{PA}$	0.74	0.47
			$MMP9_{PA}$	0.46	0.5
			$FBLN3_{PA}$	0.54	0.52

REFERENCES

1) Ahram M, Petricoin EF (2008) Proteomics discovery of disease biomarkers. Biomark Insights 3: 325– 333.
2) Biomarkers Definitions Working Group. (2001) Biomarkers and surrogate endpoints: preferred definitions and conceptual framework. Clin Pharmacol Ther 69: 89–95.
3) Burger M, Catto JWF, Dalbagni G, Grossman HB, Herr H, Karakiewicz P, Kassouf W, Kiemeney LA, La Vecchia C, Shariat S, Lotan Y (2013) Epidemiology and risk factors of urothelial bladder cancer. Eur Urol 63: 234–241.
4) Cancer Genome Atlas Research Network, Comprehensive molecular characterization of uothelial bladder carcinoma, Nature, 507 (7492) (2014), pp. 315-322.
5) Edwards NJ, Oberti M, Thangudu RR, Cai S, McGarvey PB, Jacob S, Madhavan S, Ketchum KA (2015) The CPTAC Data Portal: A resource for cancer proteomics research. J Proteome Res 14: 2707–2713.

6) Gogalic S, Sauer U, Doppler S, Preininger C (2015) Bladder cancer biomarker array to detect aberrant levels of proteins in urine. The Analyst 140: 724–735.
7) J.S. Ross, K. Wang, R.N. Al-Rohil, T. Nazeer, C.E. Sheehan, G.A. Otto, et al. Advanced urothelial carcinoma: next-generation sequencing reveals diverse genomic alterations and targets of therapy, Mod Pathol, 27 (2) (2014), pp. 271-280.