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BioNews Survey
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Wishing our Readers a Happy and Prosperous 2009

Applied Biosystems SOLiD™ System Named Life Science Innovation of the Year

CARLSBAD, Calif.-Dec. 4, 2008-Applied Biosystems, today announced that its technology for next-generation genomic analysis, the SOLiD™ System, has been named the Life Science Innovation of the Year for 2008 by The Scientist, a leading scientific publication focused on the life science industry. The SOLiD™ System received the top award based upon its ability to significantly reduce the cost of DNA sequencing, which will enable basic and clinical researchers who may not have previously considered genomic approaches to re-evaluate their experimental workflow. The technology is defining a new industry standard in DNA sequencing by delivering a combination of high throughput, unmatched accuracy, and low cost per project that was previously unavailable in the life science community.

IN THE NEWS

Researchers at the University of Cambridge and Applied Biosystems (AB) Use SOLiD™ to Study Gene Expression in Single Mouse Embryonic Stem (ES) Cells

Researchers at the University of Cambridge and Applied Biosystems and have used ABI's SOLiD™ sequencing system to profile gene expression in single stem cells, one of the first times that researchers have used second-generation sequencing to analyze single cells.

The work was described for the first time in September at two research symposia in New Jersey and Connecticut that were organized by ABI in collaboration with academic institutions. "It strikes me as really exciting work [and] as an important direction to go because we know that in any dish of, say, stem cells, the cells are not the same," said Ken Kosik, a researcher at the University of California, Santa Barbara whose lab studies neurons and stem cells.

The ABI-Cambridge study resulted from a long-standing collaboration between Kai Lao, a principal scientist at ABI, and Azim Surani, a professor of physiology and reproduction at the University of Cambridge, on single-cell gene expression. In prior studies, they had used real-time PCR and microarrays, according to Lao, which are "good tools for expression profiling of known transcripts."

In order to discover new transcripts and transcript variants, they started using SOLiD™ sequencing in May, studying single mouse embryonic stem cells that were manually extracted from embryos at the four-cell stage. The goal of the project, which used embryos that had specific genes knocked out, is to understand gene regulation by maternal microRNAs in mature oocytes, according to Lao.



SNP Basics

Single nucleotide polymorphisms or SNPs (pronounced "snips") are DNA sequence variations that occur when a single nucleotide (A, T, C, or G) in the genome sequence is altered. "SNPs", which make up about 90% of all genetic variation, occur every 500 to 1000 bases across the human genome. The abundance of these alterations in various genomes makes them a desirable tool to study population diversity or to understand genetic predisposition and drug response. For a variation to be considered a SNP, it must occur in at least 1% of the population. A SNP has to be validated in a population before screening the population. SNP typing is method for identification and screening of these single base changes.

Important points to keep in mind before planning a SNP project would be:

1. Understanding the level of polymorphism

Before starting a SNP project one should have a fair idea about the level of polymorphism, an understanding of the region of interest and have accurate sequence data surrounding the expected SNP. If the SNP is validated, it will produce successful results.

2. Obtaining good quality DNA

The most significant factor in reducing the success of SNP genotyping is the quality of DNA. All platforms, whether it be sequencing or SNP genotyping using fragment analysis or Real-Time PCR rely on good quality DNA to produce high quality results. Therefore, good quality DNA will yield a higher call rate and a greater accuracy per call than poor quality DNA.

3. Choosing the right technology

DNA sequencing technology using Sanger Chain termination method is an efficient tool for identifying a SNP. Techniques like (SSCP will also provide information regarding base changes but one has to confirm by sequencing. For SNP screening or genotyping many techniques are available such as single base extension technology which can be performed on any of AB's Genetic Analyzers as well as Mass Spectrometers. Real-Time based assays for SNPs can also be designed using Taqman® based chemistry.

TaqMan® Sample-to-SNP™ Kit

- Fast—Raw biological samples to SNP genotyping results in less than one hour
- Simple—A brief protocol with few pipetting steps
- Robust—Highly accurate results for virtually any sample
- Flexible—Validated with many types of TaqMan® SNP genotyping assays

The TaqMan® Sample-to-SNP™ Kit provides a streamlined protocol for performing TaqMan chemistry-based genotyping analysis from any sample with a single kit. The kit is comprised of two parts: the DNA Extract All Lysis Reagents and the TaqMan® GTXpress™ Master Mix. The DNA Extract All Lysis Reagents reduce prolonged procedures for the release of real-time PCR-ready DNA to a 5 minute protocol. They can process a wide variety of samples ranging from blood to buccal swabs to plant tissues. The TaqMan GTXpress Master Mix enables robust PCR amplification in less than 50 minutes.

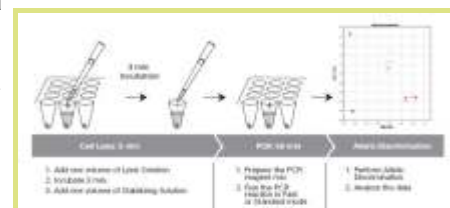


Figure 1. TaqMan® Sample-to-SNP™ Kit workflow. The DNA Extract All Lyses Reagents require only 5 min to release DNA into a lysate solution that is compatible with TaqMan® GTXpress™ Master mix. The TaqMan® GTXpress™ Master mix enables robust PCR amplification in less than 5 min

Robust Reagent System

Many master mix products available today can perform reasonably well with highly purified DNA. However, even purified DNA from inhibitory samples such as blood or FFPE tissues can still pose challenges for these mixes. The TaqMan GTXpress Master Mix has been formulated to handle a broad spectrum of inhibitors contained in samples as varied as blood and cotton.

Concordance with Purified DNA

The TaqMan Sample-to-SNP Kit streamlines the SNP genotyping workflow without purifying genomic DNA. The kit was tested extensively for call concordance between the DNA lysate and purified DNA. As shown in Figure 2, the DNA lysate provides excellent cluster separation when compared to purified DNA. While the actual clustering is assay-dependent, a broad study comparing the genotyping call concordance between purified DNA and the DNA lysate across 46 EDTA-treated blood samples and two 'no template' controls showed excellent agreement. These 46 samples were genotyped with a 400 assay panel including 200 TaqMan® Pre-designed SNP Genotyping Assays, 100 TaqMan® Drug Metabolism SNP Genotyping Assays and 100 TaqMan® Custom SNP Genotyping Assays.

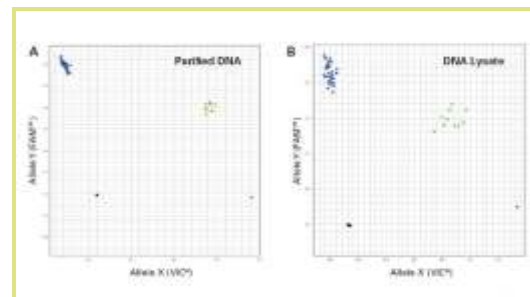


Figure 2. Example of genotyping cluster plots using purified blood (A) or the blood DNA lysate obtained with the TaqMan Sample to SNP™ Kit (B). DNA lysates or purified DNA were mixed with the GTXpress™ Master mix for assay C_8814556_30 and amplified on a Dual 384 well GeneAmp PCR system 9700. Allelic discrimination was performed on an Applied Biosystem 7900HT Fast Real-Time PCR System with 384-well block.

Product Description	Part number
TaqMan® Sample-to-SNP™ Kit, Mini-Pack (5ml sample prep, 1 ml PCR)	4403313
TaqMan® Sample-to-SNP™ Kit, 1-Pack (2.0ml sample prep, 10 ml PCR)	4403083

Basmati Verifiler™: World's First Kit for Basmati Testing

- World's first kit-based product for testing the authenticity of Basmati rice samples
- Specific microsatellite profiles of loci common to all major Basmati varieties to distinguish traditional Basmati from evolved and non-Basmati unambiguously
- "Single-tube assay" to co-amplify eight microsatellite loci
- High throughput analysis enabled via five-dye fluorescent DNA technology
- Integrated system available including reagents, Applied Biosystems Genetic Analysis instrumentation, software and technical support

World's First Single-tube, Multiplex, Microsatellite Assay-based Kit for Basmati Authentication

LABINDIA is pleased to announce the release of the Basmati Verifiler™ Kit; the world's first product for establishing the authenticity of Basmati rice samples. The kit is manufactured and marketed by Labindia and was developed by a group of scientists from the Centre for DNA Fingerprinting and Diagnostics (CDFD) in Hyderabad, India. The kit uses a PCR amplification technique based on Simple Sequence Repeats (SSR) that provides the single most discriminating assay for Basmati genotyping. The high resolution of the fluorescence-based microsatellite assay provides highly reproducible data with as low as 5 ng of DNA per PCR reaction. The Basmati Verifiler Kit simultaneously amplifies 8 SSR loci in a single, robust amplification reaction.

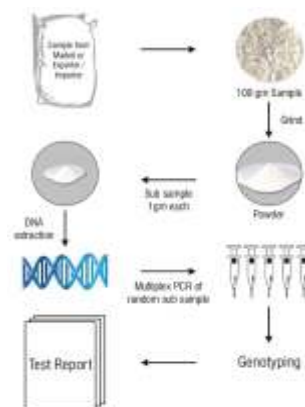
Technical Procedure

The procedure involves the following basic steps

DNA Extraction: Isolate DNA from rice grains using any commercial column-based DNA extraction kit. Each rice sample should have at least 100g of grain powder, from which a minimum of three sub-samples of 1g each should be randomly drawn and bulked for DNA extraction. Quantify the DNA and adjust to an optimum level.

PCR Amplification: Set up a 10µl PCR reaction comprising of DNA template, PCR mixture (AmpliAq Gold®, dNTPs, MgCl) along with labeled primers. After an initial denaturation step, the PCR mix is subjected to a fixed number of amplification cycles followed by the extension step.

Genotyping: This can be performed on any of the AB Genetic Analyzers using specific running modules. The PCR product is mixed with size standard GeneScan™ 500 LIZ before being injected on the instrument. Subsequently, allele sizes are called using the GeneMapper software from AB.



Speed and Throughput

The Basmati Verifiler Kit uses unique and laboratory tested primer sequences. Allele sizes range between 70 to 350 base pairs for robust PCR amplification of all loci. When used with an AB platform, the kit provides an integrated approach, and the flexibility to choose from a wide range of Applied Biosystems (AB) Genetic Analyzers depending on the throughput requirement.

Five Dye Technology

The use of fluorescent dyes (6 FAM, VIC or NED) to label DNA fragments for automated fragment analysis has drastically increased throughput. With the increased number of dyes now available it has become easier to multiplex more loci in a single capillary injection. The new dyes 6 FAM, VIC, NED and LIZ offer a wider spectral range extending to 610 nm. The expanded spectral profile minimizes spectral overlap thus leading to more reliable data.

Integrated System for Generating and Analysing Data

LABINDIA offers a completely integrated system including reagents, instruments (from AB) and software for generating and analyzing data via the Basmati Verifiler Kit. DNA samples amplified using this kit can be analyzed on a variety of AB Genetic Analysis instruments that accommodate the throughput levels of different individual laboratories. (The instrument must be equipped with a version of data collection software that is capable of five dye analysis and the instrument calibrated with suitable matrix standards).

Please contact Yogeendra Dawalkar at dawalkarym@labindia.com (Cell No. 09871596284) for purchase enquiries.

Please visit www.labindia.com/basmati for more information.

Product Description	Part number
Basmati Verifiler Kit (100 rxns)	BV81001

StepOnePlus™ Real-Time PCR System



Applied Biosystems' latest introduction to real-time PCR, the StepOnePlus™ Real-Time PCR System, makes it simple and easy to get high-quality real-time PCR results. This remarkably simple 96 well, 4 color, real-time PCR system is designed with a user-friendly, yet powerful, interface for researchers of all experience levels.

Remarkably Simple System

The StepOnePlus™ system brings advanced real-time PCR technology to a new level of accessibility. Beginning at the StepOnePlus software homepage, you can seamlessly navigate through all aspects of the real-time PCR method including sample and reaction set-up, thermal cycling, and fluorescent detection. Focused application software analyzes and interprets experimental results. Depending on the experimental design, the system can even help you select and order real-time PCR reagents online by means of convenient links in the Design Wizard.

Simply Remarkable Results

Because the StepOnePlus system is factory-calibrated for optical and thermal accuracy, simply remarkable real-time PCR results are available right out of the box. It can discriminate between 2 populations of 5,000 and 10,000 template copies of a TaqMan® Assay with 99.7% confidence.

Top Ten Pitfalls in Quantitative Real-time PCR Primer/Probe Design and Use

1. Primer and/or probe melting temperature (T_m) is not optimal for the real-time PCR reaction.

The primer melting temperature (T_m) of each PCR primer should be between 58°C –60°C, and TaqMan® probe T_m should be ~ 10°C higher than the primer T_m. Also, the T_m of both primers should be within 1°C. It is important to note that the minor groove binder (MGB) moiety increases the T_m of the probe by several degrees, so the sequence of a TAMRA™ quenched probe and MGB-NFQ quenched probe are not completely interchangeable. (See # 4).

2. Concentration of primers and/or probe are incorrect.

Reconstitute primers and probe into working stock concentrations accurately. Ensure proper concentration of the resuspended primer/probe by measuring the spectrophotometric absorbance at 260 nm. It is also important to take into account the volumes that will be routinely pipetted (we recommend a minimum of 5 µL) from working stocks of primers and probe when setting up real-time PCR assays. A common range of working stock concentrations for primers is 10–100 µM and for probes is 2–10 µM.

3. Primers and probes were designed against low complexity sequence.

Regions of low-complexity sequence can create problems in designing unique primer and probe sequences. The best option would be to select an alternative region. If that is not possible, choose longer primer and probe sequences with higher T_m, to increase specificity. Also, optimization of the thermal cycling protocol may be necessary to help reduce nonspecific binding.

4. The probe was designed with MGB and ordered as TAMRA, or vice-versa.

It is necessary to verify that the correct probe (sequence, reporter, and quencher) is being used in the real-time PCR assay. If the wrong probe is used, it is possible that the T_m of that probe is incorrect for the real-time experiment. This will greatly affect PCR efficiency and there is very little thermal cycling optimization that can rescue the reaction.

5. Primers or probes were designed against low integrity sequence.

Sometimes there are template sequence discrepancies/inaccuracies, which can lead to failed assays caused by poor binding, or no binding of primers and probes. It is important to verify the sequence and check for the presence of single nucleotide polymorphism (SNP) sites. It is recommended that multiple sequencing reactions be performed to remove any sequence ambiguities, and to use public databases with curated sequences such as NCBI (National Center for Biotechnology Information) and dbSNP (Single Nucleotide Polymorphism database) to determine the quality of the sequence. Increasing the primer length without increasing the annealing temperature would allow for more wobble (primer-template mismatch).

6. Amplicon was too long

Designing primers that generate a very long amplicon may lead to poor amplification efficiency. Ideally, amplicon length should be 50 to 150 bases for optimal PCR efficiency. In cases in which longer amplicons are necessary, optimization of the thermal cycling protocol and reaction components may be required.

7. Primers and/or probes are designed against wrong region of the gene.

Care should be taken to design the primers and probes to the right target sequence, especially in the case of known splice variants, mutant genes, or targets from a large gene family, etc. Sometimes the primers/probe may span a wrong splice site or perhaps not interrogate the correct transcript from the gene family. If mutations are the target, probes should ideally be designed with the mutation in the middle of its sequence. Primer or amplicon sequences may be BLASTed (Basic Local Alignment

Search Tool) against the public database, to ensure that the correct target is being amplified.

8. Primers and/or probes are designed against wrong species.

If you are designing primers and probes to targets from mixed source samples (e.g., transgenic samples, pools of bacteria or viruses etc.), before starting the search for primers and probes, check your target sequence for possible homologies with sequences from other organisms by applying a BLAST (Basic Local Alignment Search Tool) search. Public BLAST servers are available on the Internet (e.g. www.ncbi.nlm.nih.gov/BLAST). The BLAST programs compare a query sequence to all sequences in a specified database. To find specific primers and probes, you should use only those target regions with minimum similarities to other sequences

9. Target detection is not transcript-specific and also amplifies background genomic DNA.

Genomic DNA (gDNA) is often co-extracted with RNA and can therefore serve as a template in downstream processes, such as PCR. False-positive results are obtained through amplification of contaminating gDNA. Hence, it is preferable to have primers/probes span exon-exon junctions (intron splice-sites) in the target mRNA to prevent amplification of the target from contaminating gDNA. In case of non-intronic sequences (e.g., from bacteria, viruses, certain plant and mitochondrial sequences), wherein such design criteria cannot be applied, it may be prudent to use good RNA isolation techniques to minimize background gDNA load and to treat the RNA sample with DNase before the reverse transcription step.

10. Ordering a probe labeled with a dye not calibrated or supported on the real-time PCR instrument being used.

Confirm that the probe was labeled with the appropriate dye and verify that the dye used is calibrated and supported on the real-time PCR instrument. A calibration may be necessary before the dye can be used on the instrument.

TaqMan® Gene Expression Assays

Providing the greatest sensitivity, specificity and reproducibility for quantitative gene expression

- Gene-specific TaqMan® probe and primer sets for quantitative gene expression studies
- Human, mouse, rat, Arabidopsis, Drosophila, C. elegans, Rhesus macaque, and canine species available
- Convenient single-tube format
- Universal cycling conditions



Applied Biosystems offers the largest family of products to meet your quantitative gene expression needs: from off-the-shelf gene-specific probe and primer sets to Custom TaqMan probes and primers manufactured to your desired sequences, and everything in between. All products use TaqMan probe-based chemistry and are designed for use on the suite of Applied Biosystems Real-Time PCR Systems—together the gold standard in quantitative gene expression offering the greatest sensitivity, specificity, reproducibility, and the broadest dynamic range.

TaqMan® Gene Expression Assays are a comprehensive collection of over 700,000 pre-designed probe and primer sets that enable researchers to quickly and easily perform quantitative gene expression studies on human, mouse, rat, Arabidopsis, Drosophila, C. elegans, Rhesus macaque, or canine genes. Each gene expression assay consists of a FAM™ dye-labeled TaqMan® MGB probe and two PCR primers formulated into a single tube. Every assay is optimized to run under universal thermal cycling conditions with a final reaction concentration of 250 nM for the probe and 900 nM for each primer. This streamlined approach and comprehensive assay selection enables a convenient, standardized process for quantitative gene expression.

New Feature

BCtect™ Kit Launched in India for Early Detection of Breast Cancer - Labindia Life Sciences will Process the Breast Cancer Blood Samples

DiaGenic ASA (Oslo) and Applied Biosystems Inc. recently announced the launch of BCtect™, a blood-based test for early detection of breast cancer. The test searches for a unique gene expression signature identified by DiaGenic using a custom TaqMan® Array manufactured for DiaGenic by Applied Biosystems. India was chosen as the first country for the introduction of BCtect™ after successful completion of a large study in the country. The samples collected for this study were processed in the Labindia Life Sciences NABL-certified genomics facility in Gurgaon.

The DiaGenic BCtect™ test addresses a significant medical need in India, where breast cancer is the second leading cause of death among women. The lack of a coordinated national screening program means that breast cancer is typically detected at a late stage, resulting in high mortality rates compared to Western countries. Last year alone, nearly 100,000 women in the country died from the disease. Breast cancer is also on the rise, with an estimated 250,000 new cases expected in India by 2015. A key problem has been the detection of only 10% of cases at an early stage, which lags far behind Western countries where detection rates reach as high as 65%.

The TaqMan Array manufactured for DiaGenic by Applied Biosystems consists of 96 TaqMan® Gene Expression Assays pre-loaded multiple times on a 384-well micro fluidic card. These 384 simultaneous real-time PCR reactions are performed without the need to use liquid-handling robots or multichannel pipettors. The array is run on the Applied Biosystems 7900HT Fast Real-time PCR System in the Labindia Life Sciences genomics laboratory in Gurgaon.

We are pleased to announce a new feature starting with the Jan./Feb. 2009 issue of BioNews. This feature will consist with an eminent scientist from India working in the area of genomics and/or molecular biology. The goal of this new feature will be to educate and inform our customers about the scientific research being conducted by these scientists as well as to highlight the accomplishments of life science research institutions in India.

We kick off this feature with an interview with Dr. J.M. Deshpande, Director, Enterovirus Research Center (ERC), Parel, Mumbai. Read on for a fascinating account of the origins, history and the mission of ERC.

Nestled in a secluded corner of the sylvan settings of the prestigious Haffkine Institute complex is an unpretentious, three story building, which houses the Enterovirus Research Center (ERC), India's nerve center for the surveillance and detection of the dreaded polio virus across the country. From its humble beginnings in 1949, ERC is now a world-class viral research laboratory using the latest genomic techniques to detect and help contain the spread of polio in India.

1. Labindia (LI): Dr. Deshpande, can you say something about the history and origin of ERC?

Dr. Deshpande (JMD): Increasing incidence of paralytic cases was observed in Mumbai in the late 1940s. Dr. CG Pandit, Director-General of Indian Council of Medical Research and Dr./ PV Gharpure, Professor of Pathology & Bacteriology, Grant Medical College & Sir JJ Group of Hospitals initiated the "Polio Research Unit", a long term grant-in-aid epidemiological study on poliomyelitis at the Grant Medical College, Mumbai in 1949. In these laboratories diagnosis and isolation of the poliovirus involved inoculation of monkeys with patient's sample and reproducing the disease in animals.

2. LI: What is the mission of ERC and some milestones?

JMD: Right from day one it was clear that PRU/ERU/ERC will study Enteroviruses. Amongst these polioviruses and paralytic poliomyelitis naturally get maximum attention. The epidemiology of poliomyelitis and polio outbreaks, design and evaluation of disease control strategies and advocating polio control and eradication has been the mission of the Centre. Scientists of the Centre investigated the 1957 polio epidemic in Andaman & Nicobar Islands. The first trial of Sabin Oral Poliovirus Vaccine was undertaken by staff of this Centre in 1963. We were involved in standardization and quality control testing of OPV production at the erstwhile Haffkine Institute (now, HBPCL) and evaluating the immunization schedule for OPV in the country.

In 1992, ERC joined Global Polio Laboratory Network of the WHO as a national Polio Laboratory. In 1997, the Centre was recognized as a Regional Reference Laboratory for Polio. In year 2000 our status in the three tier global network was elevated to one of the seven "Global Specialized Polio Laboratory" of the WHO.



Dr. J. M. Deshpande

- ▶ B. Sc Microbiology, M. Sc Biophysics
- ▶ PhD Applied Biology, Mumbai University, 1981
- ▶ Director Enterovirus Research Centre, Since July 1996
- ▶ Member of India Expert Advisory Group on polio for the Government of India
- ▶ Member of the WHO Polio Working Group that decides the global research agenda
- ▶ Member, Expert Review Committee (AFP Case Classification)

Blood-based Gene Expression Analysis to Detect Early Stage Breast Cancer Using the Applied Biosystems TaqMan® Array Platform

Introduction:

DiaGenic ASA (Oslo) develops diagnostic tests by detecting disease specific gene expression patterns in whole blood. India has no screening programme for breast cancer despite a rising incidence of the disease. Mammography is the choice screening method; however its performance is worse in younger women due to dense breast tissue. In India, the average age of first diagnosis is lesser than in the Western world suggesting that mammography may not be an optimal diagnostic tool. A gene expression test could provide a more patient-friendly alternative to complement existing practices. A prototype based on cohorts from the European Union (EU) and the United States (US) was developed for this market and a new, large, Indian study was completed using informative transcripts identified from EU/US women. The India study provides a new, independent cohort and therefore represents a rigorous validation of the transcript set. The DiaGenic BCtect™ early breast cancer detection kit (see the margin article on page 6) was developed based on this study.

Applied Biosystems TaqMan® Array Platform

Discovery studies have been performed showing the high potential for such a test to diagnose breast cancer. The Applied Biosystems (AB) whole genome array was compared against Agilent's whole genome array. The AB platform gave slightly higher diagnostic performance. The TaqMan platform gave highly reproducible expression data making it the choice platform for future development.

Study	Diagnostic accuracy
In house macro arrays ¹	82%
Agilent whole genome microarray ²	75%
AB whole genome microarray ³	80%
Prototype study (TaqMan® Array Platform) ⁴	82%

Methods

Blood samples were collected using PAXgene™ tubes. All handling and shipping was performed as per the manufacturer's instructions. All blood tubes were sent to the Labindia genomic custom service group for RNA extraction. Quality control was performed by measurement of 28S/18S, RIN value (RNA Integrity Number), A260/A230 and A260/A280 ratios as well as the RNA concentrations. TaqMan Array analysis was performed using two 96 assay formats selected from prior studies. The cards were run on a 7900HT Fast machine at the Labindia, NABL-certified genomics laboratory. Gene expression QC was performed using the QC control provided with the 7900HT Fast instrument as per QC procedures developed by DiaGenic. Multivariate statistical analysis was performed by DiaGenic.

Results

The interim analysis was performed on 113 donors. This population consisted of early and late breast cancer patients, and healthy controls with either benign findings or no mammographic findings. All findings were confirmed by histological and/or cytological analysis. The diagnostic performance of the test is presented as a ROC analysis that plots sensitivity against 1-specificity. Specificity is the ability to correctly predict healthy subjects, whilst sensitivity is the ability to correctly predict diseased subjects. The diagnostic performance of the test is retained with an India population. In addition the performance of the test is favorable compared to mammography in younger women where dense breast tissue is a confounding factor in mammography imaging.

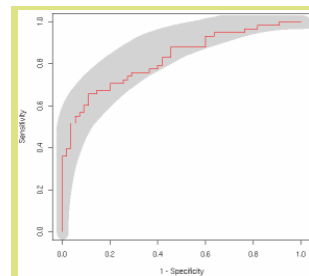


Figure 1. Grey ROC curve from earlier studies. Red curve shows India interim results

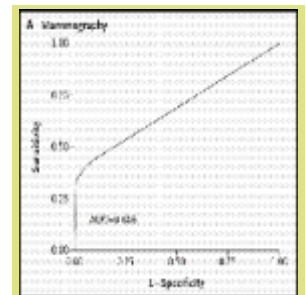


Figure 2. ROC curve of mammography in high risk women ⁵

Conclusion

The EU/US transcript set is able to classify healthy vs breast cancer patients in a new, independent, Indian population. The LDA format provides a high quality platform for gene expression analysis for diagnostic use across diverse populations. The data supports the use of the DiaGenic TaqMan® Array based test for breast cancer diagnosis

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Results of the Survey Conducted in the Sept.-Oct. 2008 Issue of BioNews

Dear Readers,

Thank you very much for your overwhelming and enthusiastic response to the survey included with the Sep.-Oct. 2008 issue of BioNews. More than 100 people responded to the survey. We are also happy to announce that the results of the survey indicate a high level of satisfaction with the design and technical content of BioNews as well as the relevance of the articles in the newsletter to your research.

The iPod Winners

As promised, two respondents will each receive an Apple iPod. The winners of the iPods are:

Dr. S. K. Shankar (M.D.)

Professor & Head
Department of Neuropathology
National Institute of Mental Health & Neuro
Sciences
(NIMHANS)
Bangalore-560 029

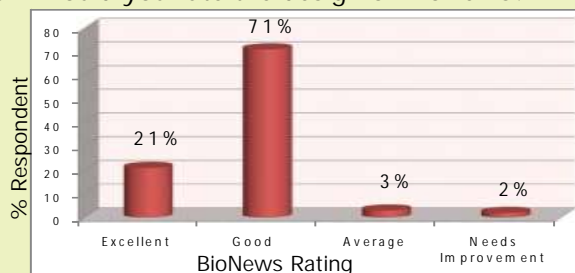
Dr. (Col.) Raghavendra B Kotabagi

Professor & HOD
Dept. of Forensic Medicine
Armed Forces Medical College (AFMC)
Pune- 411 040

Both winners will be receiving their iPods shortly....

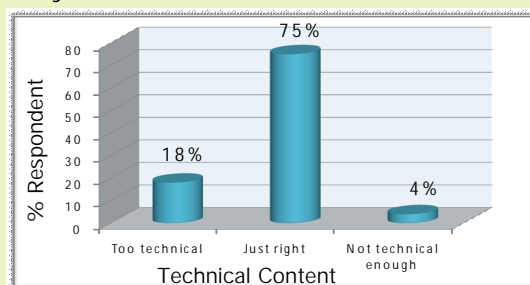
A Sampling of the Survey Results

How would you rate the design of BioNews?



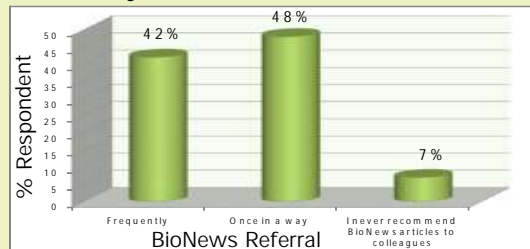
Excellent - 21%
Good - 71%
Average - 3%
Needs Improvement - 2%

How do you rate the technical content of BioNews?



Too Technical - 18%
Just Right - 75%
Not technical enough - 4%

How often do you recommend articles in BioNews to your colleagues?



Frequently - 42%
Once in a way - 48%
Never recommend - 7%