약 력

1. 인적사항

성 명	Sunny Song
소속기관	Agilent Technologies Inc.
직 위	R&D Scientist
전자메일	Sunny_Song@Agilent.com / SunnySong04@Yahoo.com

2. 학력/경력

연 도	학교 / 기관	전공 / 직위	학위 / 비고
2005 - present	Agilent Technologies, Inc. Santa Clara, California	R&D Scientist	Senior
2003 - 2005	Agilent Technologies, Inc. Palo Alto, California	R&D Scientist	Senior
2002 - 2003	Agilent Technologies, Inc.Palo Alto, California	R&D Scientist	Junior
2001 - 2002	University of California at Berkeley	Fellow	Post doc
1995 - 2001	University of Colorado Health Sciences Center	Student	Ph.D

3. 주요연구실적(개조식, 간단하게)

AGILENT TECHNOLOGIES INC 3500 Deer Creek Rd., Palo Alto, CA 94304, Life Sciences & Chemical Analysis
12/2002 to Present

R&D SCIENTIST - Gene Expression Microarray.

1. Developed fluorescent nucleic acid labeling reagents for Gene expression or Comparative Genome Hybridization microarrays (aCGH) which has a potential new business revenue of $1 million per year.
2. Interacted/collaborated with customers & potential business partners for technology evaluation for the commercialization of new reagent kit for gene expression/genomic microarray.
3. Trained employees for microarray data analysis.
4. Developed the Standard operation procedures (SOP) of gene expression/CGH microarray data analysis for internal or external use.
5. Supported Marketing/Order Fulfillment/Quality as a product specialist to provide customer solutions and troubleshooting.
6. Intellectual Property activity - Invention Disclosure for Patent filing.

7. Life Cycle documentation activity for Standard Product transition.
8. Consulting activity to support Proteomics team (East Coast site). Evaluated Affibody technology for developing immuno-affinity column.

UNIVERSITY OF CALIFORNIA-BERKELEY - 119 Morgan Hall MC3104, Berkeley, CA 94720
12/2001 to 12/2002
POST DOCTORAL FELLOW - Dept of Nutrition & Toxicology

1. Investigated retinoid metabolism in mammalian cells focused on retinoid binding proteins & enzymes using HPLC/MassSpec.
2. Site-directed mutagenesis, DNA sequence alignment, and Computer Protein Structure Modeling of enzyme aiming to modulate the substrate binding specificity & discrimination of retinoid binding proteins.

AVIDITY, LLC- 1899 Gaylord st. Denver, CO 80206
Producer of the patented biotin-accepting peptide (AviTagTM) technology used by researches in 22 countries.
4/2000 to 9/2001
MONOCLONAL ANTIBODY & BIACORE R&D CONSULTANT

1. Collected, analyzed and interpreted technical data on monoclonal antibody-antigen interactions using BIAcore.
2. Co-conceived a new product to efficiently purify biotinlyated fusion peptide (AviTagTM + hexahis) tagged proteins using affinity resin and monoclonal antibody, and conceived a ELISA type bioassay kit to screen tagged ligands in high-throughput mode.

UNIVERSITY OF COLORADO HEALTH SCIENCES CENTER, 4200 East 9th ave. Denver, CO 80262
9/1995 to 11/2001
RESEARCH ASSOCIATE, PH.D CANDIDATE - Dept of Biochemistry & Molecular Genetics.

1. Biochemical & biophysical characterization of DNA Polymerase III Holoenzyme in E.coli. Cloning, expression, purification of Recombinant Protein DNA polymerase in Fermentor scale. Extensive experience in both nucleic acid chemistry i.e. isolation, labeling, analysis of nucleic acid, and the kinetic analysis of DNA polymerase as well as biomolecular interaction analysis i.e. polymerase subunit-subunit interaction, Antibody-antigen interaction, & DNA-protein interaction.
2. Developed new analytical methods to screen/characterize the monoclonal antibodyagainst native DNA polymerase enzyme using Surface Plasmon Resonance (SPR) analysis (BIAcore), affinity column, LC/FPLC/HPLC, ELISA, and bead techniques.
3. Optimized a high throughput epitope mapping analysis using Phage-display peptide library and synthetic peptides to identify functional epitopes of DNA Polymerase.
4. PDB & GCG protein/DNA sequence data analysis for homology comparison of DNA polymerase family.

4. 발표시 사용 기자재

CD for LCD

* LCD projector의 사용을 원칙으로 합니다.
* LCD 사용을 위해 CD나, 저장 매체에 담아 오시는 것을 권장하며, Zip드라이브는 학회에서 준비하지 않습니다.

Quantitative analysis using decreasing amounts of genomic DNA to assess the performance of the oligo CGH microarray

Sunny Song[1], Vladimir Lazar[2], Anniek De Witte[1], Diane Ilsley[1]

[1]Agilent Technologies, Palo Alto, CA 94304
[2]Institut Gustave-Roussy (IGR), Paris, France

Comparative genomic hybridization (CGH) is a technique for studying chromosomal changes in cancer. As cancerous cells multiply, they can undergo dramatic chromosomal changes, including chromosome loss, duplication, and the translocation of DNA from one chromosome to another. Chromosome aberrations have previously been detected using optical imaging of whole chromosomes, a technique with limited sensitivity, resolution, quantification, and throughput. Efforts in recent years to use microarrays to overcome these limitations have been hampered by inadequate sensitivity, specificity and flexibility of the microarray systems.

The oligonucleotide CGH microarray system overcomes several scientific hurdles that have impeded comparative genomic studies of cancer. This new system can reliably detect single copy deletions in chromosomes. The system includes a whole human genome microarray, reagents for sample preparation, an optimized microarray processing protocol, and software for data analysis and visualization.

In this study, we determined the sensitivity, accuracy and reproducibility of the new system. Using this assay, we find that the performance of the complete system was maintained over a range of input genomic DNA from 5 ug down to 0.15 ug.

Quantitative analysis using decreasing amounts of genomic DNA to assess the performance of the oligo CGH microarray.

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Abstract

Comparative genomic hybridization (CGH) is a technique for studying chromosomal changes in cancer. As cancerous cells multiply, they can undergo dramatic chromosomal changes, including chromosome loss, duplication, and the translocation of DNA from one chromosome to another. Chromosome aberrations have previously been detected using optical imaging of whole chromosomes, a technique with limited sensitivity, resolution, quantification, and throughput. Efforts in recent years to use microarrays to overcome these limitations have been hampered by inadequate sensitivity, specificity and flexibility of the microarray systems.

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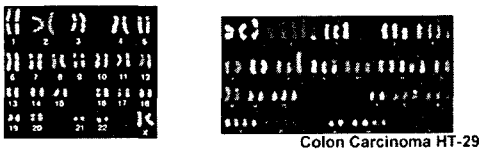
CGH (Comparative Genomic Hybridization) A method to identify and quantify DNA copy number changes throughout the genome in a single experiment.

Normal Human Genome
Stable diploid copy number even in most diseases, e.g. cardiovascular, neurological.

Cancer Genome
Multiple genome-wide chromosome aberrations including copy number changes and rearrangements



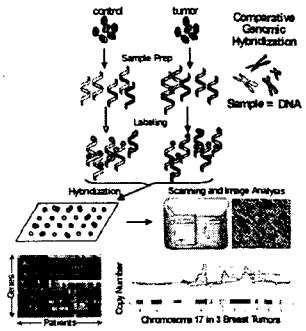
Colon Carcinoma HT-29

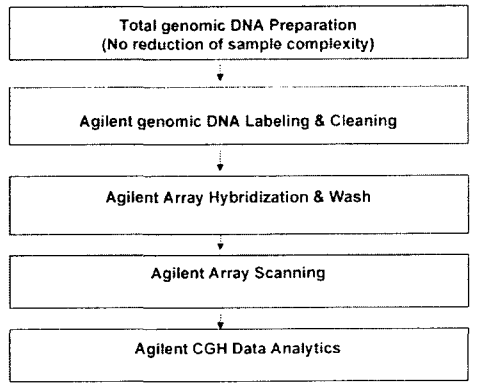
- Major application: Cancer Genetics
  - Understand cancer development and progression.
  - Identify new oncogenes (amplified regions) and tumor suppressor genes (deleted regions) → new therapeutic targets.
  - CGH profiles can be used to develop subclassification and diagnostics.

Fig.1 Array Comparative Genomic Hybridization (CGH) Whole Platform Solution

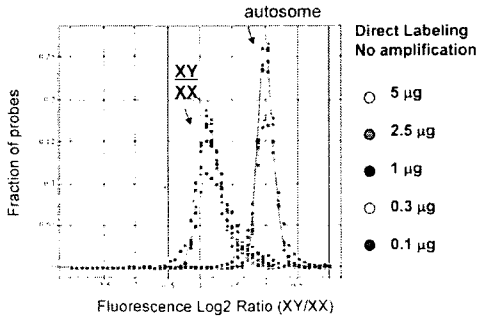
Probe Type	Ease of Manufacture	Resolution	Theoretical Coverage
BAC	Poor	100 kb	Complete
cDNA	Good	2 kb	Genes only
Oligo	Excellent	0.06 kb	complete

- Total genomic DNA
- *In situ* synthesized 60 mer oligo probes
- Potential for optimized selection and design of probes
- (e.g. Tm, homologies, kinetics, etc)
- Customizable designs enable:
  - Genome-wide/selected region(s) arrays.
  - Select genes/inter-genic regions.
  - Tissue-specific and model system arrays.

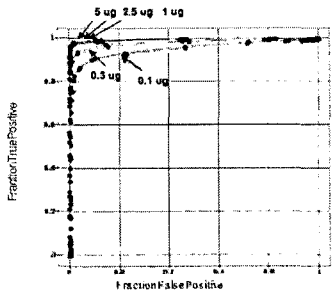




Distributions and medians of Log2Ratios from X-chromosome oligo nucleotide probes in XY/XX hybridization using a range of genomic DNA.



Accuracy Comparison using a range of genomic DNA: ROC Curve Analysis from X-chromosome oligonucleotide probes in XY/XX hybridization

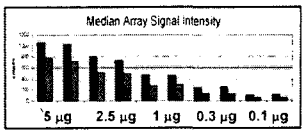


Direct Labeling
No amplification

	ROCArea
5 ug gDNA	0.98377
5 ug gDNA	0.98621
2.5 ug gDNA	0.98406
2.5 ug gDNA	0.97734
1 ug gDNA	0.97919
1 ug gDNA	0.97704
0.3 ug gDNA	0.94255
0.3 ug gDNA	0.94812
0.1 ug gDNA	0.87188
0.1 ug gDNA	0.87415

Performance Metrics Comparison using a range of genomic DNA input

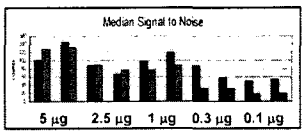
high signal



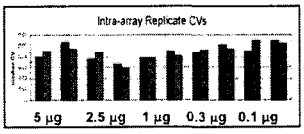
Direct Labeling
No amplification

cy5
cy3

high signal
to noise ratio

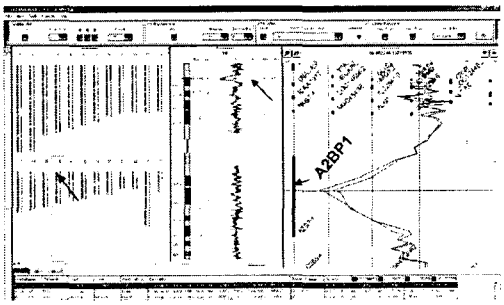


reproducible
intra array
replicate probes



User Reproducibility: Colon Carcinoma HT-29 1 µg Direct Labeling

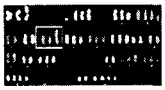
User1 Sunny Song, R&D Scientist.
Experiment done at Agilent Technologies,
Palo Alto Lab, CA
Chromosome 16p Homozygote deletion A2BP1
(Ataxin2 binding protein1)

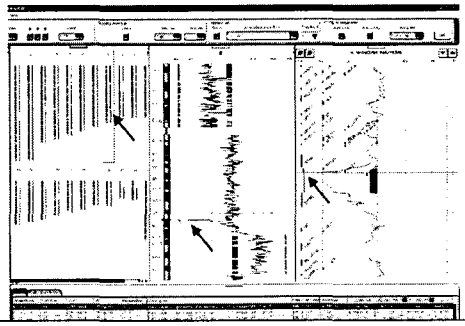


Replicates
dye swap

User Reproducibility: Colon Carcinoma HT-29 1 µg Direct Labeling

User1 Sunny Song. R&D Scientist.
Experiment done at Agilent Technologies,
Palo Alto Lab, CA
Chromosome 8p Loss (Single Copy deletion),
8q Gain (Amplicon), 8q22 Homozygote deletion

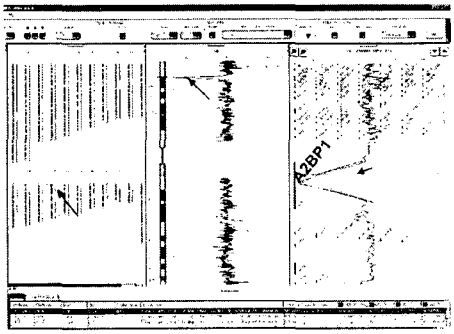




Replicates
dye swap

User Reproducibility: Colon Carcinoma HT-29 1 µg Direct Labeling

User2 Vladimir Lazar & Anniek De Witte.
R&D Scientists.
Experiment done at IGR, Paris Lab in France.
Chromosome 16p Homozygote deletion A2BP1
(Ataxin2 binding protein1)



Replicates
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User Reproducibility: Colon Carcinoma HT-29 1 µg Direct Labeling

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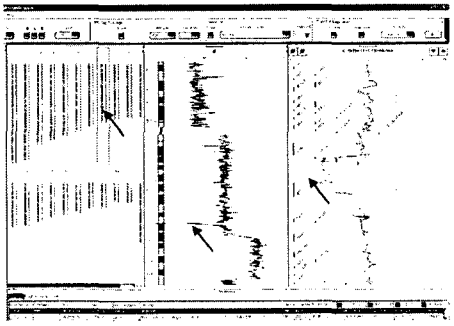

Replicates
dye swap

Conclusions

Oligonucleotide array CGH whole platform solution allows researcher to identify homozygote deletions, single copy number deletions and mapping the amplicon boundaries in CGH analysis.

1. Use total genomic DNA. No reduction of sample complexity, no PCR.
2. Excellent Signal to Noise Ratio. Very Low Background.
   ex) >30 with 0.3 ug input genomic DNA direct labeling
3. Performance consistency over a range of input genomic DNA from 5 ug down to 0.15 ug.
4. Reproducibility in inter user comparison.
5. Detection of Homozygote Deletion
   ex1) chromosome 3p14, FHIT, ex2) chromosome 3q26, novel ex3) chromosome16, A2BP1 in human colon carcinoma HT-29.
6. Detection of Single Copy Loss. ex) chromosome 18q in HT-29
7. Mapping Amplicon Boundaries. ex) chromosome 18q in HT-29