

SPECIAL ISSUES IN BREAST CANCER
GENE EXPRESSION PROFILING IN BREAST CANCER

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Selim M. NASSER



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ABSTRACT • Gene expression profiling has been increasingly used to determine new cancer markers. This technology holds major promises for improving the management of patients with breast cancer in which traditional clinicopathologic parameters do not account for all the heterogeneity of this disease and its distinct prognostic groups. Gene expression profiling has resulted in new classification of breast cancer and new assays are being developed and commercialized as prognostic and predictive tests.

However, the use of these tests in a clinical setting presents many issues. The accuracy of this new technology is often overestimated and its limitations should be addressed. Although early results are promising, further validation and well designed clinical trials are required before incorporating these tests in routine clinical practice.

RÉSUMÉ • Le profil d'expression génétique est de plus en plus utilisé pour découvrir de nouveaux marqueurs tumoraux. Cette technique a le potentiel d'améliorer la prise en charge des patients du cancer du sein, surtout que l'utilité des paramètres clinicopathologiques traditionnels est limitée face à l'évolution hétérogène de ce cancer. Cette technique a proposé une nouvelle classification du cancer du sein et de nouveaux tests cliniques à visée pronostique et prédictive sont développés et commercialisés. Cependant, l'utilisation clinique de ces tests pose des problèmes. Cette technique est limitée par de nombreux facteurs et sa précision est souvent surestimée. Malgré des résultats préliminaires encourageants, ces tests doivent être validés par des études supplémentaires surtout par des études cliniques prospectives et ceci avant leur adoption, en routine, dans la prise en charge du cancer du sein

INTRODUCTION

Breast cancer is the most common cancer in women. Current prognosis and management is based on clinical and histological parameters including TNM and tumor grade [1-2]. Despite their utility, these parameters fail to account for different clinical courses and outcomes in patients presenting with tumors showing similar features. Moreover, many women diagnosed with breast cancer get treatments from which they will not benefit and which may result in unnecessary toxicity and side effects.

Hundreds of markers have been tested in breast cancer in search for prognostic and predictive factors but despite years of research, only estrogen receptors, progesterone receptors, and HER2 have proven their utility in the routine clinical setting.

Technologic advances in the field of molecular biology have resulted in the ability to examine the expression of several genes simultaneously resulting in the recognition of patterns of gene expression. Current studies are showing that these patterns may serve as powerful tumor markers.

GENE EXPRESSION PROFILING. WHAT IS IT?

Gene-expression profiling is the simultaneous quantification of the expression of multiple genes. In other terms, it is the measurement of the activity of several genes in breast cancer cells. Such measurements are known as gene expression profiles. Several methods have been developed to look at the activity of hundreds or thousands of genes simultaneously. The most commonly used method is what we call "microarray analysis" or "gene expression array". Another common method is reverse transcriptase-polymerase chain reaction (RT-PCR).

Detailed description of these methods is beyond the scope of this review. In brief, RT-PCR is the amplification detection and quantification of mRNA of a set of predetermined genes in a given sample. RT-PCR can be performed on fresh-frozen and formalin-fixed-paraffin-embedded tissues (FFPE).

Microarray analysis requires fresh-frozen tissues. It is performed by placing a segment of DNA representing a single gene onto a spot adhered to a solid medium, such as a glass slide or "chip". Using this method, one can place hundreds or even thousands of DNA spots, each representing a single gene, onto a slide or chip, therefore creating an array of genes [3]. Next, RNA is extracted from the cells under study (such as breast cancer cells), amplified, labeled with a fluorescent dye, and then placed on the chip for hybridization with the complementary

Department of Pathology, Clemenceau Medical Center, Beirut; Lebanese American University Medical School.

Correspondence: *Selim M. Nasser, MD. Clemenceau Medical Center. Dept. of Pathology. P.O. Box 11-2555. Beirut. Lebanon.*
Tel.: +961 1 372888 ext 1952
e-mail: *selim.nasser@lau.edu.lb*

DNA sequence present within the spots on the chip. In most cases a control RNA sample from normal cells (such as leukocytes) is placed on the same chip but labeled with a different fluorescent dye. The chip is then placed in a scanner and relative levels of fluorescence, from each spot, representing increased or decreased levels of RNA messages compared to the control, are collected and analyzed using special software and statistical techniques [3-4]. In most cases, only a minority of genes are found to be over or under-expressed resulting in what we call gene expression pattern or gene expression profile. Special computer algorithms can cluster specimens based on similarity of gene expression patterns allowing the recognition of tumors that share so-called "signatures."

APPLICATIONS OF GENE EXPRESSION PROFILING IN BREAST CANCER

Gene expression profiling has been extensively used in breast cancer. It has resulted in refining our understanding, classification and grading of breast cancer as well as in the development of new prognostic and predictive tests.

Molecular classification of breast cancer

In their seminal paper Perou et al. [4] using microarray analysis identified distinct gene expression signatures, or "molecular portraits" when normal breast tissue was compared with breast cancer cells. The initial classification included basal-like, HER2 positive, luminal, normal, and categories of invasive breast cancer. Refining their earlier observation, these investigators reported that breast cancer could be grouped into six categories, which they designated basal-like; HER2-positive; normal; and luminal types A, B and C. Studies have shown that these classes are prognostic [5-7].

– *Tumors of the luminal groups* are ER positive and two thirds of them are of low or intermediate histological grade. Luminal A type breast cancers have the highest expression of estrogen and progesterone hormone receptors and have a better outcome than the other categories.

– *Basal-like cancers* are ER-negative and HER2-negative and most are high grade. The basal-like group has been associated with the so-called "triple-negative" breast cancer phenotype (ER negative, PR negative, and HER2 negative), but the basal-like genotype can be divided into multiple additional subgroups [8-9].

– *Basal-like and HER2-positive/ER-negative subtypes* are more sensitive to anthracycline-based neoadjuvant chemotherapy than are the luminal breast cancers [10]. They are also associated with the highest rates of pathologic complete response to neoadjuvant multiagent chemotherapy [11].

This molecular-based classification is not flawless and it appears that conventional parameters such as histological grade and hormonal receptors will complement the molecular classification rather than being replaced by it. Indeed, there are subtypes of luminal tumors that

have poor outcomes despite being ER-positive and these consistently share the histopathological feature of being higher grade [6, 12-13]. Moreover, a recent statistical meta-analysis of previous studies concluded that only three subtypes are consistently identifiable across datasets: HER2 positive, ER positive/HER2 negative, and ER-negative/HER2 negative [14-15].

Genomic grading

Sotiriou et al. identified genes that were capable of reclassifying the traditional three histological grades of breast cancer into only two distinct molecular grades: High-Genomic Grade Index (GGI) and Low-GGI [16]. In that study, high and low GGI were strongly associated with histologic grades 1 and 3, but patients with histologic grade 2 tumors appeared to be similar to either the grade 1 or grade 3 tumors in their molecular profiles. Moreover, patients with histologic grade 2 and High-GGI had a higher risk for recurrence than patients with grade 2 and Low-GGI. These results suggest that histologic grade 2 is actually a mixture of grade 1 and grade 3 tumors. Loi et al. used GGI to define two ER-positive molecular subgroups of breast with a statistically distinct clinical outcome in both untreated and tamoxifen-treated patients [17].

It seems that the discrepancy between histologic grade and GGI can be accounted for by the instability of the mitotic figures component in the "Bloom-Richardson score" histologic grading system. Interestingly, van Diest et al. [18] reported that the tumor proliferative index assessed by Ki-67 immunostain could serve as a surrogate for mitotic figures counting, leading to better correlation between histologic and genomic grading.

Gene expression profiling prognostic and predictive tests

Gene expression profiling allowed the development of several prognostic and predictive tests for breast cancer. Currently the best known tests are the Mammaprint and the Oncotype DX.

Mammaprint • This is the first commercially available, FDA approved, microarray-based test. It is currently designed as a prognostic assay for women under the age of 61 with lymph node negative breast cancer. It is performed on either fresh-frozen tumor samples or tumors preserved into an RNA preservative solution. The test results indicate either a high risk or low risk of disease recurrence. This test was developed in the Netherlands Cancer Institute. Using DNA microarray analysis on archived frozen tissue from 117 node-negative women with breast cancer for whom 10 or more years of follow-up was available, van't Veer et al. [7] identified a gene expression signature, composed of 70 genes, that is predictive of rapid metastasis ('poor prognosis' signature). These results were validated in other retrospective studies [19-20]. According to these results, the 70-gene profiler predicted outcomes more accurately than all other clinicopathologic parameters. The functions of the 70 genes

are associated with proliferation, invasion, metastasis, stromal integrity, and angiogenesis.

Oncotype DX • Also called 21-gene recurrence score assay. This is the first commercially available, RT-PCR-based test. It is performed in a Clinical Laboratory Improvement Act (CLIA) licensed centralized laboratory. It is currently designed as a prognostic and predictive assay to determine the 10-year risk for disease recurrence for women with ER-positive, lymph node-negative breast cancer. It is performed on formalin-fixed-paraffin-embedded samples. The test results report a recurrence score (RS) assigned into three risk categories: low, intermediate and high. This test was developed by Paik et al. [21] who profiled archived breast cancer samples that were available from patients who participated in clinical trial NSABP B-20 and from patients from two other data sets. These investigators identified 21 genes, including five control genes; the differential expression of which was used to generate a recurrence score employing a constructed algorithm. The recurrence score was able to identify three groups of patients based on risk of recurrence with median follow-up of 10.9 years: low (recurrence rates of 10% or less), intermediate (recurrence rates of 10% to 30%), and high (recurrence rates of 30% or more). Similar results were obtained from a validation study on samples from a second NSABP trial, B-14, which has a median follow-up exceeding 14 years and includes node-negative, ER-positive patients [22]. These studies suggest that this assay predicts overall prognosis in addition to adjuvant therapy benefit in that group of patients and could identify a subset of patients, which would have excellent prognosis with hormonal therapy alone. The functions of the genes selected for this test are associated mainly with proliferation and estrogen receptors pathways.

Breast Cancer Two-Gene Expression Ratio (H/I) • This is an RT-PCR based assay testing the expression of the HOXB6 and IL17BR genes. It is performed on formalin-fixed-paraffin-embedded tissues. It predicts recurrence in patients with ER-positive, lymph node-negative primary breast cancer [23-26].

Celera Metastasis Score • This is an RT-PCR based assay testing the expression of 14 genes on formalin-fixed-paraffin-embedded tissues in ER-positive, lymph node-negative tumors. Preliminary studies indicate that this test predicts a 3.5-fold difference in risk for disease recurrence between the women at the highest risk and the women at the lowest risk [27].

The Breast BioClassifier • This is another RT-PCR based assay performed on formalin-fixed-paraffin-embedded tissues. It measures the expression of 50 genes to identify the different biological subtypes of breast cancer (luminal-A, luminal-B, HER2, and basal-like), provides a prognostic risk assessment and may identify groups of patients that may potentially benefit from personalized therapy [28].

The Rotterdam Signature • Also known as the 76-gene assay. This is a microarray-based performed on

fresh-frozen tumor samples or tumors preserved into an RNA preservative solution. This assay is validated to predict prognosis in lymph node-negative patients independently of hormone receptor status [29-32].

Invasiveness Gene Signature • Another microarray-based test that measures the expression of 186 genes to predict prognosis in both node-negative and node-positive and both ER-negative and ER-positive patients [33].

NuvoSelect • This is a microarray-based assay that combines evaluation of several gene sets and claims to provide prognostic information as well as predictive therapeutic response to chemotherapy. It also provides ER and HER2 status [34-36].

Cytochrome p450 CYP2D6 Genotyping • ER-positive breast cancer patients with low or absent levels of CYP2D6 enzyme cannot activate tamoxifen and therefore would benefit more from aromatase inhibitors. Several assays using different technologies to determine CYP2D6 status are available, some are FDA approved [37-39].

The applications of gene expression profiling will only be expanding. Recently, a study reported that gene expression profiling could predict local recurrence after breast conserving surgery [40].

GENE EXPRESSION PROFILING IN THE CLINICAL SETTING : LIMITING FACTORS AND PITFALLS

Hundreds of markers have been tested and evaluated in thousands of publications, but only a few markers have been used successfully in clinical practice. Gene expression profiling has been the object of high profile studies and carries much hope; however, modern, complex and new techniques should undergo the same validation processes as the most basic ones. Adopting a test for routine clinical use requires standardization, proper validation, demonstration of diagnostic, prognostic, and predictive performance, demonstration of clinical benefit in routine clinical use and cost-effectiveness [41].

Although some tests are already commercially available, none of the gene expression profiling assays satisfies all these requirements and clinicians should be aware of the following limitations:

Study design and proper validation

Until now, tumor marker research has depended mostly on small studies with incomplete validations [42-43]. Current molecular profiling studies suffer from the same problems. It appears that the validation performance of several proposed signatures is inflated. Michiels et al. [44] showed that five of seven published molecular profiles do not actually perform better than chance. The first evaluation of the 70-gene signature showed near perfect accuracy, while the validation study revealed specificity of about 40% only [20].

According to Ein-Dor et al. [45], proper selection of appropriate genes in molecular profiling studies, requires sample size about 100-fold larger than the sample sizes

that have been used. Level I evidence for adopting new tumor markers requires analysis in prospective clinical trials designed to address the relevance of these markers in a clinical context [46-47]. None of the previous gene expression profiling studies is based on prospective trials. Up till now, only two of the current assays are being evaluated in prospective clinical trials and the first data will not be available before 2010 (see below).

Limitations of gene expression profiling data

Data from gene expression profiling are limited to specific tumor types and categories of patients. For example, Oncotype DX has been developed for estrogen-positive, lymph node-negative tumors only. Moreover, in the molecular classification, basal-like cancers have been associated with a less favorable outcome. But Weigelt et al. [48] showed that some special types of breast cancer associated with a good prognosis, such as medullary and adenoid cystic carcinomas, display also a basal-like profile. In addition, according to Esteva et al. [49] Oncotype DX failed to predict the risk of distant disease recurrence in patients with node-negative breast cancer who did not receive systemic therapy. Mina et al. [50] reported that Oncotype DX recurrence score did not correlate with pathologic complete response in patients, with newly diagnosed stage II or III breast cancer, who received preadjuvant chemotherapy.

Clinicians should be aware that data from gene profiling studies are limited to certain categories of patients and tumor types and cannot be applied in all clinical situations. Also, traditional clinicopathologic parameters should be integrated with data from gene expression profiling for proper patient's management.

Standardization of gene expression profiling-based assays

Standardization of molecular tests is necessary to ensure that genes activity can be measured and analyzed in the same conditions in different patients. However, variability and therefore biases may derive from the sampling of the specimens. For example mRNA extracted from a breast cancer specimen with a healing biopsy site, from a previous intervention, can give an inaccurate high proliferative profile. The timing of processing after surgery, fixation, specimen preservation and the nature of the biopsy (core vs. excision) can impact gene expression profiling [51-53].

Cost

Gene expression profiling based tests are very expensive and many are available only in the companies that developed them.

CURRENT GUIDELINES AND PROSPECTIVE CLINICAL TRIALS

The 2007 ASCO guidelines [54] state that 21-gene recurrence score assay (Oncotype DX) can be used to predict the risk of recurrence in women with newly diagnosed, node-negative, ER-positive breast cancer who will be

receiving tamoxifen and to identify patients who are predicted to obtain the most therapeutic benefit from adjuvant tamoxifen and therefore, not require chemotherapy. The guidelines also state that the present data are insufficient to recommend use of other assays (including the MammaPrint, the Rotterdam Signature and the H/I breast cancer gene expression ratio).

It appears however, that the true clinical relevance of these tests needs additional studies to be determined. Two ongoing clinical trials may bring some needed answers:

– *The TAILORx (Trial Assigning Individualized Options for Treatment) Trial*. This prospective clinical trial is sponsored by the National Cancer Institute and involves 900 sites in North America [55-56]. It will use Oncotype DX to guide treatment selection. This trial plans to enroll at least 10,000 women with estrogen or progesterone-positive HER2-negative, lymph node-negative breast cancer. Patients with low Recurrence Score will receive hormonal therapy alone, patients with high Recurrence Score will receive hormonal therapy and chemotherapy, and patients with intermediate Recurrence Score will be randomized into either hormonal therapy alone or hormonal therapy plus chemotherapy. Results from this trial will not appear before 2013.

– *The MINDACT (Microarray in Node-Negative Disease May Avoid Chemotherapy) Trial*. This prospective clinical trial is sponsored by the European Organization for Research and Treatment of Cancer and opened in August of 2007 [57]. It plans to compare the 70-gene MammaPrint assay against the standard clinicopathologic prognostic factors included in Adjuvant Online, in selecting node-negative breast cancer patients for adjuvant chemotherapy. Preliminary results from MINDACT may be presented in 2010.

CONCLUSION

Gene expression profiling in breast cancer has had important implications on our understanding of breast cancer. It will likely greatly impact prognostic assessment and prediction of response to therapy. However, despite the potential of this field and while the list of commercialized assays is expanding, several challenges remain and many issues need to be addressed. Will one assay prove to be superior to the others? Will newer and better panels emerge? Also, adoption of these assays by clinicians unfamiliar with their limitation is a serious concern and may cause harm to the patients if these tests are used in the wrong clinical setting. It is clear that large prospective studies and more clinical experience are needed to establish guidelines for gene expression profiling assays and additional studies are needed to confirm their scientific validity and their true clinical utility.

REFERENCES

1. American Joint Committee on Cancer. <http://www.cancerstaging.org/cstage/index.html>
2. Elston CW, Ellis IO. Pathological prognostic factors in

- breast cancer. I. The value of histological grade in breast cancer: experience from a large study with long-term follow-up. *Histopathology* 1991 ; 19 : 403-10.
3. Eisen MB, Spellman PT, Brown PO et al. Cluster analysis and display of genome-wide expression patterns. *Proc Natl Acad Sci USA* 1998 ; 95 : 14863-8.
 4. Perou CM, Jeffrey SS, van de Rijn M et al. Distinctive gene expression patterns in human mammary epithelial cells and breast cancers. *Proc Natl Acad Sci USA* 1999 ; 96 : 9212-17.
 5. Perou CM, Sorlie T, Eisen MB et al. Molecular portraits of human breast tumours. *Nature* 2000 ; 406 : 747-52.
 6. Sorlie T, Perou CM, Tibshirani R et al. Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications. *Proc Natl Acad Sci USA* 2001 ; 98 : 10869-74.
 7. van't Veer LJ, Dai H, van de Vijver MJ et al. Gene expression profiling predicts clinical outcome of breast cancer. *Nature* 2002 ; 415 : 530-6.
 8. Nielsen TO, Hsu FD, Jensen K et al. Immunohistochemical and clinical characterization of the basal-like subtype of invasive breast carcinoma. *Clin Cancer Res* 2004 ; 10 : 5367-74.
 9. Kreike B, van Kouwenhove M, Horlings H et al. Gene expression profiling and histopathological characterization of triple-negative/basal-like breast carcinomas. *Breast Cancer Res* 2007 ; 9 : R65.
 10. Carey LA, Dees EC, Sawyer L et al. The triple negative paradox: Primary tumor chemosensitivity of breast cancer subtypes. *Clin Cancer Res* 2007 ; 13 : 2329-34.
 11. Rouzier R, Perou CM, Symmans WF et al. Breast cancer molecular subtypes respond differently to preoperative chemotherapy. *Clin Cancer Res* 2005 ; 11 : 5678-85.
 12. Sorlie T, Tibshirani R, Parker J et al. Repeated observation of breast tumor subtypes in independent gene expression data sets. *Proc Natl Acad Sci USA* 2003 ; 100 : 8418-23.
 13. Sotiriou C, Neo SY, McShane LM et al. Breast cancer classification and prognosis based on gene expression profiles from a population-based study. *Proc Natl Acad Sci USA* 2003 ; 100 : 10393-8.
 14. Kapp AV, Jeffrey SS, Langerød A et al. Discovery and validation of breast cancer subtypes. *BMC Genomics* 2006 ; 7 : 231.
 15. Kapp AV, Tibshirani R. Are clusters found in one dataset present in another dataset? *Biostatistics* 2007 ; 8 : 9-31.
 16. Sotiriou C, Wirapati P, Loi S et al. Gene expression profiling in breast cancer: Understanding the molecular basis of histologic grade to improve prognosis. *J Natl Cancer Inst* 2006 ; 98 : 262-72.
 17. Loi S, Haibe-Kains B, Desmedt C et al. Definition of clinically distinct molecular subtypes in estrogen receptor-positive breast carcinomas through genomic grade. *J Clin Oncol* 2007 ; 25 : 1239-46.
 18. van Diest PJ, van der Wall E, Baak JP. Prognostic value of proliferation in invasive breast cancer: A review. *J Clin Pathol* 2004 ; 57 : 675-81.
 19. van de Vijver MJ, He YD, van't Veer LJ et al. A gene-expression signature as a predictor of survival in breast cancer. *N Engl J Med* 2002 ; 347 : 1999-2009.
 20. Buyse M, Loi S, van't Veer L et al. TRANSBIG Consortium. Validation and clinical utility of a 70-gene prognostic signature for women with node negative breast cancer. *J Natl Cancer Inst* 2006 ; 98 : 1183-9.
 21. Paik S, Shak S, Tang G et al. A multigene assay to predict recurrence of tamoxifen-treated, node-negative breast cancer. *N Engl J Med* 2004 ; 351 : 2817-26.
 22. Fisher B, Jeong JH, Bryant J et al. Treatment of lymph-node-negative, oestrogen receptor-positive breast cancer : Long-term findings from National Surgical Adjuvant Breast and Bowel Project randomized clinical trials. *Lancet* 2004 ; 364 : 858-68.
 23. Ma XJ, Wang Z, Ryan PD et al. A two-gene expression ratio predicts clinical outcome in breast cancer patients treated with tamoxifen. *Cancer Cell* 2004 ; 5 : 607-16.
 24. Ma XJ, Hilsenbeck SG, Wang W et al. The HOXB13 : IL17BR expression index is a prognostic factor in early-stage breast cancer. *J Clin Oncol* 2006 ; 24 : 4611-19.
 25. Goetz MP, Suman VJ, Ingle JN et al. A two-gene expression ratio of ho-meobox 13 and interleukin-17B receptor for prediction of recurrence and survival in women receiving adjuvant tamoxifen. *Clin Cancer Res* 2006 ; 12 : 2080-7.
 26. Wang Z, Dahiya S, Provencher H et al. The prognostic biomarkers HOXB13, IL17BR, and CHDH are regulated by estrogen in breast cancer. *Clin Cancer Res* 2007 ; 13 : 6327-34.
 27. Garber K. Genomic medicine. Gene expression tests foretell breast cancer's future. *Science* 2004 ; 303 : 1754-5.
 28. Perreard L, Fan C, Quackenbush JF et al. Classification and risk stratification of invasive breast carcinomas using a real-time quantitative RT-PCR assay. *Breast Cancer Res* 2006 ; 8 : R23.
 29. Wang Y, Klijn JG, Zhang Y et al. Gene-expression profiles to predict distant metastasis of lymph-node-negative primary breast cancer. *Lancet* 2005 ; 365 : 671-9.
 30. Foekens JA, Atkins D, Zhang Y et al. Multicenter validation of a gene expression-based prognostic signature in lymph node-negative primary breast cancer. *J Clin Oncol* 2006 ; 24 : 1665-71.
 31. Yu JX, Sieuwerts AM, Zhang Y et al. Pathway analysis of gene signatures predicting metastasis of node-negative primary breast cancer. *BMC Cancer* 2007 ; 7 : 182.
 32. Desmedt C, Piette F, Loi S et al. TRANSBIG Consortium. Strong time dependence of the 76-gene prognostic signature for node-negative breast cancer patients in the TRANSBIG multicenter independent validation series. *Clin Cancer Res* 2007 ; 13 : 3207-14.
 33. Liu R, Wang X, ChenGY et al. The prognostic role of a gene signature from tumorigenic breast-cancer cells. *N Engl J Med* 2007 ; 356 : 217-26.
 34. Ayers M, Symmans WF, Stec J et al. Gene expression profiles predict complete pathologic response to neoadjuvant paclitaxel and fluorouracil, doxorubicin, and cyclophosphamide chemotherapy in breast cancer. *J Clin Oncol* 2004 ; 22 : 2284-93.
 35. Rouzier R, Pusztai L, Delaloge S et al. Nomograms to predict pathologic complete response and metastasis-free survival after preoperative chemotherapy for breast cancer. *J Clin Oncol* 2005 ; 23 : 8331-9.
 36. Gong Y, Yan K, Lin F et al. Determination of oestrogen-receptor status and ERBB2 status of breast carcinoma : A gene-expression profiling study. *Lancet Oncol* 2007 ; 8 : 203-11.
 37. Goetz MP, Rae JM, Suman VJ et al. Pharmacogenetics of tamoxifen biotransformation is associated with clinical outcomes of efficacy and hot flashes. *J Clin Oncol* 2005 ; 23 : 9312-18.

38. Jin Y, Desta Z, Stearns V et al. CYP2D6 genotype, antidepressant use, and tamoxifen metabolism during adjuvant breast cancer treatment. *J Natl Cancer Inst* 2005 ; 97 : 30-9.
39. Goetz MP, Knox SK, Suman VJ et al. The impact of cytochrome P450 2D6 metabolism in women receiving adjuvant tamoxifen. *Breast Cancer Res Treat* 2007 ; 101 : 113-21.
40. Malmström EN, Krogh M, Malmström P et al. Gene expression profiling in primary breast cancer distinguishes patients developing local recurrence after breast-conservation surgery, with or without postoperative radiotherapy. *Breast Cancer Res* 2008 ; 10 (2) : R65.
41. Ioannidis JP. Is molecular profiling ready for use in clinical decision making ? *The Oncologist* 2007 ; 12 : 301-11.
42. Altman DG, Royston P. What do we mean by validating a prognostic model ? *Stat Med* 2000 ; 19 : 453-73.
43. Vergouwe Y, Steyerberg EW, Eijkemans MJ et al. Validity of prognostic models : When is a model clinically useful ? *Semin Urol Oncol* 2002 ; 20 : 96-107.
44. Michiels S, Koscielny S, Hill C. Prediction of cancer outcome with microarrays : A multiple random validation strategy. *Lancet* 2005 ; 365 : 488-92.
45. Ein-Dor L, Kela I, Getz G et al. Outcome signature genes in breast cancer : Is there a unique set ? *Bioinformatics* 2005 ; 21 : 171-8.
46. Hayes DF, Bast R, Desch CE et al. A tumor marker utility grading system (TMUGS) : A framework to evaluate clinical utility of tumor markers. *J Natl Cancer Inst* 1996 ; 88 : 1456-66.
47. Hayes DF, Trock B, Harris A. Assessing the clinical impact of prognostic factors : When is "statistically significant" clinically useful ? *Breast Cancer Res Treat* 1998 ; 52 : 305-19.
48. Weigelt B, Horlings HM, Kreike B et al. Refinement of breast cancer classification by molecular characterization of histological special types. *J Pathol* 2008 ; 216 (2) : 141-50.
49. Esteva FJ, Sahin AA, Cristofanilli M et al. Prognostic role of a multigene reverse transcriptase-PCR assay in patients with node-negative breast cancer not receiving adjuvant systemic therapy. *Clin Cancer Res* 2005 ; 11 : 3315-19.
50. Mina L, Soule SE, Badve S et al. Predicting response to primary chemotherapy : gene expression profiling of paraffin-embedded core biopsy tissue. *Breast Cancer Res Treat* 2006 ; 103 : 197-208.
51. Pusztai L, Mazouni C, Anderson K et al. Molecular classification of breast cancer: Limitations and potential. *The Oncologist* 2006 ; 11 : 868-77.
52. Abdullah-Sayani A, Bueno-de-Mesquita JM, van de Vijver MJ. Technology insight : Tuning into the genetic orchestra using microarray : limitations of DNA microarrays in clinical practice. *Nat Clin Pract Oncol* 2006 ; 3 : 501-16.
53. Rosenwald A, Wright G, Chan WC et al. The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma. *N Engl J Med* 2002 ; 346 : 1937-47.
54. Harris L, Fritsche H, Mennel R et al. American Society of Clinical Oncology 2007 Update of Recommendations for the Use of Tumor Markers in Breast Cancer. *J Clin Oncol* 2007 ; 25 : 5287-312.
55. Lo SS, Norton J, Mumby PB. Prospective multicenter study of the impact of the 21-gene recurrence score assay on medical oncologist and patient adjuvant breast cancer treatment selection. *J Clin Oncol* 2007 ; 25 (18 suppl) : 577.
56. Sparano JA. TAILORx : Trial assigning individualized options for treatment. *Clin Breast Cancer* 2006 ; 7 : 347-50.
57. Bogaerts J, Cardoso F, Buyse M et al. TRANSBIG Consortium. Gene signature evaluation as a prognostic tool : Challenges in the design of the MINDACT trial. *Nat Clin Pract Oncol* 2006 ; 3 : 540-51.