EGFR Expression Predicts BRCA1 Status in Patients with Breast Cancer

To the Editor: In their article, Lakhani et al. (1) report on the value of basal phenotype markers for the prediction of BRCA1 status. One of the useful features pointing to “BRCA1-ness” appeared to be high expression of the epidermal growth factor receptor (EGFR). No rationale is given by the authors for including EGFR in the analysis. There is a clear one, however: EGF (likely acting through EGFR) was related to the basal phenotype in breast cancer by DiRenzo et al. (2). Furthermore, the finding of high EGFR expression in BRCA1-related breast cancer confirms previous data from our published study (3). We examined EGFR expression by immunohistochemistry in the invasive breast cancers from 21 proven carriers of BRCA1 germ line mutations, as well as from a control group of 430 invasive breast cancers from patients unselected for a family history of breast cancer. Of the 21 BRCA1-related breast cancers, 14 (67%) showed EGFR overexpression. In the control group of 430 tumors, EGFR overexpression was found in only 70 (16%) (P < 0.001, two-sided Fisher’s exact test). Also, the full ER−/erbB2−/EGFR+ phenotype was statistically significantly more frequent in BRCA1 mutation carriers (P < 0.001).

We hypothesize that this EGFR overexpression is probably largely posttranscriptionally regulated, as amplification of the EGFR gene seems to be very rare in invasive breast cancer (4), gains at the EGFR locus were not observed by comparative genomic hybridization (5), and increased EGFR mRNA expression was not observed in two gene expression studies in hereditary breast cancer (6, 7). We therefore urge further investigation into the mechanisms of EGFR overexpression in hereditary breast cancer and into new preventive strategies through EGFR targeting.

As the first article relating EGFR to the basal phenotype and the previously published EGFR expression results in BRCA1-related breast cancer were not referred to, and mechanisms behind the interesting finding of high EGFR expression in BRCA1-related breast cancer were not discussed, we would like to bring this to the attention of the Clinical Cancer Research readership.

Paul J. van Diest
Petra van der Groep
Elsken van der Wall
Departments of Pathology and Internal Medicine, University Medical Center Utrecht, Utrecht, the Netherlands

References
EGFR Expression Predicts BRCA1 Status in Patients with Breast Cancer

Paul J. van Diest, Petra van der Groep and Elsken van der Wall


Updated version  Access the most recent version of this article at:
http://clincancerres.aacrjournals.org/content/12/2/670

Cited articles  This article cites 7 articles, 5 of which you can access for free at:
http://clincancerres.aacrjournals.org/content/12/2/670.full.html#ref-list-1

Citing articles  This article has been cited by 1 HighWire-hosted articles. Access the articles at:
/content/12/2/670.full.html#related-urls

E-mail alerts  Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions  To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions  To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.