



The value of the human epidermal growth factor receptor-2 (HER2) as a prognostic marker

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Abstract

The prognosis for patients with breast cancer is determined by well-established pathological features associated with biological aggressiveness, histological grade, tumour size and nodal involvement. These remain the key determinants, despite the identification of numerous other potential biological markers. The use of prognostic indices, such as the Nottingham Prognostic Index (NPI), which combines and weights these factors, enables clinicians to predict outcome with a certain amount of accuracy. Approximately 20–30% of breast cancers express very high quantities of the human epidermal growth factor receptor-2 (HER2) protein and this is almost always associated with gene amplification. With the use of sensitive techniques, such as the radio-immunohistochemical method (rIHC) described herein, to quantify HER2 protein levels, up to a further 50% of such cancers will be found to express the HER2 receptor at least 4-fold higher than normal breast cells. Adding HER2 expression to the NPI helps to determine more accurately the prognosis for individual patients, particularly those with node-negative disease. Overall, the main value of HER2 measurement is likely to be in the prediction of response to therapies targeting the *HER2* gene and protein. © 2001 Elsevier Science Ltd. All rights reserved.

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1. Introduction

Factors accepted as being important in the prognosis of breast cancer include the size of the primary tumour, stage of disease at diagnosis, hormone receptor status and the number of axillary lymph nodes involved [1]. The single most reliable prognostic indicator is axillary lymph node involvement [2]. However, combining these factors has been shown to produce more accurate prognostic information. For example, the Nottingham Prognostic Index (NPI) [3] utilises a scoring system that combines tumour grade (1–3), number of positive lymph nodes (1=no nodes; 2=1–3 nodes; 3=>3 nodes) and tumour size $\times 0.2$ to classify breast cancer patients into three groups: group 1, score 2–3.4; group 2, score 3.5–5.6; and group 3, score ≥ 5.7 . This classification system efficiently stratifies patients in terms of mortality risk. Breast cancer patients treated in Glas-

gow who are classified as NPI group 1 have a 10-year survival rate of 88%, compared with 66% in NPI group 2 and 28% in NPI group 3 (Dr T. Cooke, Royal Infirmary, Glasgow). Thus, standard pathological factors provide accurate and useful prognostic information and these factors are used most commonly in clinical practice.

Other non-pathological prognostic factors include proliferation markers, vessel invasion and markers of angiogenesis, and mitotic index, which have all been shown to have some value in determining prognosis [4]. Furthermore, for many years, molecular factors have also been investigated for their potential prognostic value. Such tumour markers include the human epidermal growth factor receptor (HER) gene family [5,6], *hst* [7], *c-myc* [8], *p53* [9,10], *H-ras* [11] and *int2* [7]. It has been demonstrated that combining tumour markers with other non-pathological factors identifies two distinct breast cancer phenotypes with differing prognosis [12]. However, one of the best studied molecular factors in breast cancer and one of the factors with greatest statistical prognostic value is the HER2 growth factor receptor.

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The HER family comprises four homologous receptors named HER1 to HER4 [13]. The members of the HER family are transmembrane tyrosine kinase receptors with growth-stimulating activity and have a recognised role in the normal development and differentiation of mammary tissue [14–17]. The HER2 receptor is a protein comprising 1255 amino acids of molecular weight 185 kD (p185^{HER2}) [18]. p185^{HER2} is recognised to have a central role in the HER family, being the preferred heterodimerisation partner for the other members [19] and forming heterodimers that have particularly high ligand-binding and signalling potency [20]. Importantly, both preclinical and clinical studies indicate that *HER2* amplification and overexpression are involved in oncogenic transformation and tumorigenesis in breast cancer [5,6,21–26].

Having identified the critical role of HER2 in both normal and abnormal breast cell growth regulation, determining whether this receptor could be used to determine prognosis, predict response to therapy and as a target for specific therapy in women with breast cancer became interesting. This review focuses on data regarding the prognostic value of HER2 in breast cancer, both at the invasive and pre-invasive stages, and its relationship with other prognostic variables.

2. HER2 status and breast cancer prognosis

As previously stated, combining pathological factors allows a relatively good estimate of breast cancer recurrence and mortality risk to be made. Women with node-positive breast cancer are recognised to be at high risk and are treated accordingly [27,28]. However, within this group patients can be stratified based on factors such as hormone receptor status and location of metastases.

Node-negative breast cancer patients are at lower risk of disease recurrence, but as many as 30% of these women develop recurrent disease after apparently curative surgery [29,30]. Adjuvant chemotherapy can reduce the relative risk of disease recurrence by as much as 40% [31–34]. However, adjuvant therapy is not without risk due to the potential for adverse effects associated with many cytotoxic agents. Therefore, there has been intensive research directed towards identifying factors that can select women with node-negative breast cancer who are at greater risk of relapse and would therefore benefit from adjuvant therapy.

2.1. Identification of *HER2* as a prognostic factor

Slamon and colleagues [35] first linked HER2 with poor prognosis in breast cancer. By examining *HER2*-gene amplification in node-positive patients, they were able to demonstrate a significant correlation with reduced time to disease recurrence ($P \leq 0.0001$) and

decreased survival ($P = 0.0011$). These correlations were independent of other prognostic factors and were as significant as the relationship between nodal status and disease recurrence and survival in this study. Furthermore, the survival duration of women with breast cancer overexpressing HER2 was 3 years on average compared with an average of 6–7 years in those whose disease did not overexpress HER2. Further studies confirmed these results and demonstrated that *HER2*-gene amplification correlates with HER2-receptor overexpression [36]. However, despite the positive data produced by Slamon and colleagues, further studies have produced differing results that have prevented the widespread use of HER2 status as a prognostic factor.

2.2. *HER2* status in node-positive and node-negative breast cancer

Since the initial work of Slamon and colleagues [35,36], numerous clinical studies using different HER2 measurement techniques have investigated the relationship between HER2 status and breast cancer prognosis. Forty-seven of these trials, involving 15 248 patients, have been retrospectively analysed by Ross and Fletcher [37]. This analysis showed that HER2 status was an independent predictor of prognosis in 60% of the trials involving 67% of the patients. Most of the large studies (> 300 patients) included in this analysis confirmed the correlation between a HER2-positive status and poor clinical outcome in HER-positive breast cancer patients [38–49]. Thus, it is generally accepted that there is a significant correlation between *HER2* amplification/overexpression and poor prognosis in patients with node-positive breast cancer.

The relationship between HER2 status and prognosis in node-negative breast cancer patients is more controversial. Many studies have shown that there is a correlation between outcome and HER2 status in these patients [29,30,47,50–54], although others have not [55,56]. The majority of the data indicate that HER2 overexpression predicts the occurrence of metastases in these patients, although the clinical significance of this association has not been clarified.

Finally, the identification of ductal carcinoma *in situ* (DCIS) is important if the development of invasive breast cancer is to be prevented. This condition is often detected on screening mammography because it is often associated with microcalcification. At this stage in development, DCIS can be effectively treated by complete mastectomy, after which the risk of progression is close to zero [57]. However, increasing numbers of patients are being treated with breast-conserving therapy, for which the risk of recurrence is considerably higher [57]. In this situation, providing patients with an estimate of their risk of recurrence would aid therapeutic decision-making.

HER2 amplification/overexpression has been associated with both the high-grade and comedo subtypes of DCIS [58–60]. The majority of cases of comedo-type DCIS seem to be *HER2*-positive. In one study, van de Vijver and associates [61] showed that all *HER2*-positive cases of DCIS were of the comedo type. This result has been supported by other studies [21]. As comedo-type DCIS is a particularly aggressive form of the disease, these data suggest that *HER2* overexpression may identify a subset of DCIS patients at risk of progression to invasive disease who should be treated aggressively. Another theory suggests that the development of invasive breast cancer may follow two pathways [62]. According to this hypothesis, invasive tumours developing from DCIS are more aggressive, express markers of poor prognosis and are associated with a higher risk of progression. Other tumours develop from atypical ductal hyperplasia, which do not overexpress *HER2*, and are lower risk, more slowly progressing tumours.

3. Effect of testing technique on the prognostic value of *HER2*

The data summarised above appear to show convincingly that *HER2* status can be used to make prognostic decisions in breast cancer. However, enough studies have yielded conflicting results, showing either that *HER2* status does not have prognostic value or that it has only univariate significance, to indicate that the clinical use of *HER2* status for prognosis remains controversial. One of the major causes of variability of data between studies is the different testing methods used in the studies performed.

Two studies have reviewed the effect of the testing technique on the findings of studies examining the association between *HER2* status and breast cancer prognosis in some detail [37,63]. In the meta-analysis by Ross and Fletcher [37], only six of 47 studies failed to reveal any association between *HER2* status and prognosis; four of these used immunohistochemistry (IHC) to detect *HER2*-protein overexpression and two used Southern blotting and slot-blot analysis to detect *HER2*-gene amplification. Thus, 41 studies revealed at least a univariate correlation between *HER2* status and breast cancer prognosis whatever technique is used. Ross and Fletcher stress that IHC on fresh or frozen sections would be “an ideal method of detection” if fresh or frozen tissue and a standardised testing technique were widely available. They also state that all the studies included in the meta-analysis that used fluorescence *in situ* hybridisation (FISH) to detect *HER2*-gene amplification revealed an association between *HER2* status and prognosis, overcoming the problem of DNA dilution that affects Southern and slot-blot analysis.

Mitchell and Press [63] concentrated on five recent studies [54,64–67]. Their conclusions were similar to those of Ross and Fletcher [35]; the IHC techniques used to date vary widely, introducing inconsistency into the results obtained, but generally reveal a correlation between *HER2* status and prognosis, whereas FISH consistently identifies a negative association between *HER2* amplification and prognosis.

4. Radio-immunohistochemistry: further evidence for the association between *HER2* abnormalities and poor breast cancer prognosis

Both IHC and FISH produce useful and accurate information if performed correctly. However, IHC can be affected by the qualitative aspect of scoring stained sections and FISH is not widely available. We have investigated the use of a new technique termed radio-immunohistochemistry (rIHC) that enables quantitative analysis of immunohistochemically-stained tumour sections. Briefly, rIHC uses a radiolabelled anti-*HER2* antibody that binds to the *HER2* protein on the membrane of *HER2*-overexpressing tumour cells in tissue sections (Fig. 1). The section is then dipped in autoradiographic emulsion, exposed and developed. This produces a tissue section on which grains of stain are visible. Using computerised image analysis, areas of the tumour section of particular interest can be selected and the number of grains per unit area counted. This produces a quantitative estimate of the level of *HER2* overexpression.

Using rIHC, we compared *HER2* expression levels in tumours and normal breast tissue from the same patients. This demonstrated that approximately 85% of 179 breast tumours studied express *HER2* at levels that range from normal to up to 1000-fold of normal [68]. The majority of these overexpress the *HER2* protein at levels of up to 15-fold of normal. However, 23% overexpress *HER2* at higher levels [68] and these patients also showed *HER2*-gene amplification in FISH analysis (Dr Tim Cooke, Royal Infirmary, Glasgow) (Fig. 2). Thus, we have been able to demonstrate that rIHC produces data linking *HER2* overexpression to breast cancer prognosis provided that appropriate cut-off levels are established. Furthermore, these overexpression cut-off levels have been shown to correlate with *HER2*-gene amplification as determined using FISH.

We have also investigated the distribution of *HER2* expression levels in DCIS ($n=21$), DCIS associated with invasive disease ($n=47$) and invasive breast cancer ($n=179$) using rIHC [22]. This demonstrated that frequency distributions for *HER2* expression were similar in DCIS with and without invasion (Mann–Whitney U test, $P=0.19$) and both were comparable with invasive breast cancer (Mann–Whitney U test, $P=0.09$ (without

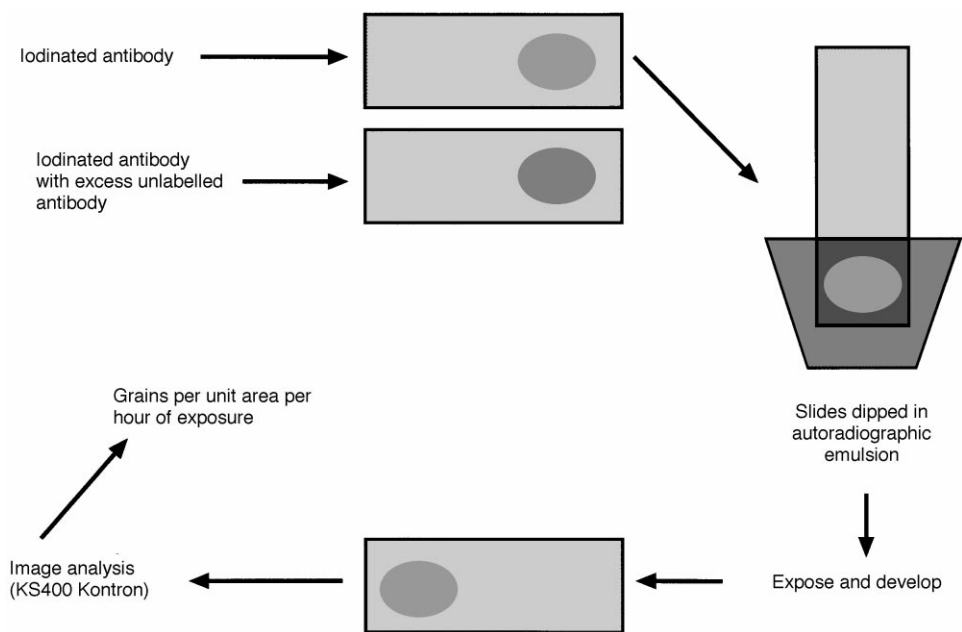


Fig. 1. Description of the rIHC technique used in the quantitative assessment of HER2 expression levels.

invasion) $P=0.83$ (with invasion) (Fig. 3). Furthermore, in tumours that showed evidence of DCIS and invasion, the expression of HER2 was similar in each component (Wilcoxon Signed Rank Test, $P=0.108$). Further studies demonstrated that HER2 expression levels were not associated with tumour grade or size, node status or HER1 levels, i.e. HER2 expression is an independent predictor of prognosis.

Further studies revealed that approximately 15% of breast cancers underexpress HER2 and that this is also associated with poor prognosis [68]. When patients in NPI groups 1–3 were subdivided into those with normal

HER2 expression levels and those with abnormal levels (overexpressors and underexpressors), HER2 expression abnormalities were shown to be able to identify patients at higher risk of disease progression and death within each NPI group (Table 1) [22].

5. Conclusions

The first suggestion that oestrogen might have a role in breast cancer was provided by Beatson in 1896 [69], who demonstrated that oophorectomy produced breast

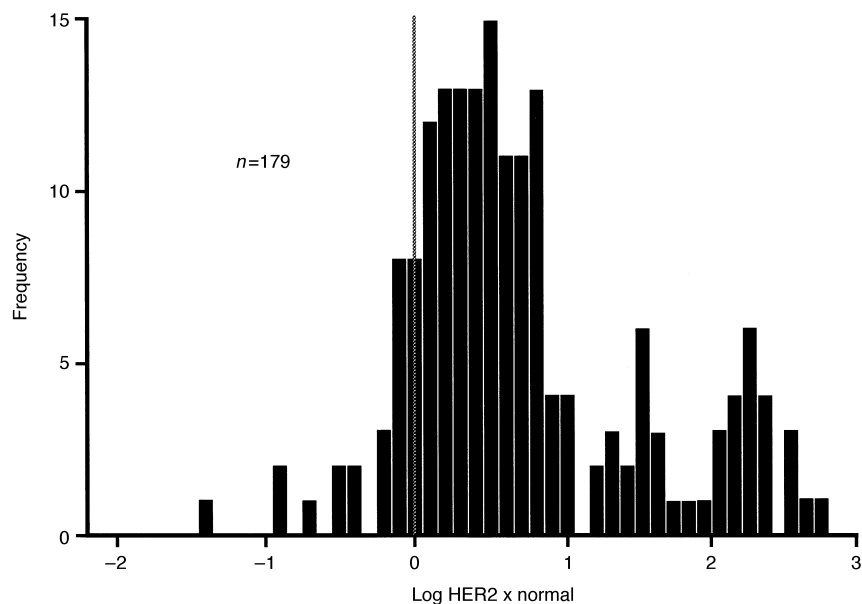


Fig. 2. HER2 expression levels in 179 breast cancer patients and the correlation between high levels of overexpression and *HER2*-gene amplification.

Table 1
Breast cancer survival at 10 years when categorised using the NPI and HER2 status

NPI ^b group	HER2 ^a status (n = 179)	
	Normal (%)	Abnormal (%)
1	92	79
2	66	29
3	29	20

$P < 0.0001$

^a HER2, human epidermal growth factor receptor-2.

^b NPI, Nottingham Prognostic Index.

cancer regression in premenopausal women. This was many years before oestrogen was first identified [70] and the mechanism of action was elucidated with the identification of the oestrogen receptor (ER) in rats [71]. Whether breast tumours express ER and/or progesterone receptors (PgR) is the best recognised molecular prognostic marker for breast cancer, with patients with ER/PgR-positive tumours having a significantly better prognosis than those with ER/PgR-negative tumours, although evidence for this was not produced until the 1970s [72,73]. Furthermore, definitive evidence that targeting the ER with anti-oestrogens produces clinical benefit in ER/PgR-positive, but not ER/PgR-negative women with breast cancer was not published until 1992 [33].

This example illustrates the difficulty of demonstrating that molecular factors have value in determining the prognosis of cancer patients and their response to therapy. Molecular biological techniques have improved, enabling factors with a potential role in cancer to be identified more easily, and many new and more sophis-

ticated tests for identifying such factors in tumour samples have been developed. This has allowed the relatively rapid screening of many molecular factors, but has also increased the potential for conflicting results to be produced.

Despite this, the data available indicate that determining HER2 status has prognostic value in breast cancer, identifying patients who are at high risk of reduced disease-free and overall survival. However, due to the variety of tests of different accuracy used to determine HER2 status over the past 20 years, this association remains controversial. We have used an accurate, quantitative and sensitive technique (rIHC) to study this association and have demonstrated that 85% of breast tumours express HER2 at higher levels than normal. Those tumours with the highest levels of HER2 overexpression (> 15-fold of normal; 23% of tumours) also showed gene amplification and these patients have a poor prognosis. Using this test, the prognostic power of HER2 status is such that the information produced is independent of other prognostic factors. Thus, relative to hormone status, information on the prognostic value HER2 status has become rapidly available.

Full acceptance of HER2 as a prognostic factor will only come as well-designed, prospective studies using quantitative, standardised techniques are performed. However, whether this will prove to be the most widely used application of HER2 status remains open to question. The latest update of the American Society of Clinical Oncology recommendations for the use of tumor markers in breast and colorectal cancer [74,75] recommends the use of ER and PgR status for making prognostic and therapeutic decisions. However, hormone receptor status is probably most widely used

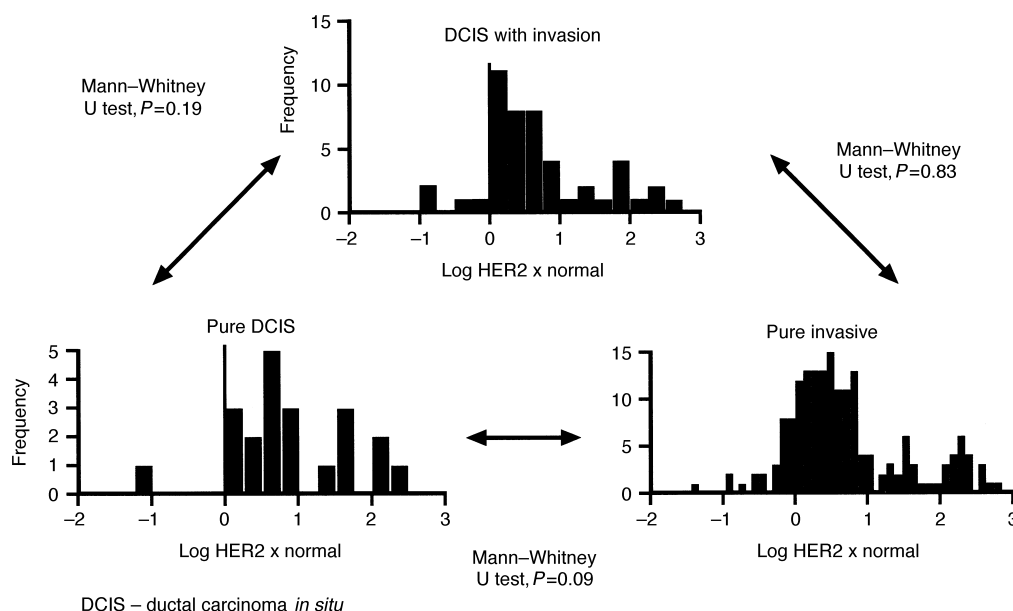


Fig. 3. Frequency distributions of HER2 expression in DCIS, DCIS associated with invasive disease and invasive breast cancer.

clinically to make therapeutic rather than prognostic decisions.

We believe that in future HER2 status will be used similarly. The availability of agents such as Herceptin® (trastuzumab), which targets the HER2 receptor [76] and produces significant survival benefits [77], together with the emerging role of HER2 status in predicting the outcome of hormonal therapy and chemotherapy [37], make knowing HER2 status important when determining the most appropriate treatment for a patient. Furthermore, a single molecular factor is unlikely to provide full prognostic information because breast cancer is characterised by multiple genetic abnormalities. In this regard, good assessment of pathological factors such as tumour grade and node status, which reflect the multiple gene defects, will probably remain the most important measure of the oncogenic potential of tumours.

In summary, HER2 status provides independent prognostic information at all stages of breast cancer from DCIS to invasive disease. Combining HER2 status with more conventional prognostic indicators, such as tumour size and grade and node status, allows high-risk groups to be identified. However, the most important application of HER2 status will be in selecting patients for targeted therapy using agents such as trastuzumab, much as hormone status is used to select patients for anti-oestrogen therapy using agents such as tamoxifen.

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