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	family were measured usin family were expressed to so of expression of the family of expression of a receptor two splice variants of the 1 aggregate expression were and TGF α , moderate expr levels of expression were Spearman's Rank Correlat Analysing the data using the	In gimmunohistochemical staining in one hundred cases of breast cancer. All of the some degree in some cases; however, individual cases showed a very wide range of from essentially none to all the factors at high levels. The highest aggregate level r was HER2 followed by HER1, then HER3, then HER4. The ligands (including NRG1 and NRG2 genes) broadly fell into three groups, those with the highest e Epigen, Epiregulin, Neuregulin 1 α , Neuregulin 2 α , Neuregulin 2 β , Neuregulin 4 ession was seen with EGF, Neuregulin 1 β and Neuregulin 3, and relatively low seen of HB-EGF, Betacellulin and Amphiregulin. Statistical analysis using tion showed a positive correlation of expression between each of the factors. the Cox Proportional Hazards model showed that, in this dataset, the most powerful
Keywords (separated by '-')	ErbB - Growth factor - Gr	rowth factor receptor - Prognosis - Breast cancer
Footnote Information	OrganizationUniversity of KentAddressCanterbury, Kent, CT1 7NJ, UKEmailEmailReceivedReceived6 February 2009RevisedAcceptedAccepted27 August 2009The levels of expression of the four receptors and eleven ligands composing the epidermal growth factor family were measured using immunohistochemical statining in one hundred cases of breast cancer. All of family were expressed to some degree in some cases; however, individual cases showed a very wide ran, of expression of the family from essentially none to all the factors at high levels. The highest aggregate level of expression were Epigen, Epiregulin, Neuregulin 1 α , Neuregulin 2 β , Neureguli and TGF α , moderate expression was seen with EGF, Neuregulin 1 β and Neuregulin 2 β , Neureguli and TGF α , moderate expression was seen with EGF, Neuregulin 1 β and Neuregulin 2 β , Neureguli and TGF α , moderate expression were Seen of HB-EGF, Betacellulin and Amphiregulin. Statistical analysis using Spearman's Rank Correlation showed a positive correlation of expression between each of the factors. Analysing the data using the Cox Proportional Hazards model showed that, in this dataset, the most power predictors of relapse free interval and overall survival were the combined measurement of only Epigen a Neuregulin 4.ls (separated by '-')ErbB - Growth factor - Growth factor receptor - Prognosis - Breast cancer	

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PRECLINICAL STUDY

The complete family of epidermal growth factor receptors 2 and their ligands are co-ordinately expressed in breast cancer 3

Emmet McIntyre · Edith Blackburn · 4

- 5 Philip J. Brown · Colin G. Johnson ·
- 6 William J. Gullick

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9 **Abstract** The levels of expression of the four receptors 10 and eleven ligands composing the epidermal growth factor 11 family were measured using immunohistochemical staining 12 in one hundred cases of breast cancer. All of the family 13 were expressed to some degree in some cases; however, 14 individual cases showed a very wide range of expression of 15 the family from essentially none to all the factors at high 16 levels. The highest aggregate level of expression of a 17 receptor was HER2 followed by HER1, then HER3, then 18 HER4. The ligands (including two splice variants of the 19 NRG1 and NRG2 genes) broadly fell into three groups, 20 those with the highest aggregate expression were Epigen, 21 Epiregulin, Neuregulin 1 α , Neuregulin 2 α , Neuregulin 2 β , 22 Neuregulin 4 and TGF α , moderate expression was seen 23 with EGF, Neuregulin 1 β and Neuregulin 3, and relatively 24 low levels of expression were seen of HB-EGF, Betacell-25 ulin and Amphiregulin. Statistical analysis using Spear-26 man's Rank Correlation showed a positive correlation of 27 expression between each of the factors. Analysing the data 28 using the Cox Proportional Hazards model showed that, in

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this dataset, the most powerful predictors of relapse free 29 interval and overall survival were the combined measure-30 ment of only Epigen and Neuregulin 4. 31 32

Keywords ErbB · Growth factor · 33 Growth factor receptor · Prognosis · Breast cancer 34

Introduction

The epidermal growth factor family of receptors and 36 ligands consist of four genes encoding receptors and at 37 least eleven genes encoding ligands [1]. Four of the 38 ligands, collectively known as the Neuregulins, are 39 expressed as multiple splice variants [2] and the latest 40 receptor to be discovered, HER4, is made in at least four 41 42 different forms also due to mRNA splicing [3]. The receptors are stabilised in an active state as homodimers or 43 heterodimers following ligand binding [4]. Exactly, which 44 45 forms are assembled in vivo is contingent on the repertoire of ligands available in the environment and their relative 46 47 affinities for each receptor type individually and possibly for preferences for binding to particular dimer pairs. We 48 have attempted previously to construct a computer simu-49 lation of this process [5] (http://www.cs.kent.ac.uk/people/ 50 rpg/em84/CellApplet1.html) in which a patch of cell 51 52 membrane can be populated with different numbers of each 53 receptor type and each of the eleven ligands can be introduced to initiate the assembly of the various receptor 54 pairwise combinations. This when run to equilibrium 55 should resemble the state of the system in a simple mem-56 57 brane bilayer.

Overexpression of most, if not all, of the receptors and 58 59 some of the ligands has been detected in breast cancer biopsies and cell lines. Antibodies or small molecule 60



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61 tyrosine kinase inhibitors have been evaluated targeted to 62 members of the system and some of these have been 63 introduced as clinical treatments for selected patients with 64 some success [6]. It would be helpful, however, to under-65 stand and predict the activation state of the system in individual patients so that the choice of the available 66 67 inhibitors can be most precisely made to ensure that 68 appropriate drugs are given and that those that are used can 69 be employed most cost-effectively. 70

Despite nearly 50 years of research and a long term appreciation of the potential importance of this family of molecules in breast and other cancer types as yet there has been no study published to our knowledge that described the expression patterns of the complete family of receptors and ligands in breast cancers at the protein level. Indeed some of the more recently described ligands such as Epigen [7] and Epiregulin [8] have not so far been studied in a series of clinical specimens. We report here using immunohistochemical staining a study describing the complete family in one hundred cases of unselected breast cancers.

81 Materials and methods

82 One hundred cases of breast cancer were obtained from 83 Professor Adrian Harris and Dr Russell Leek. Cancer 84 Research UK, Oxford, UK in the form of a tissue array. 85 Ethical approval for use was obtained from Oxfordshire 86 Clinical Research Ethics Committee. The patients were 87 treated by standard protocols, which were updated regu-88 larly according to national guidelines. ER positive patients 89 received tamoxifen for 5 years, node positive patients 90 under 60 also received 6 cycles of intravenous CMF. 91 Patients treated with wide local excision also received 92 adjuvant radiation therapy. The composition of the patients 93 is described in Supplementary Table 1 including age range, 94 grade, tumour size, ER status, node status, menopausal 95 status, whether treated by chemotherapy or hormonal 96 therapy and follow up. The study was conducted and 97 reported cohering to the guidelines published in McShane, 98 LM, et al. Reporting recommendations for tumour marker 99 prognostic studies. J Clin Oncol. 2005 Dec 20; 23(36): 100 9067-9072.

101 The antibodies used were mostly produced in the labo-102 ratory of Professor Gullick (Table 1). The antibody to EGF 103 was a kind gift of the late Dr Harry Gregory. The anti-104 bodies to Epigen (Catalogue number AF1127) and to 105 Epiregulin (Catalogue number AF1195) were purchased 106 from R&D Systems, Minneapolis, USA and the antibody to 107 TGFalpha (Catalogue number GF10) from Calbiochem, 108 San Diego, USA. Immunohistochemical staining was per-109 formed using the primary antibodies described earlier and 110 the StreptABCcomplex HRP Duet Mouse/Rabbit detection

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Table 1 Antibodies used in this study

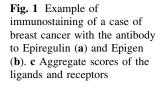
EGF receptor	F4	Mouse mAb	Gullick et al. [9]
HER2	21 N	Rabbit polyclonal	Gullick et al. [10]
HER3	RTJ2	Mouse mAb	Rajkumar et al. [11]
HER4	HFR1	Mouse mAb	Srininvasan et al. [12]
EGF		Rabbit polyclonal	From H Gregory
TGFalpha	GF10	Mouse mAb	CalBiochem
Amphiregulin	55AR	Rabbit polyclonal	Saeki et al. [13]
HB-EGF	111HB	Rabbit polyclonal	Chobotava et al. [14]
Epigen	AF1127	Goat polyclonal	R&D Systems
Epiregulin	AF1195	Goat Polyclonal	R&D Systems
Betacellulin	97BTC	Rabbit polyclonal	Srinivasan et al. [15]
NRG1a	76HRG	Rabbit polyclonal	Normanno et al. [16]
NRG1 β	102HRG	Rabbit polyclonal	Srinivasan et al. (15)
NRG2a	121NRG	Rabbit polyclonal	Dunn et al. [17]
NRG2 β	120NRG	Rabbit polyclonal	Dunn et al. [17]
NRG3	122NRG3	Rabbit polyclonal	Dunn et al. [17]
NRG4	123NRG4	Rabbit polyclonal	Dunn et al. [17]
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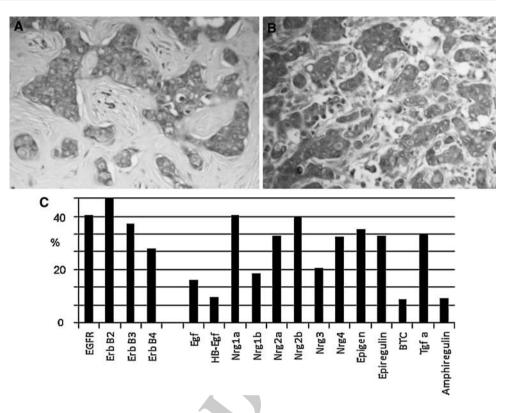
kit from Dako, Denmark. For detection of Epigen and 111 Epiregulin rabbit anti-goat biotinylated IgG (Dako) was 112 used with the kit. Optimisation of the concentration of each 113 antibody was performed prior to its use on the tissue arrays. 114 Tumours were scored for intensity of staining by inspection 115 on an Olympus BX40 microscope with a "double head" by 116 WJG and EM using a scale of 0 = negative, 1 = weak, 117 2 =moderate and 3 =strong. 118

119

Results

120 Each antibody detected specifically its cognate protein in a proportion of cases. Results with antibodies to Epigen and 121 Epiregulin, which have not previously been measured in 122 breast cancer, are shown in Fig. 1a and b. In order to assess 123 124 the overall expression levels for each protein we summed the scores for the hundred cases. The highest aggregate 125 score for the four receptors was for HER2. It should be 126 noted that this does not reveal heterogeneity of expression 127 between cases, for instance many previous studies have 128 reported that about 20% of breast cancers score 3+ for 129 HER2 but this would not be apparent in this analysis. 130 However, it does demonstrate, in particular with the 131 132 ligands, some of which have not previously been studied, that there are broad categories of expression present. 133 Highest scoring ligands included Epigen, Epiregulin, 134 Neuregulin 1 α , Neuregulin 2 α , Neuregulin 2 β , Neuregulin 135 4 and TGF α , moderate expression was seen with EGF, 136 Neuregulin 1 β and Neuregulin 3 and low levels of 137 expression were seen of HB-EGF, Betacellulin and 138 Amphiregulin. 139





140 The data obtained was analysed for any associations 141 between expression of each ligand and receptor with each 142 of the others using Spearman's Rank Correlation. From the 143 data in Fig. 2a, it can be seen that all the ligands and 144 receptors were positively associated. To provide a visual 145 representation of this large dataset, we have shown the 146 cases ordered on the ordinate in ascending score for total ligands (Fig. 2b, left axis, range 0-33) and shown the total 147 148 receptor score (range 0-12, right axis). The data reveal a 149 strong association between increasing total ligand score 150 and increasing total receptor score. It is also apparent that 151 there are some cases that essentially lack any receptor or 152 ligand expression at the cut of value scored while other 153 cases showed high levels of almost all the ligands and 154 receptors suggesting very great heterogeneity in the pres-155 ence of this highly interactive family of signalling molecules between individual cases. 156

In order to assess the relationship between the expres-157 sion of the ligands and receptors and clinical and molecular 158 159 variables, the tumours were divided in three ways. First, 160 they were dichotomised by low and high ligand levels; second, by low and high receptor levels and finally, by low 161 and high aggregate ligand and receptor levels. No signifi-162 163 cant associations were found although the strongest rela-164 tionship was between receptor levels and tumour size 165 (P = 0.06) (Supplementary Table 2).

Kaplan–Meier curves for overall survival (OS) weregenerated for all the receptors and ligands based on lack of

expression (0) or any level of expression (1-3) (Fig. 3). 168 Several of the factors have not previously been studied in 169 breast cancer and thus the dichotomisation of the data was 170 chosen to ensure as far as possible similar numbers of cases 171 in each category. HER2 expression would normally be 172 divided into low (0-2) versus high (3) as this has been 173 shown previously to give the best discrimination between 174 good and poor survival but it was considered more 175 appropriate in this study to maintain consistency within the 176 analysis. HER2 was separately analysed as a single factor 177 as low (0-2) versus high (3) and, as expected, high 178 expression was associated with reduced OS. Analysis of 179 the survival data using Cox's Proportional Hazards model 180 identified Epigen and Neuregulin 4 as the factors most 181 strongly associated with OS. 182

183 Interestingly, expression of Epigen was positively associated with improved survival, and NRG expression 184 was associated with worse OS. Various laboratory studies 185 have shown that different activation states of the EGF 186 family may induce either growth or differentiation and thus 187 in the light of our still imperfect knowledge of the system it 188 is not unexpected that some factors may have opposite 189 effects. In further analysis using the model omitting 190 sequentially the weakest factor (backwards elimination 191 dropping the factor with the smallest positive or negative 192 193 coefficient), the combination of Epigen (P = 0.003) and NRG4 (P = 0.01) retained the strongest association with 194 195 OS (Table 2). In order to assess the influence of these

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Α	AR	Tgf α	BTC	Epireg	Epigen	Nrg4	Nrg3	Nrg2 β	Nrg2 α	Nrg1 β	Nrg1α	HB-Egf	Egf	ErbB4	ErbB3	ErbB2	
EGFR	0.42	0.70	0.38	0.28	0.40	0.50	0.64	0.59	0.50	0.67	0.64	0.51	0.67	0.60	0.59	0.66	
p-value	5.52E-06	2.20E-16	4.23E-05	0.00244	1.57E-05	3.53E-08	1.76E-13	4.10E-11	5.23E-08	6.25E-15	2.16E-13	2.31E-08	5.24E-15	7.70E-12	3.85E-11	1.78E-14	
ErbB2	0.49	0.58	0.42	0.34	0.46	0.62	0.59	0.64	0.62	0.64	0.69	0.44	0.59	0.56	0.51		
p-value	8.24E-08	4.40E-11	6.24E-06	0.0002	6.28E-07	2.15E-12	3.70E-11	2.90E-13	1.63E-12	2.38E-13	< 2.2e-16	1.74E-06	3.13E-11	4.24E-10	1.62E-08		
ErbB3	0.41	0.54	0.48	0.33	0.34	0.59	0.51	0.57	0.55	0.59	0.60	0.42	0.59	0.56			
p-value	6.89E-06	1.76E-09	1.20E-07	0.00038	0.00023	3.84E-11	1.72E-08	1.44E-10	7.81E-10	2.01E-11	7.85E-12	4.61E-06	3.08E-11	4.65E-10			
ErbB4	0.37	0.68	0.38	0.30	0.42	0.63	0.54	0.49	0.65	0.56	0.67	0.37	0.51				
p-value	7.41E-05	1.55E-15	3.30E-05				1.36E-09		4.84E-14	3.36E-10		6.14E-05	1.59E-08				
Egf	0.57	0.56	0.56	0.18	0.50	0.54	0.63	0.53	0.57	0.60	0.65	0.61					
p-value			3.92E-10				7.38E-13					5.42E-12					
HBEfg	0.59	0.39	0.65	0.32	0.36	0.53	0.55	0.52	0.47	0.56	0.51						
p-value			6.35E-14				9.64E-10				1.80E-08						
Nrg1α	0.57	0.68	0.54	0.30	0.45	0.67	0.66	0.75	0.65	0.70							
p-value			2.11E-09				2.78E-14			2.20E-16							
Nrg1β	0.52	0.57	0.53	0.22	0.32	0.60	0.65	0.63	0.54								
p-value			6.08E-09			1.11E-11		3.90E-13	2.29E-09								
Nrg2α	0.43	0.66	0.51	0.37	0.59	0.70	0.62	0.65									
p-value			2.44E-08					7.60E-14									
Nrg2β	0.61	0.59	0.64	0.36	0.51	0.66	0.60										
p-value			1.28E-13				9.14E-12										
Nrg3	0.58	0.58	0.58	0.24	0.50	0.56											
p-value			8.05E-11			5.01E-10	_		and the second se								
Nrg4	0.45	0.52	0.51	0.35	0.37	_				۹.				and the second second			
p-value			1.62E-08		7.14E-05	В									_		
Epigen	0.32	0.46	0.39	0.46							2				_		
p-value			1.85E-05	3.75E-07							1			-			
Epireg	0.26	0.38	0.22								14		-				
p-value	0.004	4.45E-05 0.37	0.01399								-						
BTC													_				
p-value	1.19E-14	7.20E-05							,	-,,		-			-,,		
Tgfα	0.35						35 3	0 25	20	15 10	5	0	2 4	6	8 1	0 12	14
p-value	0.00014						Total L	igand							To	otal Rece	ptor

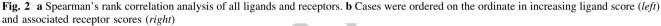
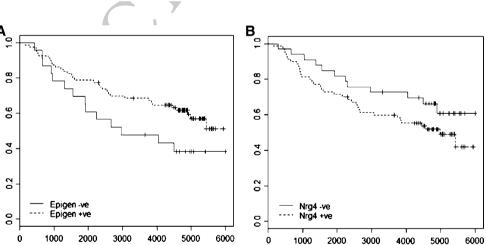


Fig. 3 Kaplan Meier charts showing the survival (days) of the patients based on the level of expression (0 vs. 1–3) of Epigen (*left*) and NRG4 (*right*)



196 factors in a more molecularly homogeneous group of cases 197 and to see if there were any major effects of treatment, the 198 oestrogen receptor positive cases were analysed separately. 199 Again positive expression of Epigen was associated with 200 good OS (P = 0.0092), but NRG2 α became the other predictive factor (P = 0.0057). The dataset was only 201 hundred cases (although 1,700 data points were acquired 202 203 for the 17 factors measured) and further studies on larger

datasets would be required to confirm or refute these 204 apparent relationships. 205

Discussion

Each ligand and each receptor were expressed at a range of 207 levels in a proportion of cases of breast cancer in this study. 208

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Table 2	Cox pro	portional	hazard	results	for	overall	survival	
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	Coeff.	Р	
EGFR	-0.6397	0.240	
ErbB2	-0.0235	0.970	
ErbB3	0.0812	0.870	
ErbB4	0.2826	0.600	
Egf	-0.1251	0.800	
HBEgf	0.2006	0.720	
Nrg1a	-0.7294	0.200	
Nrg1b	0.2555	0.570	
Nrg2a	0.2613	0.660	
Nrg2b	0.8110	0.260	
Nrg3	-0.5034	0.270	
Nrg4	1.0819	0.062	
Epigen	-1.1589	0.019	
Epiregulin	0.7059	0.230	
BTC	0.3027	0.600	
Tgfa	-0.3076	0.570	
Amphiregulin	-0.6340	0.230	

209 Statistical analysis of the data revealed a strong associate 210 between the expression of any member of the family and 211 all other members. Although breast cancer is acknowl-212 edged, both clinically and by analysis of molecular factors, 213 to be a heterogeneous disease it is still perhaps surprising 214 how different the composition of the factors between cases 215 were. In some individuals (at the precision of measurement 216 available from simple immunostaining), there were essen-217 tially no ligands or receptors present. In other individuals, all the receptors and essentially all the ligands were present 218 at the highest quartile of measurement. This suggests that 219 220 the family may be, in some cases, relatively unimportant 221 whereas in others it clearly has the potential to be an 222 important influence on cell activity. This may also reflect a 223 sensitivity or lack of sensitivity to drugs designed to inhibit 224 this system.

225 Individual receptors and ligands were, in some cases, 226 associated negatively or positively with shorter relapse free 227 interval or survival. This was not unexpected as some 228 ligands are known to provoke increased rates of cell growth 229 while others appear to stimulate differentiation. Using the 230 Cox's Proportional Hazards model, we show that a com-231 bination of Epigen and Neuregulin 4 in this series of cases 232 together gives the greatest separation of aggressive from 233 indolent disease. This result could not be predicted as we 234 are currently unaware of their individual activities in any 235 detail nor their effect on the balance between growth on the 236 one hand and differentiation on the other. It is likely, 237 however, that measuring a subset of the family may allow 238 prediction of the natural history of the disease in some 239 cases. Here two factors emerged, but further test datasets would be required to determine whether this was general-240 isable. The Neuregulins are produced as multiple splice 241 variants for instance, five have so far been identified as 242 products of the NRG4 gene [18] and these have very dif-243 ferent destinations within or without the cell and as such 244 245 may also have different functions. The antibodies used here to the ligands (where known) are directed to the EGF-like 246 sequence which is shared by all the so far reported splice 247 variants and should thus detect the sum of the expressed 248 249 gene products. The use of reagents which can discriminate between the splice variants may give a better ability to 250 predict their involvement and influence in the disease. 251

The use of computer simulations of the EGF system has 252 been an area of considerable study as we have a reasonable 253 knowledge of its constituents and some understanding of 254 255 how they function. It may be in the future that a "reading" of the family of receptors and ligands (or a subset of them) 256 may be able to more accurately predict prognosis and, 257 more importantly, select patients for treatment with par-258 ticular combinations of signal transduction inhibitor drugs. 259

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