O-124. Regional recurrence (RR) after 4 axillary node sampling (4ANS)

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The protocol at Nottingham City Hospital has been to carry out 4 Axillary Node Sampling (4ANS) in all cases of primary invasive carcinoma (excluding locally advanced tumours) aged 70 or less.

Those with positive nodes were advised to undergo axillary Radiotherapy or clearance.

To test the accuracy of 4ANS the rates of RR were examined in all cases diagnosed in 1990–1999 and only then in those in which 4 or more nodes had been obtained.

	Nodes +ve	*n*	RR (*n*)	RR at 10 years (%)
4 ANS				
LN −ve		1294	59	4.6
LN +ve	<4	544	23	4.2
LN +ve	4+	133	17	12.8
4 LN minimum				
LN −ve		953	29	3.0
LN +ve	1	272	7	2.6
LN +ve	2–3	207	7	3.4
LN +ve	4+	133	17	12.8

When a minimum of 4 lymph nodes are obtained only 3% developed RR in the absence of prophylaxis.

Cases with 4 or more lymph nodes involved at sampling developed RR in 13% of cases despite axillary prophylaxis.

4 node sampling appeared at least as accurate as sentinel lymph node biopsy using radio colloid, in the prediction of node positivity. Based on this Macmillan has presented a parallel series of blue dye assisted 4 node sampling (BDA4NS) ($n = 350$). Only 1 RR has occurred.

DBA4NS has practical and economic advantages over SLNB using dye and colloid, better prediction of survival and RR and is at least as accurate.

OS-1. Are conventional clinical markers outperformed by microarray gene expression profilers in breast cancer prognosis?

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The predictive diagnostic power of cDNA microarray gene expression profilers is confronted with those of conventional prognostic markers for breast cancer patients using both established prognostic indices and novel combinations of conventional markers. This is done using several data sets containing both microarray gene expression measurements and clinical variables for breast cancer patients. State-of-the-art classification tools and statistical procedures are used for the analysis. It is concluded that conventional markers are by no means outperformed by gene expression measurements using cDNA microarrays. Hence, at least for the time being, one should not overvalue the power of microarray gene expression data as clinical prediction tools.

Nevertheless, microarray tumor expression data add knowledge in terms of insights into the important genes and pathways underlying disease outcomes.