

Lymph node involvement using One-Step Nucleic Acid Amplification (OSNA) according to BRAF gene mutation status in patients with papillary thyroid carcinoma submitted to lymph node dissection

Carles Zafon, Oscar González, Jordi Temprana, Gabriel Obiols, Amparo García-Burillo, Xavier Serres, José María Balibrea, Joan Castell, Jordi Mesa, Carmela Iglesias

Hospital General Universitari Vall d'Hebron. Barcelona. Spain

Introduction

The relationship between BRAF gene mutation and lymph-node metastases is controversial in papillary thyroid cancer (PTC). OSNA (One-Step Nucleic acid Amplification) is a molecular technique that measures the number of copies of mRNA of cytokeratin 19 (CK 19) and it is used as a marker of lymph node metastasis.

Aim

To analyze the influence of BRAF mutation status in the characteristics of lymph nodes in patients with PTC submitted to lymph node dissection.

Patients and methods

Patients and tumour characteristics		N = 20	Lymph node characteristics	N = 277	CK 19 copy number	result	definition
Gender, n (%)		Female 12 (60) Male 8 (40)	sentinel, n (%)	36 (13)	< 100	-	negative
Age (years), mean (SD)		50 (15)	Compartment, n (%)	Central 179 (64.6) Lateral 95 (34.3) Unknown 3 (0.1)	100 – 250	-	Isolated tumor cells
Histologic variants, n (%)		Classical 16 (80) Follicular 2 (10) Cystic 2 (10)	Weight (g), median (IQR)	0.09 (0.04-0.18)	250 – 5000	+	Micrometastases
Size (cm), mean (SD)		2.6 (1.8)	Diameter (cm), median (IQR)	0.5 (0.3 – 0.8)	> 5000	++	Macrometastases

OSNA interpretation

Results

BRAF status	Lymph node dissections		N = 21	Lymph nodes		OSNA-N0	OSNA-N1	p-value
	Nodes per patient, median (IQR)	Global result, n (%)		N, n (%)	Weight (g), median (IQR)	Diameter (cm), median (IQR)	Tumour load per node, median (IQR)	
BRAF-M1	Nodes per patient, median (IQR)	11 (8-16)		OSNA-N0 3 (14.3)	0.08 (0.03 – 0.15)	0.40 (0.30 – 0.70)	6700 (1900 – 18000)	
BRAF-M1	Global result, n (%)	OSNA-N0 3 (14.3) OSNA-N1 18 (85.7)						
BRAF status	Positive nodes, median (IQR)	2.5 (1-7)		Type of M1, n (%)				
BRAF status	Percentage positive nodes, median (IQR)	25 (16.8 – 55.2)		Isolated tumour cells	6 (6.8)			
BRAF status	Total tumour load (TTL), median (IQR)	26390 (2853 – 215598)		MicroM1	38 (43.2)			
BRAF status	TTL/ total nodes, median (IQR)	2446 (327 – 10053)		MacroM1	44 (50)			
BRAF status	TTL/ positive nodes, median (IQR)	4850 (1675 – 49963)						
Lymph node dissections		N = 21	Positive Lymph node dissections		N = 18			
		BRAF-0 BRAF-1 p-value			BRAF-0 (n = 5) BRAF-1 (n = 13) p-value			
OSNA-0	2	1			Nodes per patient, median (IQR)	9 (4.7 – 11) 13 (8 – 17.5) 0.05		
OSNA-1	5	13			Positive nodes, median (IQR)	2 (1.7 – 3.2) 3 (1 – 7.2) 0.42		
		0.24			Percentage positive nodes, median (IQR)	25 (22.5 – 45.9) 25 (12.5 – 55.2) 0.92		
Lymph nodes		N = 277			Total nodes Weight (g), median (IQR)	0.75 (0.51 – 1.45) 1.11 (0.64 – 3.06) 0.38		
		BRAF-0 BRAF-1 TOTAL p-value			Total tumour load (TTL), median (IQR)	3900 (2852 – 267727) 29860 (3875 – 142397) 0.92		
OSNA-0, n (%)	53 (79)	136 (65)	189		TTL/ positive nodes, median (IQR)	3900 (1426 – 76202) 5100 (2900 – 23364) 1		
OSNA-1, n (%)	14 (21)	74 (35)	88					
TOTAL, n (%)	67 (100)	210 (100)	277					
Patients		N = 20	OSNA-N1 Lymph nodes		BRAF-0	BRAF-1	p-value	
		BRAF-0 BRAF-1 p-value						
N, n (%)	7 (35)	13 (65)		N, n (%)	14 (16)	74 (84)		
Age (years), mean (SD)	46.3 (13)	52.4 (17)	0.37	Weight (g), median (IQR)	0.09 (0.04 – 0.17)	0.12 (0.05 – 0.33)	0.25	
Tumour size (cm) mean (SD)	2.2 (1.8)	2.8 (1.9)	0.47	Diameter (cm), median (IQR)	0.45 (0.30 – 0.60)	0.60 (0.4 – 1)	0.08	
Tumour multifocality, n (%)	3 (42.8)	6 (46.1)	0.88	Tumour load per node, median (IQR)	17950 (1300-8900)	6700 (2050 – 12000)	0.77	
Tumour vascular invasion, n (%)	1 (14.3)	5 (38.5)	0.26	Type of M1, n (%)			> 0.05	
Tumour ETE, n (%)	2 (28.6)	6 (46.1)	0.44	Isolated tumour cells	0	6 (7.1)		
				MicroM1	7 (50)	31 (41.9)		
				MacroM1	7 (50)	37 (50)		

Conclusions

There were no differences in morphological characteristics of dissected lymph nodes according to BRAF mutation. However, the probability of node metastasis is higher among those nodes with BRAF mutated tumours than in BRAF not mutated samples.

