ORIGINAL ARTICLE



Usefulness of *NRAS* codon 61 mutation analysis and core needle biopsy for the diagnosis of thyroid nodules previously diagnosed as atypia of undetermined significance

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Abstract A repeat fine needle aspiration (FNA) is recommended for thyroid nodules diagnosed as atypia of undetermined significance (AUS) in a previous cytology. We evaluated the utility of NRAS codon 61 (NRAS61) mutation analysis and core needle biopsy (CNB) for the diagnosis of thyroid nodules previously diagnosed as AUS. This study enrolled 236 patients who underwent both NRAS61 mutation analysis and CNB of thyroid nodules previously diagnosed as AUS at cytology. The NRAS61 mutation was detected in 36 nodules and was more frequently detected in the AUS and follicular neoplasm (FN)/suspicious for follicular neoplasm (SFN) categories, as determined by histological analysis of CNB, than in the benign group (p = 0.005). Sixty-one patients underwent surgery, and 29 nodules were finally diagnosed as malignant after surgery. Among 61 patients who underwent

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surgery, nodules with the *NRAS*61 mutation (42–65 %) had a significantly higher malignancy rate than nodules with wild-type *NRAS*61 (7–37 %, p = 0.038). The association between malignancy and the *NRAS*61 mutation was significant after adjusting for age, sex, nodule size, and histological diagnosis of CNB (p = 0.01). *NRAS*61 mutation analysis together with CNB could be helpful for arriving at a clinical decision in patients with thyroid nodules showing AUS in a previous cytology.

Keywords Thyroid nodule \cdot Thyroid neoplasm \cdot Thyroid cancer \cdot Biopsy \cdot *NRAS* oncogene

Introduction

The Bethesda System for Reporting Thyroid Cytopathology defined the 'atypia of undetermined significance (AUS)/follicular lesion of undetermined significance (FLUS)' category because some cytopathologies are difficult to classify into benign, suspicious, or malignant categories in thyroid fine needle aspiration (FNA) cytological examinations [1]. The AUS category constitutes a heterogeneous group, and malignancy rates in AUS are reported to range from 6 to 48 % [2–4]. Repeat FNA and/or molecular testing is recommended for thyroid nodules classified as AUS with further evaluation of worrisome clinical and ultrasonographic features [5, 6].

FNA is a cost effective and safe procedure for assessing thyroid nodules [7, 8]. However, 10–50 % of cases show inconclusive findings even after repeat FNA of thyroid nodules initially classified as AUS [9–12]. Core needle biopsy (CNB) is an alternative procedure that uses a large and hollow needle. CNB was reported to provide a large tissue sample and facilitate precise histological diagnosis

[12, 13]. Recent studies showed that CNB resulted in a better diagnosis of thyroid malignancy than repeat FNA in nodules with nondiagnostic or AUS cytology. Inconclusive findings were reported to be 2-27 % for CNB and 49-50 % for repeated FNA in such settings [11, 12].

Molecular analysis has been used to detect thyroid malignancy in thyroid nodules. BRAF V600E, RAS point mutations, RET-PTC, and PAX8-PPARy rearrangement are frequently associated with thyroid cancer [14, 15]. Molecular analysis of thyroid nodules with AUS cytology could improve the diagnostic value of FNA. A previous study reported that the malignancy rate of thyroid nodules with AUS cytology was 88 % in any mutation positive nodules and only 5.9 % in mutation negative nodules [16, 17]. Among various genetic alterations, RAS point mutations are the most frequent mutations found in thyroid nodules with AUS cytology [16-18], and the NRAS codon 61 (NRAS61) mutation was the most common among six hot-spot mutations of *RAS* genes [19]. The malignancy risk was reported to be 84 % in RAS mutation positive nodules with AUS cytology [16].

To date, there is no study to evaluate the diagnostic performance of using CNB and molecular analysis for the diagnosis of indeterminate thyroid nodules. In this study, we evaluated a diagnostic utility of performing *NRAS61* mutation analysis on CNB samples of thyroid nodules previously assigned to the AUS category.

Material and methods

Patients

Between April 2013 and June 2014, patients who had undergone both *NRAS*61 mutation analysis and CNB of nodules previously diagnosed as AUS by FNA at Asan Medical Center, Seoul, Korea were enrolled in this study. Only patients who had thyroid nodules with a size of 1 cm or larger were included. A total of 236 patients were included in this study. This study protocol was approved by the institutional review board of Asan Medical Center.

Ultrasonography (US)-guided CNB procedure

All US examinations were performed using one of three US systems: iU22, HDI-5000 (Philips Healthcare, Bothell, WA), or EUB-7500 unit (Hitachi Medical Systems, Tokyo, Japan). The US systems were equipped with a linear, high-frequency probe (5–14 MHz). A comprehensive US evaluation of the neck and thyroid gland was performed in all cases, and the size, location, and composition of any nodules were evaluated. US-guided CNBs were performed

using a 1.1, 1.6, or 2.0 excursion, disposable, 18-gauge, double-action, spring-activated needle (TSK Ace-cut; Create Medic, Yokohama, Japan) after local anesthesia using 1 % lidocaine as previously reported [20]. Briefly, the core needle was approached with a free hand technique from the isthmus and directed to the solid component of the nodule. The stylet and cutting cannula of the needle were fired after the tip of the biopsy needle was advanced to the edge of the nodule. An additional CNB was performed if the lesion was considered to have been inaccurately targeted or if an inadequate tissue core was obtained according to visual inspection. Tissue cores were placed in 10 % buffered formalin immediately after biopsy. After the biopsy, all patients were requested to compress the biopsy site for 10-20 min. When a patient complained of neck pain or swelling at the biopsy site, an US examination was performed to check for complications.

Histological diagnosis

CNB samples were classified histologically into six categories broadly based on those of the Bethesda System for Reporting Thyroid Cytopathology [1]: nondiagnostic, benign, AUS, follicular neoplasm (FN)/suspicious for follicular neoplasm (SFN), suspicious for malignancy, and malignancy. An experienced endocrine pathologist (D.E.S), who was blinded to the clinical information, reviewed the results of histological analysis. Nondiagnostic findings included the absence of any identifiable follicular thyroid tissue (skeletal muscle or fibrous adipose tissue only), the presence of only normal thyroid gland, and the presence of tissue containing only a few follicular cells [12, 21]. The AUS category was assigned to CNBs that included some atypical cells with nuclear and/or architectural atypia and for which there was insufficient evidence for the diagnosis of FN/SFN, suspicious for malignancy, or malignancy because of extensive secondary degeneration, equivocal presence of tumor capsule, and clinically lymphocytic thyroiditis or mutinodular goiter background [20, 22]. The FN/SFN category for CNB included nodules which revealed architectural atypia such as microfollicular/trabecular/solid growth pattern with tumor capsule in the absence of clinical background of lymphocytic thyroiditis or mutinodular goiter. The suspicious for malignancy or malignancy categories for CNB were similar to those of 'Bethesda System for Reporting Thyroid Cytopathology [1]. A diagnostic criterion of CNB was defined as FN/SFN, suspicious for malignancy, or malignancy categories of CNB because these should be considered for thyroid surgery. The final diagnosis of the thyroid nodules was confirmed by histological examination of the surgical specimen after thyroidectomy.

Analysis of NRAS61 mutation

Genomic DNA from formalin-fixed fresh CNB tissues was extracted using the QIAamp DSP DNA Mini Kit (Qiagen, Hilden, Germany) as previously reported [23]. Polymerase chain reaction (PCR) was performed on genomic DNA to generate amplified fragments of NRAS61 with the following primers: forward, 5'-TTGCATTCCCTGTGGTTTTT-3'; reverse, 5'-TCCGCAAATGACTTGCTATT-3') using KOD FX polymerase (Toyobo, Osaka, Japan). Genomic DNA was amplified in a 10-µL reaction volume that contains 50 ng genomic DNA, 0.3 µL of 10 µM primers with 1 μ L of 10 \times PCR buffer and 1 μ L of MgCl₂ (2 mM). The amplification protocol consisted of an initial denaturation at 94 °C for 2 min, followed by 40 cycles at 98 °C for 10 s, 55 °C for 40 s, and 68 °C for 30 s, followed by a final extension step at 68 °C for 7 min. PCR products were analyzed on 2 % agarose gels that were stained with ethidium bromide. For purification of PCR amplified product, 1 µL of exonuclease I (1 unit/µL); (USB Corp., Cleveland, OH, USA) was incubated with 1 µL of PCR amplified products in 10 µL of the reaction for 40 min at 37 °C and 15 min at 85 °C. Sequencing reactions were performed in 1 µL of treated PCR amplified products with BigDye Ready Reaction Kit (ABI PRISM BigDye Terminator version 3.1; Applied Biosystems, Foster City, CA, USA) with the forward primer. The final products were analyzed on ABI PRISM Genetic Analyzer 3100 automatic DNA sequencer, Applied Biosystems).

Statistical analysis

R version 3.0 and R libraries prodlim, car, Cairo, and survival were used to analyze data (R Foundation for Statistical Computing, Vienna, Austria, http://www.R-project.org). Continuous variables between two groups were compared using Student's t test. Categorical variables were compared using the Chi-squared test or Fisher's exact test. The multivariate analysis included age, sex, nodule size, CNB, and NRAS61 mutation analysis. We evaluated the diagnostic values of NRAS61 mutation analysis and histological analysis of CNB by calculation of sensitivity, specificity, negative predictive value, positive predictive value, and accuracy. Diagnostic values were calculated using the folcriteria: sensitivity = [true positive lowing (TP)/ $\{TP + false negative (FN)\} \times 100$, specificity = [true negative (TN)/{TN + false positive (FP)}] \times 100, negative predictive value (NPV) = $[TN/(TN + FN)] \times 100$, positive predictive value (PPV) = $[TP/(TP + FP)] \times 100$, and accuracy = $[(TP + TN)/(TP + TN + FP + FN)] \times 100.$ McNemar's test was used to compare the diagnostic value between two kinds of diagnostic tools. All p values were twosided, and p < 0.05 was considered statistically significant.

Results

Baseline characteristics

The mean age of the 236 patients was 54.1 ± 12.1 years, and 42 patients (18%) were male. The mean longest diameter of the target nodules measured by US was 2.2 ± 1.1 cm. The needle was passed once into the target nodule in 187 patients (79%), twice into the target nodule in 48 patients (20%), and three times into the target nodule in one patient (0.4%). The mean number of tissue cores was 1.2 ± 0.5 . Eighty-nine biopsies (38%) were obtained with a 1.1-cm excursion needle, 137 (58%) with a 1.6-cm excursion needle, and 10 (4%) with a 2.0-cm excursion needle.

Histological diagnosis of CNB

Thyroid nodules were classified into six categories by histological diagnosis of CNB (Table 1): nondiagnostic (n = 8, 3%), benign (n = 90, 38%), AUS (n = 99, 42%), FN/SFN (n = 32, 14%), suspicious for malignancy (n = 3, 1%), and malignancy (n = 4, 2%). A CNB was helpful for arriving at a clinical decision in 129 cases (55\%): 39 nodules were assigned for surgical treatment (FN/SFN, suspicious for malignancy, or malignancy), and 90 were benign nodules.

NRAS61 mutation

The *NRAS*61 mutation was found in 36 of 236 CNB samples (15 %, Table 1). *NRAS*^{Q61R} was detected in 32 nodules (89 %), and *NRAS*^{Q61K} was detected in 4 nodules (11 %). There were no differences in age, sex, nodule size, number of needle passes, number of tissue core, or type of excursion needle between patients with nodules with the *NRAS*61 mutation and those with nodules with wild-type *NRAS*61.

NRAS61 mutation analysis and histological diagnosis of CNB

The *NRAS*61 mutation was only found in the thyroid nodules of benign, AUS, and FN/SFN groups based on the analysis of CNB samples: seven in 90 nodules (8 %) of the benign group, 21 in 99 nodules (21 %) of the AUS group, and eight in 32 nodules (25 %) of the FN/SFN group (Table 1). It was not detected in CNB samples from patients in the inadequate, suspicious for malignancy, or malignancy groups. The *NRAS*61 mutation was more common in AUS and SFN/FN groups than in the benign group (p = 0.005). Seven nodules in the benign category and 21 nodules in the AUS category had the *NRAS*61 mutation. Therefore, in addition to CNB, *NRAS*61 mutation

Groups	Diagnosis by CNB	Subjects		Mutant NRAS61		Malignancy confirmed	% of malignancy	
		Total	Surgery	No.	%	by surgery	Total ^a (%)	Surgery ^b (%)
Overall	Nondiagnostic	8	1	0	0	0	0	0
	Benign	90	6	7	8	2	2	33
	AUS	99	26	21	21	11	11	42
	FN/SFN	32	23	8	25	11	34	48
	Suspicious for malignancy	3	2	0	0	2	67	100
	Malignancy	4	3	0	0	3	75	100
	Total	236	61	36	15	29	12	48
Mutant NRAS61	Nondiagnostic	0	0	0	NA	0	NA	
	Benign	7	2	7	100	1	14	50
	AUS	21	13	21	100	7	33	54
	FN/SFN	8	8	8	100	7	88	88
	Suspicious for malignancy	0	0	0	NA	0	NA	
	Malignancy	0	0	0	NA	0	NA	
	Total	36	23	36	100	15	42	65
Wild-type NRAS61	Nondiagnostic	8	1	0	0	0	0	0
	Benign	83	4	0	0	1	1	25
	AUS	78	13	0	0	4	5	31
	FN/SFN	24	15	0	0	4	17	27
	Suspicious for malignancy	3	2	0	0	2	67	100
	Malignancy	4	3	0	0	3	75	100
	Total	200	38	0	0	14	7	37

Table 1 Malignancy rate according to the results of NRAS codon 61 mutation analysis and core needle biopsy in nodules with AUS cytology

^a Malignancy rate among total patients

^b Malignancy rate among patients who underwent surgery

AUS atypia of undetermined significance, CNB core needle biopsy, NRAS61 NRAS codon 61, FN/SFN follicular neoplasm/suspicious for follicular neoplasm

analysis was helpful at arriving at a clinical decision for surgery in these 28 patients (12 %), and 15 of these patients underwent surgery. The other 13 patients did not choose thyroid surgery even after physician's recommendation. Most of them were closely followed up by regular US examination. In 5 patients who were diagnosed as suspicious for malignancy or malignancy by CNB, two patients did not undergo surgery. Physician recommended thyroid surgery for these two patients, but they did not undergo surgery and were not followed up anymore in our institution.

Comparison of malignancy rates according to the results of *NRAS61* mutation analysis

Sixty-one patients (26 %) underwent thyroid surgery after CNB, and 29 of these patients were finally diagnosed as having a malignant tumor (Table 1).The *NRAS*61 mutation was present in 36 of 61 patients, and 15 of these (65 %) were finally diagnosed as having a malignant tumor. The malignancy rate was significantly higher in patients with the *NRAS*61 mutation (42–65 %) than in those with wild-

type *NRAS61* (7–37 %; OR: 3.15, p = 0.038; Table 1). The association between final diagnosis of malignancy and the presence of mutant *NRAS61* was significant after adjusting for age, sex, nodule size, and histological diagnosis of CNB (OR: 6.63, p = 0.006; Table 2).

Malignancy rate according to the results of NRAS61 mutation analysis and diagnostic categories of CNB

The *NRAS61* mutation was found in thyroid nodules belonging to benign, AUS, and FN/SFN groups based on CNB histological analysis. Therefore, we compared the malignancy rate of these three groups. We determined the malignancy rates both in total patients and in patients who underwent surgery (Table 1).

In the benign group, the malignancy rate of the mutant *NRAS*61 group (14–50 %) was similar to that of the wild-type *NRAS*61 group (1–25 %; p = 0.99). One follicular variant papillary thyroid carcinoma (FV-PTC) was found in the mutant *NRAS*61 group, and one follicular thyroid carcinoma (FTC) was found in the wild-type *NRAS*61 group. The mean size of mutant *NRAS*61 group was 2.1 ± 0.7 cm

Variable	Univariate			Multivariate		
	OR	95 % CI	р	OR	95 % CI	р
Age (≥45 years)	1.65	0.545-5.23	0.38	2.91	0.75-11.28	0.12
Sex (male)	1.83	0.475-7.88	0.39	2.95	0.65-14.36	0.18
Nodule size (\geq 4 cm)	-	-	0.99	-	-	0.99
CNB (FN/SFN, suspicious for malignancy, and malignancy)	2.05	0.745-5.83	0.17	2.72	0.835-8.9	0.10
NRAS codon 61 mutational testing (mutant)	3.21	1.115–9.87	0.03	6.63	1.735-25.48	0.006

Table 2 Univariate and multivariate analyses for factors associated with thyroid malignancy in 61 patients who underwent thyroid surgery

FN/SFN follicular neoplasm/suspicious for follicular neoplasm

and that of wild-type *NRAS*61 group was 2.4 ± 1.3 cm. There was no difference in nodule size between two groups of benign category of CNB (p = 0.42).

In the AUS group, no significant difference in the malignancy rate was detected between the *NRAS61* (3–54 %) mutation group and the wild-type *NRAS61* group (5–31 %; p = 0.43). The mutant *NRAS61* group had six FV-PTCs and one FTC. There were three FV-PTCs and one FTC in the wild-type *NRAS61* group.

In the FN/SFN group, the malignancy rate of the mutant *NRAS*61 mutation group (88 %) was significantly higher than that of the wild-type *NRAS*61 group (17–27 %; OR: 16.5, p = 0.009). The mutant *NRAS*61 group had three FV-PTCs and four FTCs (88 %). There were three FTCs and one FV-PTC (17–27 %) in the wild-type *NRAS*61 group.

Diagnostic values of *NRAS61* mutational analysis and CNB analysis in patients who underwent thyroid surgery

The diagnostic values of *NRAS61* mutation analysis and CNB in 61 patients who underwent thyroid surgery are summarized in Table 3. There was no significant difference in sensitivity or specificity between *NRAS61* mutation analysis and CNB analysis. *NRAS61* mutation analysis and CNB together had better sensitivity (82.8 %) than *NRAS61* mutation analysis alone (51.7 %, p = 0.02) or CNB analysis alone (55.2 %, p = 0.01).

We determined the diagnostic value of *NRAS*61 mutation analysis alone for thyroid nodules belonging to the AUS group of CNB in patients who underwent thyroid surgery. Eleven of twenty-six thyroid nodules (42 %) in this category were confirmed as having thyroid malignancy. The sensitivity and specificity of *NRAS*61 mutation analysis for the diagnosis of thyroid malignancy were 63.6 and 60 %, respectively (Table 3). Seven of thirteen thyroid nodules were diagnosed as malignant in the mutant *NRAS*61 group (PPV = 53.8 %), and 9 of 13 thyroid nodules were diagnosed as benign in the wild-type group (NPV = 69.2 %).

Discussion

This study demonstrated that *NRAS*61 mutation analysis combined with CNB histological analysis has the potential to diagnose thyroid malignancy in AUS thyroid nodules previously identified by FNA. The *NRAS*61 mutation was found in 15 % of nodules with AUS cytology. The *NRAS*61 mutation was only found in thyroid nodules belonging to benign, AUS, and FN/SFN categories of CNB. Nodules with the *NRAS*61 mutation had a significantly higher malignancy rate than nodules without the *NRAS*61 mutation. This association between malignancy and the *NRAS*61 mutation was significant after adjusting for age, sex, nodule size, and CNB histological analysis.

The AUS category defined according the Bethesda system is a heterogeneous group, which has a wide range of cytological features, including benign, FN, and suspicious for malignancy [1, 24]. The proportion of the AUS category among thyroid nodules is 2-18 %, and the malignancy rate in the AUS category is 5-15 % [1, 5, 24]. However, several studies reported malignancy rates of 6-48 %, which are higher than those in the original Bethesda system [2–4]. The AUS category has the highest degree of variability for malignancy rate among the six Bethesda categories, which is one reason why there is considerable variability in the malignancy rate. Several factors influence the decision to perform thyroid surgery or extent of surgery to the AUS category of thyroid nodules. Patients who have a nodule with a size over 4 cm, a family history of thyroid cancer, a past history of radiation exposure, or suspicious US features for thyroid malignancy were reported to have a high risk of malignancy in AUS nodules [25-31].

With the technical improvement of CNB provided by US guidance, CNB was recently revived for the diagnosis of thyroid cancer [32, 33]. CNB was reported to have a higher adequacy rate and better diagnostic value than a repeat FNA in nodules with AUS cytology [11, 12]. The amount of tissue obtained by CNB is larger than that obtained by FNA. Also, CNB is less dependent on operator

Diagnostic values	<i>NRAS</i> 61 mutation analysis alone $(n = 61)$	CNB only $(n = 61)$	<i>NRAS</i> 61 mutation analysis and CNB $(n = 61)$	<i>NRAS</i> 61 mutation analysis alone in AUS category of CNB $(n = 26)$
Sensitivity (%)	51.7	55.2	82.8	63.6
Specificity (%)	75.0	62.5	40.6	60.0
Negative predictive value (%)	63.1	60.6	72.2	69.2
Positive predictive value (%)	65.2	57.1	55.8	53.8
Accuracy (%)	63.9	59.0	60.7	61.5

 Table 3 Diagnostic value of NRAS codon 61 mutation analysis and core needle biopsy for thyroid malignancy in 61 patients who underwent surgery

CNB core needle biopsy, NRAS61, NRAS codon 61, AUS atypia of undetermined significance

The histologies of CNB samples were classified into six categories broadly based on the 'Bethesda System for Reporting Thyroid Cytopathology': nondiagnostic, benign, atypia of undetermined significance (AUS), follicular neoplasm (FN)/suspicious for follicular neoplasm (SFN), suspicious for malignancy, and malignancy. A diagnostic criterion of CNB was defined as FN/SFN, suspicious for malignancy, or malignancy categories of CNB. The AUS category of CNB included nodules with some atypical cells for which there was insufficient evidence for the diagnosis of FN, suspicious for malignancy, or malignancy

skill than FNA for successful penetration of the nodule [12, 34]. In this regard, CNB could be more useful as a secondary diagnostic tool than repeat FNA for thyroid nodules with AUS cytology determined in a previous cytology analysis. However, the utility of CNB analysis alone is limited because a considerable number of cases (42 %) could be classified into the AUS category according to this study. Therefore, other diagnostic tools are needed to improve the diagnostic performance of CNB for thyroid nodules in this category.

The malignancy risk of thyroid nodules having both AUS cytology and a RAS mutation were reported to be 84 % [16]. The NRAS point mutation was the most commonly detected genetic alteration in FV-PTC and FTC using targeted next generation sequencing (Thyroseq), which was designed to target 12 cancer-related genes with 284 mutational hot spots [35]. The RAS mutation is involved in early carcinogenesis of thyroid cancer and cancer progression [14]. It is found not only in thyroid cancers such as FV-PTC or FTC but also in benign thyroid tumors [36, 37]. However, RAS mutations are more frequent in FTC than in FA or NH [38, 39]. Several studies also reported that RAS mutation, especially the NRAS codon 61 mutation, is associated with poor prognosis and distant metastasis of FTC [38-40]. Therefore, we considered that NRAS61 mutation analysis could be a useful diagnostic option for the diagnosis of FV-PTC or FTC in this setting. A previous study reported that benign thyroid nodules bearing RET/PTC rearrangements grew more rapidly than those nodules without *RET/PTC* [41]. Like benign nodules harboring RET/PTC, benign nodules harboring NRAS61 mutation could grow faster than those with wild-type NRAS61. However, there was no difference in nodule size between mutant NRAS61 group and wild-type NRAS61 group of benign category of CNB. Unfortunately, we could not evaluate the changes in size of thyroid nodules according to the *NRAS*61 mutational status during long-term periods, so we could not compare the rapidity of growth in benign nodules according to the *NRAS*61 mutation status.

This study is limited by its retrospective design. The low prevalence of suspicious for malignancy or malignancy categories in the CNB results might be related to selection bias. The results of this study could not demonstrate a role for CNB in the diagnosis of nodules with AUS cytology, because we included thyroid nodules that underwent both NRAS61 mutation analysis and CNB. Only a limited number of patients underwent thyroid surgery because physicians tend to prefer watchful observation of thyroid nodules, most of which are likely to be benign. This might be the reason for the low diagnostic rate for benign thyroid nodules and limited sensitivity or negative predictive values of NRAS61 mutation analysis. Therefore, we described the % of malignancy corresponding to total patients and patients who underwent surgery. In the AUS group, there was no significant difference in the malignancy rate between mutant NRAS61 group and the wild-type NRAS61 group. Only 26 of 99 patients (26 %) underwent surgery in AUS group. Most of patients in AUS category were not included in the analysis because they did not undergo surgery. This might cause no difference in the malignancy rate between mutant NRAS61 group and the wild-type NRAS61 group of AUS category. Four thyroid nodules with wild-type NRAS61 were diagnosed as malignant in the AUS group by histological analysis of CNB. Molecular analyses of more genes, including BRAF, RAS, RET-PTC, and PAX8-PPARy, might provide a better diagnostic performance for detecting thyroid malignancy than NRAS61 mutation analysis alone. Combination of NRAS61 mutational analysis and CNB showed a lower specificity than CNB alone. We regarded combination of two tests as any positive result of two tests, so combination of two tests had a lower specificity than each single test.

In summary, CNB was useful for diagnosing and arriving at a clinical decision concerning thyroid nodules previously classified as having AUS cytology. The *NRAS*61 mutation was significantly associated with a high malignant rate in thyroid nodules. Additional *NRAS*61 mutation analysis along with CNB helped arrive at a clinical decision in 12 % of patients with a previous cytological diagnosis of AUS in thyroid nodules, and it improved diagnostic sensitivity. These findings indicate that performing *NRAS*61 mutation analysis in addition to histological analysis of CNB could be useful for the diagnosis of thyroid nodules with AUS cytology.

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Compliance with ethical standards

Conflict of interest The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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