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Thyroid Nodules & Goiter Thursday Poster Clinical

EXPERIENCE WITH THE GENOMIC SEQUENCING CLASSIFIER IN >100 CYTOLOGICALLY INDETERMINATE THYROID NODULES

Endo M., Nabhan F., Roll K., Sipos J.Ohio State University, Columbus, OH

The Afirma Genomic Sequencing Classifier (GSC) was designed to improve specificity for identification of benign thyroid nodules among cytologically indeterminate thyroid nodules (ITN) as compared to its predecessor the Gene Expression Classifier (GEC). Here we report the performance of GSC at our institution. The retrospective study of ITN at The Ohio State University submitted for GSC or GEC from 2/2011 to 6/2018. The treating physician determined patient management. Statistical analysis was performed with Fisher's extract test. Two-sided P values of less than 0.05 were considered statistically significant.114 samples from cytologically ITN were collected for GSC: 87(76.3%) with Bethesda III and 27(23.7%) with Bethesda IV. 113 (99%) samples were adequate for GSC testing. GSC was benign in 83 nodules (73.5%), suspicious in 30 (26.5%). Twenty-two of 30 GSC suspicious cases underwent surgery: 4 classic papillary thyroid carcinoma (PTC), 2 PTC oncocytic variant, 3 follicular variant PTC, 2 follicular thyroid carcinoma, 1 noninvasive follicular thyroid neoplasm with papillary-like nuclear features and 10 benign nodules. One of 83 GSC benign cases underwent surgery with benign results. The positive predictive value (PPV) of GSC was 54.6% for operated GSC suspicious patients with sensitivity 100% and specificity of 89.2%. Overall, 44.7% of GEC tested nodules underwent surgery. Among 403 ITN nodules adequate for GEC testing between 2/2011 and 7/2017, the benign call rate, PPV, NPV, sensitivity, and specificity among GEC tested nodules were 48.4%, 33%, 95%, 98%, and 15%, respectively. Long-term follow up is needed to confirm the benign nature of all molecularly benign unoperated nodules. Our GSC experience shows statistically significant increases in benign call rate compared to GEC.