

## Whole Exome Sequencing Identifies Somatic *ATRX* Mutations in Pheochromocytomas and Paragangliomas

Lauren Fishbein MD, PhD, MTR<sup>1</sup>; Sanika Khare MB<sup>2</sup>; Bradley Wubbenhorst MS<sup>2</sup>; Daniel DeSloover BS<sup>2,5</sup>; Kurt D'Andrea BS<sup>2</sup>; Shana Merrill MS<sup>2</sup>; Nam Woo Cho BS<sup>6</sup>; Roger A. Greenberg MD, PhD<sup>6,8</sup>; Tobias Else MD<sup>9</sup>; Kathleen Montone MD<sup>4</sup>; Virginia LiVolsi MD<sup>4,8</sup>; Douglas Fraker MD<sup>7,8</sup>; Robert Daber PhD<sup>4,5</sup>; Debbie L. Cohen MD<sup>3</sup>; Katherine L. Nathanson MD<sup>2,8</sup>

<sup>1</sup>Department of Medicine, Division of Endocrinology, Diabetes and Metabolism;

<sup>2</sup>Department of Medicine, Division of Translational Medicine and Human Genetics

<sup>3</sup>Department of Medicine, Division of Renal and Hypertension

<sup>4</sup>Department of Medicine, Division of Pathology and Laboratory Medicine

<sup>5</sup>Department of Medicine, Division of Center for Personalized Diagnostics

<sup>6</sup>Department of Medicine, Division of Cancer Biology

<sup>7</sup>Department of Medicine, Division of Surgery, Division of Oncologic Surgery

<sup>8</sup>Abramson Cancer Center, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, PA 19104

<sup>9</sup>Department of Medicine, Metabolism, Endocrinology and Diabetes, University of Michigan Health System, Ann Arbor, MI 48109

**Background:** Pheochromocytomas and paragangliomas are tumors of the autonomic nervous system. Approximately one-fourth of tumors are malignant, defined by the presence of distant metastases. There are eleven known susceptibility genes for which the presence of a germline mutation will increase the risk of developing a pheochromocytoma or paraganglioma (PCC/PGL). However, very little is known about the somatic genetic mutations leading to tumorigenesis or malignant transformation.

**Methods:** In order to identify somatic genetic changes which may be drivers in PCC/PGL tumorigenesis and malignant transformation, we performed whole exome sequencing in 21 matched tumor and germline DNA samples from patients with either sporadic or inherited PCC/PGL, enriching for those with germline mutations in *VHL* or *SDHB* to represent tumors of low and high malignant potential, respectively.

**Results:** We identified somatic variants in *ATRX* in two of seven *SDHB* associated tumors in the discovery set. In a separate validation set of 103 samples, we found somatic *ATRX* variants of undetermined significance or deleterious or likely deleterious variants in 13.6% of tumors. PCC/PGLs with somatic *ATRX* variants were associated with alternative lengthening of telomeres and clinically aggressive behavior.

**Conclusions:** *ATRX* functions in chromatin remodeling and is somatically mutated in several cancer types including pancreatic neuroendocrine tumors. Our findings indicate that *ATRX* is the most frequently somatically altered genes in PCC/PGL, other than genes involved in the inherited syndromes. Although our sample set of PCC/PGL with *ATRX* variants is small, many had clinically aggressive features, inherited *SDHx* mutations and alternative lengthening of telomeres. Our findings suggest that mutations in genes involved in epigenetic regulation may be important for tumorigenesis in pheochromocytomas and paragangliomas with clinically aggressive behavior.