Low frequency of somatic mutations in uterine sarcomas: a molecular analysis and review of the literature.

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Source

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Abstract

OBJECTIVE:

The rarity of uterine sarcomas along with their pathological and molecular heterogeneities render their study particularly challenging. We evaluated a panel of somatic mutations principally centering on the tyrosine kinase gene family and their downstream signaling cascades in an attempt to identify potential candidate markers that may assist in diagnostic or therapeutic decisions in these tumors.

METHODS:

We performed mutational analysis of 20 exons from 9 genes (EGFR, CDKN2A, MET, KIT, RAS, BRAF, PI3KCA, HER-2 and PDGFR-alpha) on biopsy material from 25 patients who underwent primary surgery for uterine sarcoma between October 1995 and October 2003. Due to the limited number of studies conducted we have also undertaken a literature review of somatic mutations in uterine sarcomas.

RESULTS:

A total of 3 different somatic mutations were identified: one KRAS (codon G12D) in a carcinosarcoma and two exon 20 PI3KCA mutations (H1047R and H1047Y) both in carcinosarcomas. Mutational status of all mutations was confirmed using germline DNA extracted from peripheral blood. Consistent with the literature data, no other mutations regarding the rest of the genes of the panel were identified. Due to the low number of somatic mutations in our series, we did not perform further clinicopathological correlations.

CONCLUSION:

The absence of somatic mutations in the majority of genes that are considered critical in neoplastic transformation hampers the identification of potential therapeutic targets in patients with uterine sarcoma.