Key Summary of Conference Abstract

Identification of Circulating IGF-1 Polymorphisms by High Resolution LC-MS

Background

- Insulin-like growth factor-1 (IGF-1) is an anabolic hormone and a biomarker for certain growth disorders.[1]
- A high resolution liquid chromatography-mass spectrometry (LC-MS) assay that is highly specific for IGF-1 was developed at Quest Diagnostics.[1]
- Reports in the literature have indicated that similar assays are able to identify single-amino-acid changes in IGF-1.[2]
- **Objective:** The investigators examined whether the IGF-1 LC-MS assay developed at Quest is capable of detecting single-amino-acid changes in IGF-1 in clinical samples.

Methods

- A search of the dbSNP and 1000 Genomes databases was conducted to identify genetic changes (single-nucleotide polymorphisms [SNPs]) that could affect IGF-1 protein size.
- LC-MS spectra from patient samples were retrospectively analyzed for molecules with a single-amino-acid substitution in the IGF-1 protein.

Results

- The database search identified 5 *IGF1* SNPs that result in an amino-acid change, with minor allele frequencies as follows:
  - A67T: 0.4% MAF
  - A70T: 0.04% MAF
  - V17M: 0.02% MAF
  - V44M and P66A: single reported incidences
- Analysis of existing LC-MS spectra indicated that multiple spectra were consistent with IGF-1 molecules containing single-amino-acid substitutions.

Conclusions

- The previously developed high-resolution LC-MS assay for IGF-1 is capable of identifying IGF-1 molecules with single-amino-acid substitutions.
- The identification of particular IGF-1 changes could affect the interpretation of test results for some patients.

Poster Presented at the 98th Annual Meeting and Expo of the Endocrine Society

Authors

Zengru Wu, Heather R Sanders, Nigel J Clarke, Michael P Caulfield, Richard E Reitz, Michael J McPhaul

Affiliation

Quest Diagnostics Nichols Institute, San Juan Capistrano, CA

ENDO 2016 Annual Meeting
Boston, MA
April 1−4, 2016
Date and time: Saturday, April 2, 2016, 1:15−3:15 PM

Webpage

https://endo.confex.com/endo/2016endo/webprogram/Paper26275.html

References

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2. Hines J, Milosevic D, Ketha H, et al. *Clin Chem*. 2015;61:990-991.