Key Summary of Conference Abstract

Borderline *CNBP* CCTG Expansions in Myotonic Dystrophy Type 2 in Over 16,000 Specimens Analyzed in a Clinical Laboratory

Background

- Myotonic dystrophy type 2 (DM2) is an adult-onset disease characterized by myotonia, muscular dystrophy, early-onset cataracts, and cardiac and endocrine dysfunction.[1]
- The disease is caused by a CCTG repeat expansion in the *CNBP* gene.[2] Normal repeat size is ≤176 base pairs (bp), whereas a repeat size of >372 bp is potentially pathogenic.[2]
- "Borderline" expansions (177-372 bp) may be premutations that expand into the pathogenic range and have been reported in a few studies.[3-4] Identifying these expansions in a larger population will provide a more accurate estimate of how often they occur.
- **Objective:** The investigators of this study examined the frequency of borderline CCTG expansions in the *CNBP* gene in samples submitted for DM2 testing.

Methods

- The study included 16,253 specimens that were sent to Quest Diagnostics for DM2 diagnostics testing.
- CCTG expansions in the *CNBP* gene were detected using routine PCR, repeat-primed PCR, and Southern blot.

Results

- Borderline *CNBP* genotypes were found in 0.97% of samples (n=158).
  - 0.86% (n=139) with 1 normal allele and 1 borderline allele
  - 0.02% (n=4) with 2 borderline alleles
  - 0.08% (n=13) with 1 borderline allele and 1 expanded allele
- The borderline alleles ranged in size from 177 to 338 bp.
  - Most alleles (58.23%) were between 180 and 186 bp.
  - Other allele sizes were rare, occurring at individual allele frequencies of <3.80%.

Conclusions

- Approximately 1% of samples received for DM2 testing contained borderline *CNBP* alleles.

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Webpage
http://submissions.mirasmart.com/Verify/AAN2017/submission/temp/radE012D.pdf

References

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