

Genetic testing in HD— the winds of change...

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Ground Rules

- You are all muted (sorry)
- There are SO MANY of you (!), we had to do it this way
- If you have a question, go to the “chat” function on the side of your screen, and write it down; we hope to have 10 minutes at the end for questions



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Introduction

- Describe complexities of the repeat sequence that are emerging as clinically important (Matt)
- Discuss research studies that at-risk patients might ask about (Martha)
- Discuss the implications of all of this on the work that genetic counselors do
- Ask whether this is a useful activity



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My background (Matt)

- The molecular diagnostics laboratory at the University of Minnesota began testing for Huntington disease in 1994
- I have been involved with predictive genetic testing for HD in our adult neurology clinic since 2001.



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Huntington disease as a 'simple' genetic disease

- I begin teaching our laboratory rotation using Huntington disease as an example of a deceptively simple test.
 - We are evaluating a single genetic 'variant' to make the diagnosis
 - Clear interpretive guidelines



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Interpretive guidelines

- Normal [9-26 CAG repeats]
 - **Expansion of 26 repeat allele [PMID:23946314]**
- Intermediate [27-35 CAG repeats]
 - **Symptoms in intermediate range [PMID:27402890]**
- Reduced penetrance [36-39 CAG repeats]
 - **Why do some individuals remain asymptomatic?**
- Full penetrance [40+ repeats]
 - **Patients with late/early onset relative to repeat number**
- The reported repeat number does not fully explain age of onset or meiotic instability.



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Changing guidelines

- Is there sufficient evidence to warrant revision?
- What are the downstream consequences?
 - Duty to recontact



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Current theories

- Tissue specific somatic expansion of repeat may be a critical factor in disease onset and/or progression.
- Somatic expansion of the repeat may be mediated by both *cis* and *trans* acting factors
- Hot topic at recent European Huntington Disease Network



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Cis acting factors

- Somatic and/or meiotic instability of the repeat may be mediated by:
 - Interruptions (or loss of interruptions) in CAG repeat
 - Extension of the pure CAG repeat due to single nucleotide variants
 - Variation in size of adjacent (CCG) repeats.
- I will focus on these for today's talk



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Trans acting factors

- Evidence suggests that in intact mismatch repair system (MSH2/MSH3) is required for somatic expansion.
 - Knocking these genes out in mice appears to preclude expansion.
- Variants in DNA repair genes identified as modifiers
 - FAN1
- This will not be the focus of today's talk



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How does the HD test actually work?

Clinical view



Counting CAG repeats

Laboratory view



Amplifying a DNA fragment and *inferring* repeat number based on several assumptions

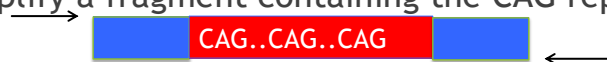


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The HD molecular test

1. Amplify a fragment containing the CAG repeat



2. Subtract the non-CAG repeat portions of the fragment



3. Divide the remaining fragment size by 3



4. Technical adjustments based on laboratory validations



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What assumptions are we making?

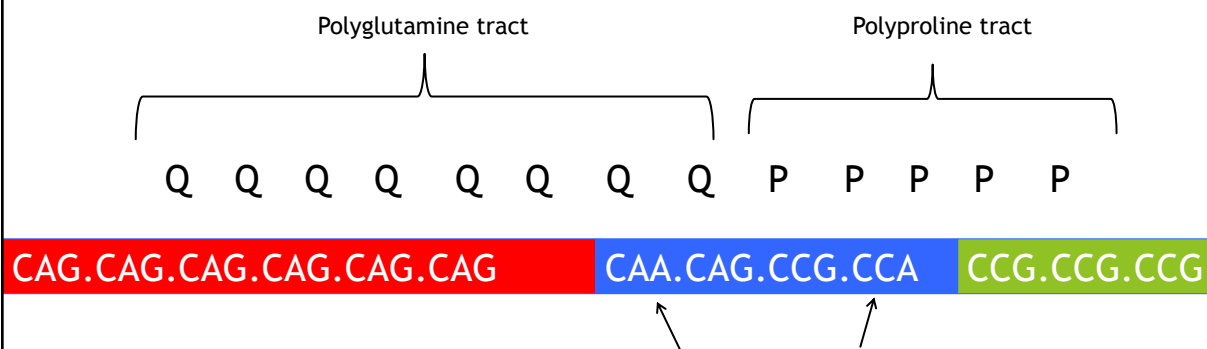
- ▶ There are no variations interfering with our primers
- ▶ The size of adjacent non-CAG repeats is irrelevant
- ▶ There are no SNPs present that would extend the CAG repeat sequence into the regions we are subtracting
- ▶ The content of the remaining fragment is purely CAG repeats



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Taking a closer look



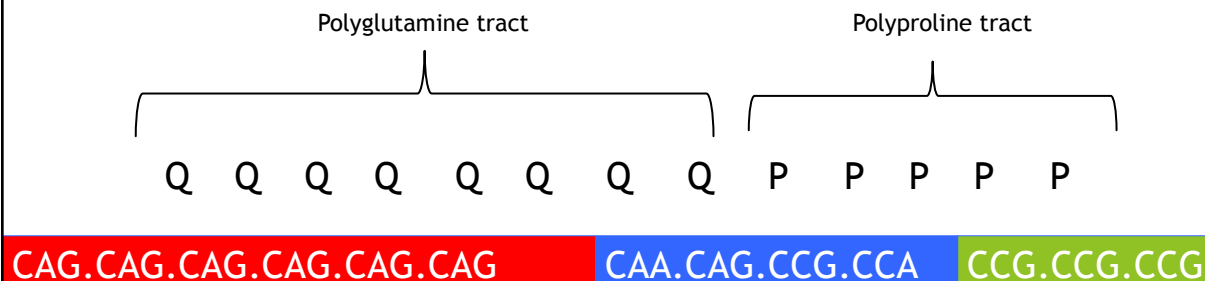
- ▶ There is a 12 base (4 codon) sequence between the “pure” CAG repeat and “pure” CCG repeat. This sequence contains two “interruptions” that also encode glutamine or proline, respectively



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Taking a closer look



- ▶ The HD diagnostic test determines the size of the 'pure' CAG repeat sequence



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Taking a closer look

CAG.CAG.CAG.CAG.CAG.CAG CAA.CAG.CCG.CCA CCG.CCG.CCG

We are not actually sequencing this region. We are *assuming* it is composed of CAG repeats

CAG.CAG.CAG.CAG.CAG.CAG

CAG.CAG.CAA.CAG.CAG.CAG

- ▶ These two alleles appear identical on molecular testing



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Taking a closer look

CAG.CAG.CAG.CAG.CAG.CAG CAA.CAG.CCG.CCA CCG.CCG.CCG

CAG.CAG.CAG.CAG.CAG.CAG CAG.CAG.CCG.CCA CCG.CCG.CCG

A single base variation in this codon can extend the CAG repeat by two- but this is always subtracted from the fragment size.

CAG.CAG.CAG.CAG.CAG.CAG CAG.CAG. CCG.CCG.CCG

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American Journal of Medical Genetics 87:91-92 (1999)

Letter to the Editor

Expansion of a 27 CAG Repeat Allele Into a Symptomatic Huntington Disease-Producing Allele

CAG.CAG.CAG.CAG.CAG.CAG CAG.CAG. CCG.CCA

CAG
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The original family with an unstable 27-repeat allele had a SNP that extended the 'pure' CAG repeat.



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Taking a closer look

CAG.CAG.CAG.CAG.CAG.CAG

CAA.CAG.CCG.CCA

CCG.CCG.CCG

The initial HD diagnostic test assumed this CCG repeat sequence was the same size in everyone.

Original (HD12) primers

CAG.CAG.CAG.CAG.CAG.CAG

CAA.CAG.CCG.CCA

CCG.CCG.CCG



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The CCG repeat actually varies from 7-12 repeats.

CAG.CAG.CAG

CAA.CAG.CCG.CCA

CCG.CCG.CCG

CAG.CAG.CAG

CAA.CAG.CCG.CCA

CCG.CCG.CCG.CCG.CCG

If we subtract a fixed number of CCG repeats (7), we may overestimate the CAG repeat number in cases where there are more CCG repeats present.



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HD 1/3 primers

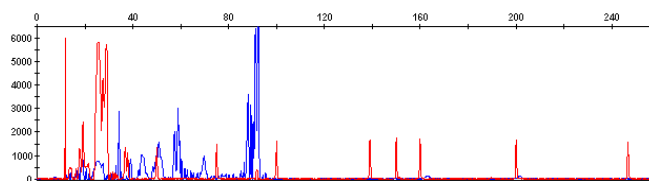
Current diagnostic primers now exclude the polymorphic CCG repeat sequence



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We still utilize HD 1/2 primers to resolve homozygosity



HD 1/3 primers yield a single fragment size

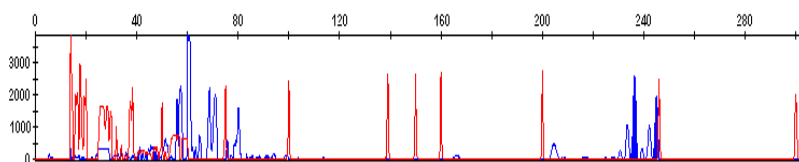
- Most likely due to homozygosity for a common CAG repeat size (e.g. 17)
- Can't exclude the presence of an extremely large expansion (>90) that failed to amplify
- If two different sized CCG repeats present, we can use the old 1/2 primers to demonstrate two distinct normal-sized alleles.



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We still utilize HD ½ primers to resolve homozygosity



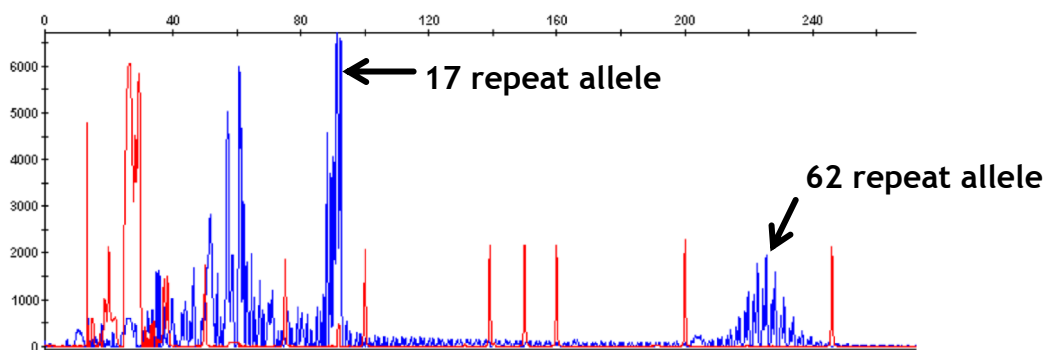
Utilizing ½ primers in cases of apparent homozygosity will often allow us to visualize two distinct normal-sized alleles.



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Can we detect evidence of somatic repeat size mosaicism with the standard diagnostic test?



- Standard PCR does not generate a single clean 'peak' for larger alleles
- Identifying somatic mosaicism on this noisy background is difficult.



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Summary

- ▶ The 'CAG repeat' in *HTT* is actually a complex repeat structure.
- ▶ Variations in the structure of these repeats may be important in mediating somatic stability/instability.
- ▶ Somatic instability may be a determinant in disease onset and progression.



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Why not sequence?

- ▶ Sequencing is costly relative to fragment analysis.
- ▶ Analyzing polymorphic repetitive sequence is extremely messy.
- ▶ Setting phase of CAG repeat size with interruptions may not be possible in a single sample.
- ▶ Any signal of somatic mosaicism in blood may be overshadowed by the noise of the PCR reaction itself.



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Should diagnostic testing include more information about the repeat

- ▶ Is there sufficient evidence that this information is clinically useful in *an individual patient*.
- ▶ Can these variations in repeat structure be reliably detected in an individual sample?
- ▶ Can these variations in repeat structure be detected in a cost-effective way to patients?



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HD Clinical Research

- ▶ Enroll-HD
- ▶ Precision HD1 and Precision HD2 (Wave Life Sciences)
- ▶ Generation HD1 (Roche)



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Enroll-HD

- ▶ Global observational study of HD, began 2012
 - ▶ Goal 20,000 subjects, currently at 19,000
 - ▶ 170 sites, 19 countries involved
- ▶ Includes gene positive, gene negative, not tested, affected, (not at risk)
- ▶ Researchers can (freely) access data and samples
- ▶ Companies look to high-enrolling Enroll sites for their drug trials
- ▶ Enroll-hd.org

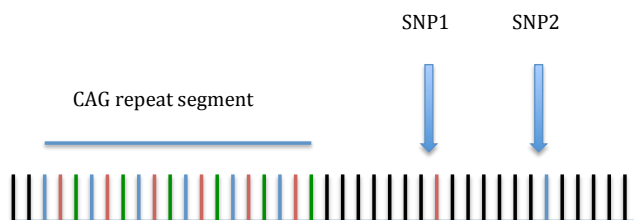


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Wave LifeSciences

- ▶ Precision HD1 and Precision HD2
- ▶ Phase 1b-2a trials of SNP-based ASO, delivered by monthly spinal infusion



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Why target the SNP?

- ▶ To selectively reduce production of mHTT
- ▶ About 70% of Caucasians with HD have SNP1, SNP2, or both on the chromosome with the expanded allele
- ▶ Establishing the presence and phase of the SNPs has been challenging
- ▶ The company is looking for less common, but relevant, SNPs to target



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Precision HD1 and Precision HD2

- ▶ US sites are planned
- ▶ Currently enrolling in Toronto and Poland

- ▶ Wavelifesciences.com, hdtrialfinder.org, clinicaltrials.gov



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IONIS-HTTRx study

- ▶ Completed 4th quarter 2017
- ▶ 46 subjects, Canada, Germany, England
- ▶ First in-human trial of ASO for HD; delivered by monthly spinal infusion for 3 months
- ▶ Goal was to reduce production of huntingtin (wild type and mutant), reflected in reduced CSF Htt levels



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Results of IONIS-HTTRx

- ▶ CSF Htt levels reduced by 40%, more lowering with bigger doses of the drug
- ▶ NO safety issues arose
- ▶ Study subjects are continuing to receive the drug on an open-label basis
- ▶ Roche (who bought Ionis) is skipping to the Phase 3 trial described above
- ▶ (Hints that some subjects had a little improvement in some clinical measures)



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Generation HD₁

- ▶ Phase 3 trial of RG6042, a nonselective ASO, to reduce huntingtin production
- ▶ 660 subjects WITH MANIFEST HD (early stages), about 90 sites, multiple countries
- ▶ The concept of the CAP score (CAG-Age Product)
 - ▶ Age x (CAG-33.66)=CAP score
- ▶ Monthly spinal infusions for 2 years
- ▶ Planned start 1st quarter 2019
- ▶ Roche is also organizing a “natural history study”, of about 100 additional subjects



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What does this have to do with genetic counseling/testing for HD?

- ▶ What can the patient do if he/she tests positive, or negative, or decides not to be tested?
 - ▶ Enroll in Enroll-HD
 - ▶ Be active in the HD community (HDSA, HDYO, etc)



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What does this have to do with genetic counseling/testing for HD?

- ▶ Can the patient get SNP testing to see if he/she is a candidate for the Wave trial?
 - ▶ NO
 - ▶ SNP testing is not clinically available
 - ▶ Wave is performing SNP testing AFTER patients have signed initial consent to be in their trial
 - ▶ The WAVE trials are targeting people who have “manifest” (diagnosable motor symptoms of) HD; gene-positive but unaffected individuals cannot enroll in the study



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What does this have to do with genetic counseling/testing for HD?

- ▶ Should an at-risk patient get a gene test “so that I can enroll in that gene therapy trial”?
 - ▶ NO
 - ▶ All of the currently proposed gene silencing trials are targeting diagnosed/affected individuals with manifest (diagnosable motor symptoms of) HD



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What does this have to do with genetic counseling/testing for HD?

- ▶ What research study can a person be in if they have tested positive but do not have symptoms of HD?
 - ▶ Enroll-HD



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Will there ever be a drug trial for gene positive people who do not have HD symptoms?

- ▶ Maybe, we don't know when. There are no such studies currently in the works.
- ▶ CAP score



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Can a person get RG6042 as part of “right to try”?

- ▶ Roche will not approve any such requests.



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In summary

- ▶ The indications for predictive testing have not changed---yet.
- ▶ We need to educate and support patients who misunderstand the relationship between having a gene test, being in a research study, having a drug available in the clinic, etc
- ▶ Patients (and centers) will be disappointed if they are not selected for these trials



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In summary

- ▶ In the future...
 - ▶ Clinical labs may need to add tests for the CAA interruption or the SNP (which will be expensive)
- ▶ We need to prepare for the time when disease-modifying treatments are available, as the floodgates will open for “predictive testing” at that point



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In summary

- ▶ Matt and Martha are happy to talk to health professionals 1:1 to make sure all this is clear
- ▶ Does this group think that this presentation was helpful?
- ▶ Are there other topics that the HD genetic counseling community would like to discuss in future webinars or in-person meetings?
- ▶ Are there people in the group who would like to be a leader rather than a participant in such activities?



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