



## Abstracts

Articles appearing in the June 2019 issue

### Novel pathogenic *XK* mutations in McLeod syndrome and interaction between *XK* protein and chorein

**Objective** To identify *XK* pathologic mutations in 6 patients with suspected McLeod syndrome (MLS) and a possible interaction between the chorea-acanthocytosis (ChAc)- and MLS-responsible proteins: chorein and *XK* protein.

**Methods** Erythrocyte membrane proteins from patients with suspected MLS and patients with ChAc, ChAc mutant carriers, and normal controls were analyzed by *XK* and chorein immunoblotting. We performed mutation analysis and *XK* immunoblotting to molecularly diagnose the patients with suspected MLS. Lysates of cultured cells were coimmunoprecipitated with anti-*XK* and anti-chorein antibodies.

**Results** All suspected MLS cases were molecularly diagnosed with MLS, and novel mutations were identified. The average onset age was  $46.8 \pm 8$  years, which was older than that of the patients with ChAc. The immunoblot analysis revealed remarkably reduced chorein immunoreactivity in all patients with MLS. The immunoprecipitation analysis indicated a direct or indirect chorein-*XK* interaction.

**Conclusions** In this study, *XK* pathogenic mutations were identified in all 6 MLS cases, including novel mutations. Chorein immunoreactions were significantly reduced in MLS erythrocyte membranes. In addition, we demonstrated a possible interaction between the chorein and *XK* protein via molecular analysis. The reduction in chorein expression is similar to that between Kell antigens and *XK* protein, although the chorein-*XK* interaction is a possibly noncovalent binding unlike the covalent Kell-*XK* complex. Our results suggest that reduced chorein levels following lack of *XK* protein are possibly associated with molecular pathogenesis in MLS.

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### HTT haplogroups in Finnish patients with Huntington disease

**Objective** To study genetic causes of the low frequency of Huntington disease (HD) in the Finnish population, we determined *HTT* haplogroups in the population and patients with HD and analyzed intergenerational cytosine-adenosine-guanosine (CAG) stability.

**Methods** A national cohort of patients with HD was used to identify families with mutant *HTT* (*mHTT*). *HTT* haplogroups were determined in 225 archival samples from patients and from 292 population samples. CAG repeats were phased with *HTT* haplotypes using data from parent-offspring pairs and other *mHTT* carriers in the family.

**Results** The allele frequencies of *HTT* haplotypes in the Finnish population differed from those in 411 non-Finnish European subjects ( $p < 0.00001$ ). The frequency of haplogroup A was lower than that in Europeans and haplogroup C was higher. Haplogroup A alleles were significantly more common in patients than in controls. Among patients with HD, haplotypes A1 and A2 were more frequent than among the controls ( $p = 0.003$ ). The mean size of the CAG repeat change was +1.38 units in paternal transmissions being larger than that (-0.17) in maternal transmissions ( $p = 0.008$ ). CAG repeats on haplogroup A increased by 3.18 CAG units in paternal transmissions, but only by 0.11 units in maternal transmissions ( $p = 0.008$ ), whereas haplogroup C repeat lengths decreased in both paternal and maternal transmissions.

**Conclusions** The low frequency of HD in Finland is partly explained by the low frequency of the HD-associated haplogroup A in the Finnish population. There were remarkable differences in intergenerational CAG repeat dynamics that depended on *HTT* haplotype and parent sex.

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B. Rhead, M. Bäärnhielm, M. Gianfrancesco, et al. 2016;2:e97. doi.org/10.1212/NXG.000000000000097

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Q. Niu, X. Wang, M. Shi, Q. Jin. 2015;1:e20. doi.org/10.1212/NXG.000000000000017

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