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A genome wide scan for Familial Idiopathic basal Ganglia Calcification (Fahrs disease) identifies new candidate regions and confirms genetic heterogeneity. *J.R.M. Oliveira[1], S. Hopfer[1], J. Papp[2], E. Spiteri[1], J. Klepper[3], J. Gilbert[4], Z.K. Wszolek[4], M. Hutton[4], F. Boller[4], M.J. Sobrido[1], D.H. Geschwind[1]*. 1) David Geffen Medical School Neurology Dept, University of California, Los Angeles, CA; 2) Department of Human Genetics, UCLA, Los Angeles, CA; 3) Department of Pediatric Neurology, University of Essen, Essen, Germany; 4) Department of Neurology, Mayo Clinic, Jacksonville, FL.

Fahrs disease, or Idiopathic Basal Ganglia Calcification (IBGC), is a neurological condition characterized by calcifications in the basal ganglia nucleus, cerebellum and occasionally the cerebral subcortical white matter. Clinical manifestations include dystonia, parkinsonism, and neurobehavioral symptoms such as psychosis. The first locus associated with IBGC resides on the long arm of the chromosome 14(IBGC1 - Geschwind et al 1999). Considering a family of Spanish origin ,with probable linkage to the same region, the critical region may be narrowed to 10.9 cM (Sobrido et al 2003).PURPOSE: To assess genetic heterogeneity in IBGC and to define new candidate regions we performed linkage analysis in several families with IBGC. METHODS: A 10cM genome wide scan was performed in 4 families with a total of 47 subjects using a ABI MD 10 marker panel. An additional family with 14 more subjects is still under analysis. Using LINKAGE and SIMWALK2 we performed multipoint and two point analysis. RESULTS: The largest single-point lod score was observer on chromosome 7 with a LOD score of 3.023 at marker D7S519 in the FB2 family (10 affected). The minimal interval defined by haplotype analysis is between the markers D7S484 and D7S506, spanning about 20cM. Three smaller families, with a total of 16 affected, had a maximum multipoint LOD score of 3.487 on chromosome 9, at a position roughly midway between D9S157 and D9S171. Haplotype analysis shows that these families share a common region around 16 cM between the markers D9S171 and D9S1817. These results reinforce preliminary studies demonstrating genetic heterogeneity in Fahrs disease and report two potential new candidate regions, one of them shared by three families.