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Genetic aspects of Huntington's Disease in Latin America.

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Huntington's disease (HD) is a progressive autosomal dominant illness characterized by involuntary choreic movements, psychiatry and cognitive disturbances. HD is caused by an expansion of CAG repeats in *HTT* gene. Western countries with major Caucasian ancestry have higher HD prevalence than those found in Asia. Data on HD in Latin America (LA) is sparse. Objective: To present a systematic review on genetic aspects of HD in Latin America. Methods: PubMed and LILACS were searched up to March 2015, reporting confirmed HD cases in LA. Case series, cross-sectional, case-control, and prospective studies were included. Results: From 534 communications, 47 met the eligibility criteria. Population-based studies were not found; minimal prevalence of 0.5-4 / 100,000 was estimated for Venezuela and Mexico. Geographical isolates were well characterized in Venezuela and in Peru. CAG repeats at *HTT* gene varied between 7-33 and 37-112 in normal and expanded alleles, respectively. Intermediate alleles were found in 4-10% of controls. Ages at onset and the expanded CAG repeats correlated with r from – 0.55 to – 0.91. While haplotype patterns of Venezuelan and Brazilian chromosomes were similar to those observed in Europeans, haplotypes from Peruvian HD patients did not match the same pattern. Conclusions: The limited number of papers addressing HD in LA suggests that HD is poorly diagnosed in the continent. Minimal prevalence seemed to be halfway between those of Caucasians and Asians. Range of CAG repeats was similar to those of Europeans. Haplotype studies indicate that majority of HD patients might be of Caucasian descent; an Asian origin for some Peruvian patients was proposed. Keywords: Huntington, genetic epidemiology, Latin America. Revisão sistemática.