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Short Report

High frequency of *OPA1* mutations causing high ADOA prevalence in south-eastern Sicily, Italy

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Optic atrophy type 1 (*OPA1*) gene mutation causes autosomal dominant optic atrophy (ADOA, MIM #165500). Prevalence of ADOA ranges from 1:50,000 in most populations to 1:12,000 in Denmark. Seventy members of nine families were analysed for the presence of *OPA1* gene mutations by polymerase chain reaction (PCR) and direct sequencing. We identified three *OPA1* gene mutations in 48 patients with variable signs of optic atrophy. Two mutations, c.784-21_784-22insAluYb8 and c.876_878delTGT, were found in two different families. The third mutation, c.869G>A, was found in 28 patients from seven families. The haplotype analysis data suggested that the c.869G>A mutation is a founder mutation. Our main result suggests a higher ADOA prevalence in south-eastern Sicily than previously found in Denmark. This is because of not only the founder effect but also to the presence of three different mutations in the geographical area of the study. Our hypothesis is that a combination of social pressure because of blindness and migration factors is involved. In fact, in Siracusa, a provincial capital in south-eastern Sicily, St. Lucy, the patron saint of the blind was born and died.

Conflict of interest

The authors report no conflicts of interest.

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Key words: ADOA – founder effect – high prevalence – *OPA1* mutations – small geographical area

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Autosomal dominant optic atrophy (ADOA) (MIM #165500) is the most common form of hereditary optic neuropathy. The disease has an insidious onset in the first decade of life, characterized by a loss of visual acuity, development of central, paracentral or coecocentral scotomas, bilateral atrophy of the optic nerve and colour disturbances (1); it shows a high degree of inter- and intra-familial expression, as well as incomplete penetrance (2).

ADOA has an estimated prevalence of 1:50,000 in most populations, but is as high as 1:12,000 in Denmark (3, 4). The prevalence of the disorder in Denmark is reported to be the highest of any geographical location and to be caused by the c.2826delT mutation, which is responsible for ADOA in approximately 42% of the Danish families examined (5). In addition, a recent epidemiological study showed a prevalence of at least 1:35,000 in North England (6).

The first locus for ADOA was mapped to chromosome 3q28-q29. Although *OPA1* is clearly a major ADOA locus, genetic heterogeneity has been suggested and other loci have recently been identified (7–11). More than 200 different *OPA1* mutations have been reported in the OPA1 site (see http://lbbma.univ-angers.fr/eOPA1) (12).