Abstract

Hereditary motor and sensory neuropathies (HMSN) or Charcot–Marie–Tooth (CMT) diseases are the most common degenerative disorders of the peripheral nervous system. However, the frequency of the different subtypes varies within distinct populations. Although more than seventy clinical and genetic forms are known to date, more than 80% of CMT patients in Western countries have genetic abnormalities associated with *PMP22*, *MPZ*, *MFN2* and *GJB1*. Given the considerable genetic heterogeneity of CMT, we emphasize the interest of both clinical and pathological specific features such that focused genetic testing could be performed. In this regard, peripheral nerve lesions in *GDAP1* mutations (AR CMT1A), such as mitochondrial abnormalities, have been newly demonstrated. Otherwise, while demyelinating autosomal recessive CMT used to be classified as CMT4 (A, B, C …), we propose a simplified classification such as AR CMT1 (A, B, C …), and AR CMT2 for axonal forms. Also, we stress that next generation sequencing techniques, now considered to be the most efficient methods of genetic testing in CMT, will be helpful in molecular diagnosis and research of new genes involved. Finally, while no effective therapy is known to date, ongoing new therapeutic trials such as PXT3003 (a low dose combination of the three already approved drugs baclofen, naltrexone, and D-sorbitol) give hopes for potential curative treatment