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Short Communication

Sarcoglycanopathies: A Novel Predictive Approach

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Abstract

Progressive Muscular Dystrophies (PMDs) are a heterogeneous family of neuromuscular diseases. Although they are considered as a rare diseases group, their severity and relatively high prevalence make them a suitable target for that kind of scientific research whose target is to give to the community a better quality of life. With this in mind, it is reasonable to think that a reliable predictive model is needed. Alas, since both PMDs subtypes prevalence and incidence among general population do not show significant statistical variations, it is not possible to base a predictive model on these data. However, the aim of this paper is to elaborate a novel approach in order to crack the code of PMDs unpredictability.

Introduction

Progressive Muscular Dystrophies (PMDs) are a heterogeneous family of neuromuscular diseases. Investigations on these hereditary disorders started a long time ago, in fact the first accurate description of Duchenne Muscular Dystrophy (DMD), was carried out in 1852 [1]. About a century later, some cases of progressive muscular dystrophy were reported, although they were clinically non-discriminable from DMD. However, such an obscure form of PMD was later called "Duchenne-like" autosomal recessive muscular dystrophy [2]. Afterwards, researchers discovered that DMD is ascribable to mutations in the dystrophin protein gene [3,4]. Both structural and functional feature of transmembrane dystrophin proteins brought to the finding of a class of dystrophin-associated proteins, that taken together form a unique transmembrane Dystrophin-Glycoprotein Complex (DGC). Within such a molecular complex, one more sub-framework was discovered, namely a four subunits-one called sarcoglycan [5]. Under a genetic point of view, the positive correlation between mutations within the sarcoglycan complex gene and sarcoglycanopathies development became clear.

Epidemiological aspects

Prevalence data about all types of sarcoglycanopathies have been calculated only for a restricted number of nations. More specifically, in India 53.8% [6], in USA it is about 15% [7], in Mexico 14% [8], in Italy 18.1% [9], United Kingdom 11.7% [10]. In Denmark, Germany and the Czech Republic the muscular dystrophies prevalence is 22.3, 23, and 2.3% [11-13]. The percentages of each of such diseases shows no statistically significant variations for about all populations, except for isolated ones, among which the founder effect is very relevant. The most common form of LGMD (Limb Girdle Muscular Dystrophy), regardless of the geographic area, is usually the 2D type. 2E and 2C forms presence is generally balanced among patients [14]. The rarest type is, in most nations, is 2F, while in India it comes after 2C [6]. 2C is also prevalent, among other forms, in North Africa [15,16].

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Novel insights

Under an epidemiological point of view, it is legit to put sarcoglycanopathies among the group of rare diseases. Nevertheless, they are worldwide acknowledged as serious genetic disorders, as they deeply affect life quality at all levels of severity. Since it has been demonstrated that significant statistical variations between LGMDs only occur among isolated populations (due to the founder effect), it is reasonable to infer that predictive models are not feasible only taking into account general population. The aim of this opinion paper is to propose a backward-wise methodological approach. The idea consists in mapping the ethnical background of LGMD patients among big communities, so that it will be possible to identify the ethnogenetic basis of these diseases. Then, ascending only to antiquely originated isolated communities; it will be relatively easy to calculate their internal LGDMs type prevalence. With this in mind, the next step it will be to ethnogenetically track the origin of patients among general population, in order to identify the LGMD cases that affect individuals ethnically linked to the above cited antiquely originated isolated communities and finally design a reliable predictive model.

References

1. Meryon E (1852) On granular and fatty degeneration of the voluntary muscles. Med Chir Trans 35: 73-84.
2. Kloepfer HW, Talley C (1958) Autosomal recessive inheritance of Duchenne-type muscular dystrophy. Ann Hum Genet 22: 138-143.
3. Koenig M, Hoffman EP, Bertelson CJ et al. (1987) Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary genomic organization of the DMD gene in normal and affected individuals. Cell 50: 509-517.
4. Hoffman EP, Brown RH Jr, Kunkel LM (1987) Dystrophin: the protein product of the Duchenne muscular dystrophy locus. Cell 51: 919-928.
5. Yoshida M, Suzuki A, Yamamoto H et al. (1994) Dissociation of the complex of dystrophin and its associated proteins into several unique groups by n-octyl beta-D-glucoside. Eur J Biochem 222: 1055-1061.
6. Meena AK, Sreenivas D, Sundaram C et al. (2007) Sarcoglycanopathies: a clinico-pathological study. Neurol India 55: 117-121.

7. Moore SA, Shilling CJ, Westra S et al. (2006) Limb-girdle muscular dystrophy in the United States. J Neuropathol Exp Neurol 65: 995-1003.

8. Gomez-Diaz B, Rosas-Vargas H, Roque-Ramirez B et al. (2012) Immunodetection analysis of muscular dystrophies in Mexico. Muscle Nerve 45: 338-345.

9. Guglieri M, Magri F, D'Angelo MG et al. (2008) Clinical, molecular, and protein correlations in a large sample of genetically diagnosed Italian limb girdle muscular dystrophy patients. Hum Mutat 29: 258-266.

10. Norwood FLM, Harling C, Chinnery PF et al. (2009) Prevalence of genetic muscle disease in Northern England: in-depth analysis of a muscle clinic population. Brain 132: 3175-3186.

11. Ginjaar HB, van der Kooi AJ, Ceelie H et al. (2000) Sarcoglycanopathies in Dutch patients with autosomal recessive limb girdle muscular dystrophy. J Neurol 247: 524-529.

12. Stehlikova K, Skalova D, Zidkova J et al. (2014) Autosomal recessive limb-girdle muscular dystrophies in the Czech Republic. BMC Neurol 14: 154.

13. Sveen ML, Schwartz M and Vissing J (2006) High prevalence and phenotype-genotype correlations of limb girdle muscular dystrophy type 2I in Denmark. Ann Neurol 59: 808-815.

14. Moreira ES, Vainzof M, Suzuki OT et al. (2003) Genotype-phenotype correlations in 35 Brazilian families with sarcoglycanopathies including the description of three novel mutations. J Med Genet 40: E12.

15. Noguchi S, McNally EM, Ben Othmane K et al. (1995) Mutations in the dystrophin-associated protein gamma-sarcoglycan in chromosome 13 muscular dystrophy. Science 270: 819-822.

16. McNally EM, Passos-Bueno MR, Bonnemann CG et al. (1996) Mild and severe muscular dystrophy caused by a single gamma-sarcoglycan mutation. Am J Hum Genet 59: 1040-1047.