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Phenotypic heterogeneity of sarcomeric gene mutations:

a matter of gain and loss?

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After several decades of intense research and various attempts of definition and classification, cardiomyopathies still remain disorders of remarkable and intriguing complexity. Once more, this aspect is elicited by the recent discovery that mutations in the cardiac ankyrin repeat protein or CARP, a protein functionally part of the sarcomere, can cause different types of cardiomyopathies, as reported in this issue (1,2), as well as a congenital heart disease (3).

ANKRD1 in normal heart and disease

CARP is a 36 kD protein encoded by the cardiac ankyrin repeat domain 1 gene *ANKRD1*, which maps on chromosome 10. *ANKRD1* is a member of a conserved gene family, coding for muscle ankyrin repeat proteins (MARPs), involved in muscle stress response such as stretch, injury and hypertrophy (4). CARP is a nuclear transcription co-factor, a signaling molecule predominantly expressed in the heart. CARP is found in the sarcomere, where it co-localize with the N2A domain of titin and myopalladin in the I-band of the Z disk (Figure 1), and in the nucleus (4). The expression of CARP is controlled, at list in part, by the titin-based mechano-transduction signaling pathway, and it is increased in heart development and conditions of injury and stress. In heart development, CARP acts as transcriptional repressor of myocyte contractile elements. In heart failure, CARP is overexpressed, suggesting a role in the "fetal gene program" characteristic of the molecular remodeling of the failing heart (5).

Since titin was previously found to be associated to both HCM and DCM (6-8), also CARP, as part of the titin complex, was hypothesized to play a role in cardiomyopathies. In this issue, two reports confirm this hypothesis and show that in fact *ANKRD1* mutations can cause both DCM and HCM $(1,2)$.

In the first article, Arimura et al. (2) report the results of the *ANKRD1* mutation screening in a large HCM population collected in Japan and in USA. In 384 index patients, they found 3

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missense mutations (*ANKRD1* Pro52Ala, Thr123Met and Ile280Val), accounting for ∼1% of HCM cases. Interestingly, they also investigated the N2A CARP-biding domain of titin, and found two additional mutations (*TTN* Arg8500 and Arg8604Gln) in their HCM cohort. In the second report, Moulik et al (1) investigated a series of 208 DCM index patients of Japanese and USA origin, and found 3 missense mutations (*ANKRD1* Pro105Ser, which was recurrent in 2 families, Val107Leu, and Met1841Ile) accounting for in 2% of DCM cases, further supporting a role of the titin mechano-transduction complex in the pathogenesis of cardiomyopathies. But, how to explain two different cardiomyopathies with opposite pathophysiology caused by the same gene?

Phenotypic heterogeneity in cardiomyopathies

Phenotypic heterogeneity (also called "allelic variants" in OMIM (9)) is a well known and common phenomenon in genetics, referring to the occurrence of more than one phenotype caused by allelic mutations at a single locus (10): examples familiar to cardiologists are Duchenne and Becher muscular dystrophies caused by the same dystrophin gene, laminopathies ranging from progeria to lipodystrophy due to lamin A/C gene, LQT syndrome and congenital conduction defect caused by the cardiac sodium channel gene *SCN5A*.

The reason for the clinical variability in allelic disorders lies in the different function of the mutant proteins. In the case of sarcomeric genes, it appears that a "gain" of function usually results in increased energy demand, inefficient ATP utilization and hypertrophy, whereas a "loss" of function in decreased contractility (Table). The two studies published in this issue seem to follow the rule. Arimura et al. (2) show that *ANKRD1* mutations in HCM increase binding of CARP to titin and myopalladin, and that titin mutations at the CARP-binding site have the same effect. On the other hand, Moulik et al. (1) show that *ANKRD1* mutations in DCM cause a loss of CARP binding to talin 1, potentially leading to loss of stretch-sensing, disruption of the link between titin complex and cytoskeletal network, and transcriptional deregulation of genes involved in cell cycle and other pathways.

However, gain and loss are not the only mechanism involved in the phenotypic heterogeneity of *ANKRD1*. Indeed, a recently publication by Cinquetti et al. (3) reports the identification of increased CARP expression or protein stability in 3 cases with total anomalous pulmonary venous return (TAPVR), a rare congenital heart defect characterized by failure of the pulmonary veins to connect to the left atrium during development. In this case, CARP overexpression or its increased activity are believed to repress normal cardiac gene expression leading to abnormal heart development.

Impact of *ANKRD1* **mutations discovery in clinical care**

The discovery of *ANKRD1* mutations in cardiomyopathies has several implications. Firstly, it contributes to fill the gap of the large number of patients in whom the cause of cardiomyopathy is still unknown, approximately 40% of cases in HCM and probably around 70% in DCM (11). Secondly, it expands our knowledge on the mechanisms leading to hypertrophy and heart failure to include abnormal stretch-based signaling in response to force: this appears to be another "common pathway" for HCM and DCM, which could be targeted by novel therapeutic strategies. Finally, it raises the question of clinical genetic testing of *ANKRD1* in HCM and DCM patients. Although the low prevalence of mutations may currently limit the routine screening of *ANKRD1* gene, we may expect that the implementation in resequencing technology will allow a systematic screening of rare cardiomyopathy genes in the patient population in the near future.

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Abbreviations

CARP, Cardiac Ankyrin Repeat Protein; ANKRD1, Cardiac Ankyrin Repeat Domain 1 Gene; DCM, Dilated cardiomyopathy; HCM, Hypertrophic cardiomyopathy.

References

- 1. Moulik M, Vatta M, Witt SH, et al. *ANKRD1*-The gene encoding cardiac ankyrin repeat protein is a novel dilated cardiomyopathy gene. J Am Coll Cardiol. 2009in press
- 2. Arimura T, Bos JM, Sato A, et al. Cardiac Ankyrin Repeat Protein Gene (ANKRD1) Mutations in Hypertrophic Cardiomyopathy. J Amer Coll Cardiol. 2009in press
- 3. Cinquetti R, Badi I, Campione M, et al. Transcriptional deregulation and a missense mutation define ANKRD1 as a candidate gene for total anomalous pulmonary venous return. Hum Mutat 2008;29:468– 74. [PubMed: 18273862]
- 4. Mootha VK, Lepage P, Miller K, et al. Identification of a gene causing human cytochrome c oxidase deficiency by integrative genomics. Proc Natl Acad Sci USA 2003;100:605–610. [PubMed: 12529507]
- 5. Zolk O, Frohme M, Maurer A, et al. Cardiac ankyrin repeat protein, a negative regulator of cardiac gene expression, is augmented in human heart failure. Biochem Biophys Res Commun 2002;293:1377–82. [PubMed: 12054667]
- 6. Itoh-Satoh M, Hayashi T, Nishi H, et al. Titin mutations as the molecular basis of dilated cardiomyopathy. Biochem Biophys Res Commun 2002;291:385–91. [PubMed: 11846417]
- 7. Gerull B, Gramlich M, Atherton J, et al. Mutations of TTN, encoding the giant muscle filament titin, cause familial dilated cardiomyopathy. Nature Genetics 2002;30:201–4. [PubMed: 11788824]
- 8. Matsumoto Y, Hayashi T, Inagaki N, et al. Functional analysis of titin/connectin N2-B mutations found in cardiomyopathy. J Muscle Res Cell Motil 2005;26:367–74. [PubMed: 16465475]
- 9. McKusick, VA. Online Mendelian Inheritance in Man, OMIM (TM). McKusick-Nathans Institute for Genetic Medicine, Johns Hopkins University; National Center for Biotechnology Information, National Library of Medicine; Baltimore, MD: Bethesda, MD: 2000.
- 10. Haines, J.; Pericak-Vance, M. Genetic analysis of complex diseases. Vol. 2nd ed.. Wiley; Hoboken, NJ: 2006.
- 11. Hershberger RE, Lindenfeld J, Mestroni L, Seidman CE, Taylor MR, Towbin JA. Genetic evaluation of cardiomyopathy--a Heart Failure Society of America Practice Guideline. J Card Fail 2009;15:83– 97. [PubMed: 19254666]
- 12. Mizra M, Marston S, Willot R, et al. Dilated cardiomyopathy mutations in three thin filament regulatory proteins result in a common functional phenotype. J Biol Chem 2005;280:28498–506. [PubMed: 15923195]
- 13. Kaski JP, Syrris P, Burch M, et al. Idiopathic restrictive cardiomyopathy in children is caused by mutations in cardiac sarcomere protein genes. Heart 2008;94:1478–84. [PubMed: 18467357]
- 14. Debold EP, Schmitt JP, Patlak JB, et al. Hypertrophic and dilated cardiomyopathy mutations differentially affect the molecular force generation of mouse alpha-cardiac myosin in the laser trap assay. Am J Physiol Heart Circ Physiol 2007;293:H284–H291. [PubMed: 17351073]
- 15. Rajan S, Ahmed RP, Jagatheesan G, et al. Dilated cardiomyopathy mutant tropomyosin mice developcardiac dysfunction with significantly decreased fractional shortening and myofilament calcium sensitivity. Circ Res 2007;101:205–214. [PubMed: 17556658]
- 16. Morimoto S. Sarcomeric proteins and inherited cardiomyopathies. Cardiovasc Res 2008;77:659–666. [PubMed: 18056765]

J Am Coll Cardiol. Author manuscript; available in PMC 2010 July 21.

Mestroni Page 4

Figure. Model for the titin-N2A signaling complex

N2A titin's sequence interacts with MARPs (CARP, ankrd2 or DARP). Myopalladin associates with MARP/N2A complex by interacting with the N-terminal domains of MARPs. Reprinted from Miller et al.(4) with permission from Elsevier.

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Mestroni Page 6