

STUDY OF MOLECULAR PATHOLOGIC MARKERS FOR HYPERTROPHIC CARDIOMYOPATHY

FINAL REPORT

Patient Name: NA	Patient Birth Date: NA
Medical reference: NA	Patient Gender: NA
Consultancy Referral Number: NA	Referring physician: NA,
Specimen Type: NA	Harvesting facility: NA
Requisition Date: NA	Referring facility: NA
Fulfillment Date: NA	Purpose: NA
Referral reason: NA	
Sample Reference: NA	
1 – Results	

This genetic study shows 1 genetic variant in the gene MYBPC3 that can be associated with hypertrophic cardiomyopathy.

1.1 – GENETIC INFORMATION

The results, described according to HGVS nomenclature (http://www.hgvs.org), are presented in the following table.

Gene	Genetic variant references		Nucleotidic change	Aminoacidic change	Observation
	HGMD	Ensembl			
MYBPC3	CM981322	-	c.772G>A	p.Glu258Lys	Mutation in heterozygosity.

Hypertrophic cardiomyopathy is mainly caused by genetic alterations that deregulate the cardiac contraction mechanism comprising the dysfunction of the mechanical, biochemical and cell bioenergetics.

MYBPC3, CM981322: The MYBPC3 gene encodes for the cardiac myosin binding protein C, a sarcomeric motor
protein important for cardiac muscle contraction. This mutation is pathogenic and associated with HCM. It abolishes
the interaction between MYBP-C and myosin-S2 and disturbs muscle contraction kinetics [1]. It is associated with
family history of HCM, early onset phenotype, moderate to severe hypertrophy, sudden cardiac death and cardiac
transplant [2, 3, 4, 5, 6].

This information is supported by peer reviewed scientific papers indexed on PubMed (http://www.ncbi.nlm.nih.gov/pubmed) and also by The Human Gene Mutation Database (HGMD Professional [®] version 2013.4) [7], accessed on 4th November 2014.

Hypertrophic cardiomyopathy has a 50% chance of being transmitted to family relatives; therefore, we recommend a carrier testing for these genetic variants to direct members of the patient.

2 – TECHNICAL INFORMATION

2.1 – METHODOLOGY

- 1. A commercial kit was used to perform DNA extraction and purification from na. DNA concentration and quality were evaluated with MultiskanGo spectrophotometer (Thermo Scientific).
- 2. Genotyping was performed through molecular analysis of 218 genetic variants in 18 genes associated with hypertrophic cardiomyopathy.
- 3. Genotyping was achieved using a high-throughput DNA Microchip platform, the iPlex MassArray system from Agena. This array platform allows an optimal genetic analysis by combining the benefits of accurate primer extension chemistry with MALDI-TOF mass spectrometry. The different masses of each generated PCR product are then converted into genotype information.

2.2 - TEST ACCURACY

The technical accuracy of this test is estimated to be 99%.

HeartGenetics applies a rigorous quality control which may not exclude the possibility of error that might influence the test results. The results presented in this report are limited to the available scientific knowledge at the time this test was developed.

2.3 – HEARTGENETICS PANEL

TCAP (NM_003673), *ACTN2* (NM_001103), *TNNT2* (NM_000364), *MYH7* (NM_000257), *TNNC1* (NM_003280), *ACTC1* (NM_005159), *TNNI3* (NM_000363), *CRYAB* (NM_001885), *TPM1* (NM_000366), *LDB3* (NM_001080116), *FHL1* (NG_015895.1), *MYBPC3* (NM_000256), *BRAF* (NM_004333), *MYL2* (NM_000432), *CSRP3* (NM_003476), *FLNC* (NM_001458), *MYL3* (NM_000258), and *LAMP2* (NM_002294).

Cantanhede, NA

TECHNICAL DIRECTION

Helenavarão

Helena Vazão Molecular Biologist, PhD Associate Laboratory Director

Susana Rodrigues Santos Human Geneticist, Specialist Molecular Biologist, PhD Laboratory Director

It has been assumed as truthful all the above declarations about patient and medical identity, the purpose of the study, index case and nature of analysed biological products. Any total or partial reproduction is prohibited.

3 – REFERENCES

- [1] W. J. De Lange, A. C. Grimes, L. F. Hegge, A. M. Spring, T. M. Brost, and J. C. Ralphe, The Journal of general physiology 142, 241 (2013).
- [2] I. Olivotto, F. Girolami, R. Sciagrà, M. J. Ackerman, B. Sotgia, J. M. Bos, S. Nistri, A. Sgalambro, C. Grifoni, F. Torricelli, et al., Journal of the American College of Cardiology 58, 839 (2011).
- [3] S. Marston, O. Copeland, A. Jacques, K. Livesey, V. Tsang, W. J. McKenna, S. Jalilzadeh, S. Carballo, C. Redwood, and H. Watkins, Circulation research 105, 219 (2009).
- [4] H. Niimura, L. L. Bachinski, S. Sangwatanaroj, H. Watkins, A. E. Chudley, W. McKenna, A. Kristinsson, R. Roberts, M. Sole, B. J. Maron, *et al.*, New England Journal of Medicine **338**, 1248 (1998).
- [5] S. J. Kindel, E. M. Miller, R. Gupta, L. H. Cripe, R. B. Hinton, R. L. Spicer, J. A. Towbin, and S. M. Ware, Journal of cardiac failure 18, 396 (2012).
- [6] S. P. Page, S. Kounas, P. Syrris, M. Christiansen, R. Frank-Hansen, P. S. Andersen, P. M. Elliott, and W. J. McKenna, Circulation: Cardiovascular Genetics 5, 156 (2012).
- [7] P. D. Stenson, E. V. Ball, M. Mort, A. D. Phillips, J. A. Shiel, N. S. Thomas, S. Abeysinghe, M. Krawczak, and D. N. Cooper, Human mutation 21, 577 (2003).

HeartGenetics is certified with ISO NP 9001:2008 for Quality Management System.

Please visit www.heartgenetics.com to find out more about other available genetic tests, namely Hereditary Thrombophilia, Familial Hypercholesterolemia, Molecular Risk Factors for Arterial Hypertension and Cardiovascular Pharmacogenetics. Ask your physician for more information.