

# APPLYING GENOMICS TO BIOMEDICINE

## DIAGNOSIS OF ARRHYTHMOGENIC RIGHT VENTRICULAR DYSPLASIA

Adrià Hernández, Genetics Degree, UAB  
adria.hernandez@e-campus.uab.cat



### INTRODUCTION

The arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C) is an inherited heart disease. It is characterized by death of myocytes in the right ventricle and their replacement by fibro-fatty tissue. Major genetic defects are found in desmosomes whose function is cell adhesion. Sudden cardiac death (SCD) is the main problem of ARVD; around of 20% of SCD are involved by ARVD (table 1). 50% of cases have familial distribution with at least one affected patient. The pattern of inheritance is AD and the prevalence range is 1:2500, but varies between populations.

TABLE 1: CAUSES OF SUDDEN CARDIAC DEATH (%) IN PEOPLE UNDER 35 YEARS OLD. Corrado et al. (1998)

CAUSES	ATHLETES	NO ATHLETES	TOTAL
Arrhythmogenic right ventricular dysplasia	22,4	8,2	10,8
Coronary arteriosclerosis	18,4	16,4	16,7
Anomalous coronary arteries	12,2	0,5	2,6
Conduction system disease	8,2	9,1	8,9
Mitral valve prolapse	10,2	9,5	9,7

### OBJECTIVES

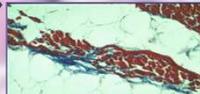
The main objective is to discuss the possibility of applying genomics to biomedicine as a genetic test for a long-term disease, for example in ARVD; extrapolating this use in many diseases such as cancer and cardiomyopathies. In particular, presentation of all features of ARVD: clinical characteristics, genetic causes, genetic testing and genetic counseling. Also, introducing a real case to explain improvement of applying genomic testing.

#### DES MOSOMES: CELL ADHESION



HAVE GENETIC ALTERATIONS

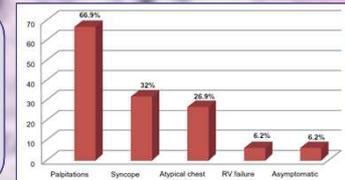
#### DEATH OF MYOCYTES



FIBRO-FATTY INFILTRATION

#### SYMPTOMS: (figure 1)

Palpitations and syncopes  
Advanced phase: RV failure and LV involvement  
Sudden Cardiac Death (SCD)



### REAL CASE

To introduce genetic testing in ARVD, here it is presented a familiar with two affected females (figure 2). They were diagnosed when they were 30-35 years old. Any genetic test hasn't been done and any mutation hasn't been found. Also, sons and daughters are too young to present any clinical symptoms. The possible genetic diagnostic is explained in this work.

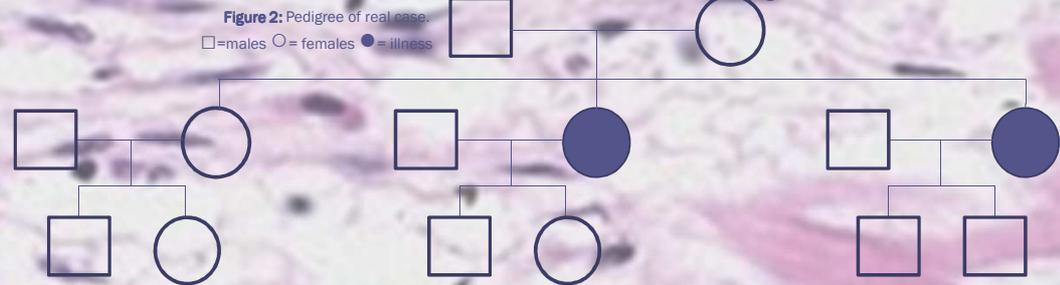


Figure 1: Symptoms of ARVD and its frequencies.

### GENETIC CAUSES

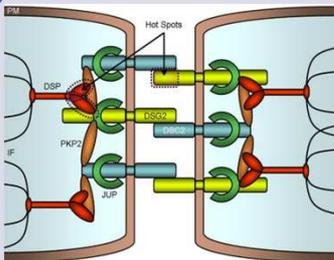


Figure 3: Molecular model of desmosomes. Genes are PKP2, DSC2, DSG2, DSP and JUP.

GENE	LOCUS	PROTEIN
CTNNA3	10q21.3	αT-catenin
DES	2q35	Desmin
DSC2	18q21	Desmocollin-2
DSG2	18q12.1	Desmoglein-2
DSP	6p24	Desmoplakin
JUP	17q21	Junction plakoglobin
LMNA	1q22	Lamin A/C
PKP2	12p11	Plakophilin-2
PLN	6q22.1	Phospholamban
TGFβ3	14q24.3	Transforming growth factor β 3
TMEM43	3p25.1	Transmembrane protein 43
TTN	2q31.2	Titin

**PKP2:** is the most prevalent gene affected in ARVD. There are more than 150 pathogenic mutations identified only in PKP2 that represent 35-40% of total ARVD cases. A lot of types of mutations have been detected (CNV, splicing, missense, nonsense and frameshift).

**DSC2, DSG2, DSP** and **JUP** are genes that encodes desmosomes, too (table 2 and figure 3). More than 200 mutations have been found in this four genes. Majority of variations are punctual changes as missense mutations. All types of mutations may be detect.

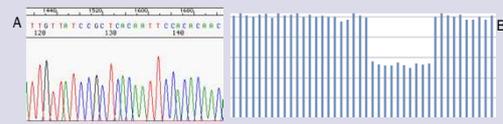
Non-desmosomal genes: recent genes have been discovered, these could relate with cases of misdiagnosis and are important in genetic test; their prevalence is low (10%). These genes are: **DES, TGFβ3, TMEM43, LMNA, TTN** and **PLN** (table 2). They encode, mainly, intermediate filaments or regulatory elements.

In ARVD/C Genetic Variants Database, it is possible to find all variants in this 12 genes with all important information. For that is a good tool for genetic diagnostic.

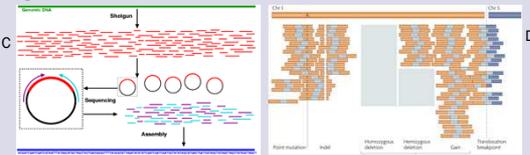
### GENETIC TESTING

The major diagnosed people has a mutation in PKP2 (40%), around 40% people is not diagnosed and other 20% is affected different other genes.

There are techniques used to find variations only in one sequence of the genome: Sanger sequencing (A) and MLPA (B). Usually, are the first steps to look for a mutation in PKP2.



More genetic causes in different chromosomes, it would be more efficient to use a whole-genome technique (C). Next Generation Sequencing (NGS) is the most useful test to find variations (D).



Identifying variations in ARVD/C Genetic Variants Database (E) to know all information of this variant.

Gene	Mutation	DNA change	Protein change	Exon	Locus	Type	Reported Classification	Grantham Score	SIFT	PolyPhen	Domain	Notes	LOVD ID
PKP2	Del exon 1-4	c.1-7_542+7del		1	12p11	Deletion	Pathogenic						

Clinical reports of this mutation in patients and controls

Article: Cox et al. Circulation 2011;123:2690-2700. article details | 0/400 | TFC+ | 1

### ETHICAL QUESTIONS

Key information and suggestions that cardiologists should know:

- Genetic testing in patients and relatives (at least two diagnosed in a family)
- Interpretation of the results: mode of inheritance and risk recurrence, molecular genetics, penetrance and natural history and variable expressivity.
- Organization of genetic counselling, principles of bioethics.
- Possible prenatal or preimplantation diagnostic if variations have been found.

### CONCLUSIONS

- ARVD is a polygenic disease and can evolve to a SCD (20%) or other malignant symptoms.
- Applying genomics to biomedicine may help as a good tool in some complicated diseases as cardiomyopathies or cancer.
- Whole-genome testing will be important in research and diagnostic to these diseases.
- Genetic causes and diagnostic of ARVD have been explained to solve real cases of affected families and the manner to help to improve their life.

### REFERENCES

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