Abstract: **P6579**

Genetic profile and predictors of positive genetic test in brugada syndrome

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Introduction: Brugada syndrome (BS) is a channelopathy with autosomal dominant transmission, incomplete penetrance and variable expression. There are 18 different gene mutations described in association with this syndrome, however 70% of patients remain without identifiable genetic cause. Genetic testing is appropriated for patients with clinical diagnosis but it is also a very important tool in familiar screening.

Aim: We aim to characterize genetic profile of patients with clinical diagnosis of BS and identify differences between patients with and without causative mutation.

Methods: We included patients followed by the arrhythmology department of our hospital with diagnosis of BS and that have performed genetic test (or patients who were identified through familiar screening and with negative genetic test in the index case). Patients identified through familiar screening with positive genetic test but no spontaneous electrocardiographic pattern, still awaiting pharmacologic provocative test at the time of enrolment – no clinical diagnosis - were excluded. Genetic test was considered positive when we found a pathogenic or probably pathogenic mutation. Mutations in PKP, SLMAP, CACNA, CACNB, SCN10A and CLASP genes considered of uncertain clinical relevance were not included as positive genetic test. We analysed differences between subset of patients with and without causative mutation regarding clinical and electrocardiographic variables. We performed multivariate analysis to find predictors of positive genetic test.

Results: From our 173 patients, 140 met the inclusion criteria and none exclusion criteria so they were enrolled. Patients were 61% male with mean age of 50±15 years old. Mean follow-up was 26±28 months; 24,4% of index cases were positive for causative mutation, 6,8% patients with pathogenic mutation in SCN5A gene and 17,6% with probably pathogenic mutation in SCN5A.

We haven’t found significant differences between the 2 groups (negative and positive genetic test) in any clinical variable included. Regarding electrocardiographic variables, patients in whom a mutation was identified had longer PR interval (192±36 Vs 170±28, p=0.001), longer QRS (121±19 VS 111±18 p=0.017), particularly when QRS>110ms (p=0.002), and longer QT (398±25 VS 370±45 p=0.015) In multivariate analysis, PR interval (p=0.032) and QRS>110ms (p=0.041) were independent predictors for positive genetic test.

Conclusion: In our BS population, there were no clinical differences between patients with and without causative mutation, also concerning events rate. Patients with positive genetic test have significantly longer PR interval and QRS>110ms than in patients with genetic test negative. Those results can be interpreted in relation to sodium channel disfunction in patients with SCN5A mutation.