GW26-e1472
More accurate way for localization of idiopathic outflow tract ventricular arrhythmia
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OBJECTIVES In consideration of the Left and right outflow tract take a kind of a relationship as before and after, we sought to investigate whether horizontal plane QRS axis would be a useful index for differentiating left from right ventricular outflow tract origin.

METHODS We analyzed the surface ECG pattern of patients with OT-Va who underwent successful catheter ablation. Based on horizontal plane QRS axis measurement method, we computed the OT-Va and Sinus rhythm(SR) the V2/V6 ratio instead of a specific electrical axis degree, and comparison the index. The V2/V6 index were calculated by computing the ratio V2(VRS)/V6(VRS) in OT-Va versus V2(RS)/V6(RS) in SR.

RESULTS A total of 221 patients (mean age 47±17 years, 39% male) who underwent successful catheter ablation from January 2008 to march 2014 were analyzed. 54 patients from LOVT, and 167 patients was in the RVOT. Patients with bundle branch block, prior myocardial infarction and failed catheter ablation were excluded. Receiver operating characteristic curve analysis for anatomic prediction of outflow tract ventricular arrhythmia (OT-Va) origin. The area under the curve (AUC) of the V2/V6 index was 0.935. A cut off value of the V2/V6 index <0.95 was used with the sensitivity of 0.97 and the specificity of 85.4%.

CONCLUSIONS Horizontal plane QRS axis and its derivative of the V2/ V6 ratio can be a useful index for differentiating LVOT from RVOT origin. This algorithm can be a more accurate way for guide clinical planning ablation strategy.

GW26-e2300
Gender differences in clinical characteristics and inpatient outcomes amongst 2442 hospitalized Chinese patients with nonvalvular atrial fibrillation: The Nanchang Atrial Fibrillation Registry
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OBJECTIVES Gender differences in risk of thromboembolism and death among patients with nonvalvular atrial fibrillation (NVAF) has been illustrated in several studies. Limited studies have investigated the impact of gender on clinical characteristics and outcomes amongst NVAF patients from China. We investigated the impact of gender on risk factors and inpatient mortality in a hospitalised cohort of 2,442 Chinese NVAF patients.

METHODS We reviewed medical records of consecutive patients admitted with NVAF during May 2011 and Dec 2013 in the second affiliated hospital of Nanchang University. The predictors of inpatient mortality were evaluated by multivariate regression analyses.

RESULTS We studied 2,442 patients (43.4% female; mean age was 70.6±11.3), whereby median length of stay was 10 days (IQR 7-14). Inpatient mortality was 2.2%. Mean age, CHADS2, and CHA2DS2-VASC scores were higher in females compared with males (All P<0.01). There was a greater increase in the prevalence of NVAF with age amongst females compared with males. Hypertension, diabetes and hyperthyroidism were more common in female AF patients, while higher incidences of coronary artery disease, cardiomyopathy, chronic artery disease and cancer were observed in males. Oral anticoagulation use during hospitalization was 33.3%, without gender differences. Length of stay and other inpatient outcomes were comparable between both genders. On multivariate analyses, the significant risk factors of inpatient death in females were previous ischemic stroke/transient ischemic attack (TIA)/thromboembolism (TE) (Hazard Ratio, HR: 5.15; 95%CI: 2.03-13.06), peripheral artery disease (HR: 5.7; 95%CI: 1.49-22.16) and chronic renal disease (HR: 5.68; 95%CI: 1.46-22.13). Amongst males, only age (HR: 1.06, 95%CI: 1.02-1.11) and previous ischemic stroke/TIA/TE (HR: 3.29, 95%CI: 1.56-6.90) were independent predictors of inpatient mortality.

CONCLUSIONS Gender related difference in clinical characteristics and stroke risk profile were evident in Chinese NVAF patients, but no gender disparity was evident in the low antithrombolytic use or inpatient mortality. Stroke/TIA/TE was an important predictor of inpatient mortality in both females and males.

GW26-e2959
Genetic and Clinical Characteristics of Patients with Brugada Syndrome
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OBJECTIVES Though much progress has been made on understanding the Brugada Syndrome (BrS) since the first report in 1989, the genetic causes and full clinical picture of this syndrome are far from clear. The rarity of this disorder has led to a fragmented state of publication where many small case reports make up the majority of the BrS literature. This study aimed to amalgamate many case studies into a deeper understanding of the clinical and genetic features of this deadly syndrome.

METHODS A literature review was conducted by culling BrS case reports (2014-2015) that contained 12-lead ECGs and adequate clinical details from PubMed. Clinical information including family history, genetic testing, cardiac events (CEs) such as presyncope, syncope, cardiac arrest, sudden cardiac death (SCD), and CE-exacerbating factors was extracted. Electrocardiographic abnormalities were evaluated for the presence of typical BrS ECG patterns, defined as coved/triangle (type-1) and/or saddle back (type-2) ST elevation with T wave inversion in the right precordial leads. QRS axis shifting and AV block (AVB) were recorded. Arrhythmias were assessed for atrial fibrillation/ flutter (AF/AF), monomorphic/polymorphic ventricular tachycardia (VVT/PVT), torsades de pointes (Tdp) and ventricular fibrillation (VF). Treatments included VT ablation and placement of implantable cardioverter defibrillators (ICD). The frequency of VT storm following ICD implantation was also assessed.

RESULTS A total of 67 BrS cases (age 43±20 years, range 0.2-85 years, 81% M) with sufficient clinical information available were studied. Patients’ ethnic origins were: Asian (39%), European (52%), Latino/Hispanic (6%) and African (3%). A family history of BrS and/or unexplained premature SCD was found in 25% of the cases. DNA sequencing (including 290 genes) and genetic testing (including 134 genes) were performed for BrS-causing and susceptible genes were reported in 33% (22/67). These were: SCN5A (10 Muts/13 SNPs); CACNA1C (2 Muts/2 SNPs); CACNB2 (1 SNP); KCNHR2 (4 Muts); KCNE1 (1 SNP); RyR2 (1 Mut); RANGRF (1 Mut); SBMA (2 Muts) and in ABCC9 (1 SNP). A transitory type-1 BrS ECG pattern was found in 91% (61/67) including 14 cases induced by febrile illness and 21 provoked by sodium channel blockers. Type-2 BrS ECG pattern was seen 19 cases, of which 15 had both type-1 and 2, and 4 cases had type-2 pattern only. There were 1st degree AVB (15%), leftward QRS axis (22%), and right or superior right axis (19%). All except one case (66/67) had ST elevations ≥0.2 mV when the BrS patterns appeared. Palpitations, pre-syncope and syncope were seen in 21%, 9% and 46% respectively. MVT, PVT and Tdp were documented in 19%, 12% and 1% of cases. VF was seen in 39% (26/67) with 7/26 induced by EPS. SCD occurred in 4/67 cases. In addition, 17 cases of SCD were traced in those with BrS family history. VT ablation was performed in 9% (6/67), and ICD was placed in 43% (29/67). In the latter, effective ICD discharges were documented in 85% (25/29) during 0.1-7 year follow-up. VT storm occurred in 34% (10/29) shortly after ICD implantation.

CONCLUSIONS Though genetic heterogeneity is large, SCN5A remains as the dominant BrS-causing gene. Functional SNPs are also very common, indicating they may play an important role in BrS genetics under certain conditions. A transitory type-1 ECG pattern, though genetic, is more common, indicating they may play an important role in BrS genetics under certain conditions. A transitory type-1 ECG pattern, though genetic, is more common, indicating they may play an important role in BrS genetics under certain conditions. A transitory type-1 ECG pattern, though genetic, is more common, indicating they may play an important role in BrS genetics under certain conditions. A transitory type-1 ECG pattern, though genetic, is more common, indicating they may play an important role in BrS genetics under certain conditions.