Genotype ECG-Phenotype Correlation in Atrial Fibrillation

Daniela Husser, MD; Martin Stridh, PhD; Leif Sörnmo, PhD; Dan M. Roden, MD; Dawood Darbar, MD; Andreas Bollmann, MD

Background—Atrial fibrillation (AF) is heterogeneous at the clinical and molecular levels. Association studies have reported that common single-nucleotide polymorphisms in KCNE1 and SCN5A may predispose to AF. In this study, we tested the hypothesis that specific AF-associated genotypes confer variation on the appearance of AF assessed by analysis of fibrillatory rate of the atria.

Methods and Results—Twenty-six nonrelated patients (21 males, mean age 55±12 years) with persistent lone AF (median AF duration 5 weeks) not taking class I or III antiarrhythmic drugs were studied. Fibrillatory rate was obtained by spatiotemporal QRST cancellation and time-frequency analysis of the index surface ECG. Genotypes at the AF-associated loci in KCNE1 (S38G) and SCN5A (H558R) were determined by direct DNA sequencing. The atrial fibrillatory rate was 418±50 fibrillations per minute (range, 336 to 521) in the study cohort. Carriers of the 38GG KCNE1 genotype (n=13) had significantly lower fibrillatory rates (392±36 versus 443±49 fibrillations per minute, P=0.006) compared to those with GS or SS genotype (n=13). Six patients (23%) with fibrillatory rates >450 fibrillations per minute, all had either the GS or SS genotype (χ² P=0.008). In contrast, both the heterozygous and homozygous SCN5A H558R polymorphism had no effect on fibrillatory rate. There were no significant associations between fibrillatory rate and clinical (age, gender, AF duration, drug treatment) or echocardiographic (left atrial diameter, left ventricular ejection fraction) variables. In multivariable regression analysis, the KCNE1 S38G genotype (SS/GS coded 0, GG coded 1) was the only independent predictor of fibrillatory rate (β=−0.437, P=0.006) with a SE of the estimate of 44 fibrillations per minute.

Conclusions—This study suggests that atrial fibrillatory rate obtained from the surface ECG is at least in part determined by KCNE1 (S38G) genotype, implying that this variant exerts functional effects on atrial electrophysiology. This intermediate ECG phenotype may be useful for elaborating genetic influences on AF mechanisms and identifying subsets of patients for variability in AF susceptibility or response to therapies. (Circ Arrhythmia Electrophysiol. 2009;2:24-28.)

Key Words: electrocardiography ■ electrophysiology ■ genetics ■ atrial fibrillation
cardiographic patient characteristics explain fibrillatory rate variance only in part.7,8

In this study, we tested the hypothesis that specific AF-associated genotypes confer variation on the ECG appearance of AF assessed by analysis of fibrillatory rate.

Methods

Study Population
The study was performed in patients prospectively enrolled in our AF registry, which consists of a clinical, a genetic, and a digital ECG registry. Inclusion criteria include age ≥18 years, and a documented history of AF or atrial flutter. At enrollment into the registry, patients gave informed consent, a detailed medical and drug history is obtained in all patients in addition to a standard 12-lead ECG and a transthoracic echocardiogram.

For this study, patients were selected if they had persistent lone AF >7 days with or without mild hypertension, not taking class I or III antiarrhythmic drugs at the time of ECG acquisition.

Left atrial and left ventricular measurements from the M-mode echocardiograms were performed by an experienced physician blinded to the genotype status of the patient. The echocardiograms were evaluated according to the recommendations of the American Society of Echocardiography.

Molecular Analysis
Genomic DNA was extracted according to standard protocols, and the KCNE1 (S38G) and SCN5A (H558R) polymorphisms were detected by direct sequencing blinded to the ECG findings.

ECG Analysis
Standard 10-s, 12-lead surface ECG recordings were acquired in all patients with the subject relaxed in a supine position. Digital ECG (500-Hz sampling rate) were retrieved from the hospital ECG database for further signal processing.

After high-pass filtering to remove baseline wander, atrial fibrillatory activity was extracted in lead V1 using spatiotemporal QRST cancellation. Because the dominant frequency component of interest is within the 4 to 9 Hz range, the resulting fibrillatory baseline signal was downsampled to 50 Hz and subjected to spectral analysis. The time-frequency distribution of the atrial signal (obtained by short-term Fourier transform) was decomposed such that each spectrum can be modeled as a frequency-shifted and amplitude-scaled version of the spectral profile. This procedure is based on a spectral profile, dynamically updated from previous spectra, which was matched to each new spectrum using weighted least squares estimation. The frequency shift needed to achieve optimal matching then yields a frequency shift needed to achieve optimal matching then yields a measure of instantaneous fibrillatory rate of a 2.5-s ECG segment (overlapping with 1 segment each second) and was trended as a function of time.6

Frequencies were converted to fibrillatory rates with its unit fibrillations per minute as advocated previously (rate = frequency × 60).9 Mean fibrillatory rate (in fibrillations per minute) defined as average of instantaneous fibrillatory rates over the 10-second ECG segment was determined (Figure 1).

Results

Patient Characteristics
Patient characteristics are summarized in Table 1. The atrial fibrillatory rate was 418±50 fpm (range, 336 to 521).

The frequencies of the KCNE1 genotypes were SS in 4%, GS in 46%, and GG in 50% and of the SCN5A genotypes HH

<table>
<thead>
<tr>
<th>Table 1. Patient Characteristics (n=26)</th>
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<tbody>
<tr>
<td>Age, y</td>
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<tr>
<td>Male/female</td>
</tr>
<tr>
<td>AF duration, wk</td>
</tr>
<tr>
<td>Mild hypertension</td>
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<tr>
<td>LAD, mm</td>
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<tr>
<td>LVEF, %</td>
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<tr>
<td>Digitalis</td>
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<tr>
<td>Beta and/or calcium channel blocker</td>
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<tr>
<td>Atrial fibrillatory rate, fpm</td>
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<td>Ventricular rate, bpm</td>
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Mean±1 SD (range). LAD indicates left atrial diameter; LVEF, left ventricular ejection fraction.
in 57%, HR in 31%, and RR in 12%. Patient characteristics according to genotype are summarized in Table 2.

**Genotype-ECG Phenotype Correlations**

Carriers of the 38GG *KCNE1* genotype had significantly lower fibrillatory rates (392±36 versus 443±49 fpm, \( P=0.006 \)) compared with those with GS or SS genotype (Table 2). Six patients (23%) with fibrillatory rates >450 fpm, all had either the GS or SS genotype (\( \chi^2\ P=0.008; \) Figure 2). Their clinical characteristics were similar to patients with lower fibrillatory rates. In particular, their AF duration ranged from 2 to 42 weeks (median, 5 weeks), similar to the remaining patients (1 to 52 weeks; median, 6 weeks). In contrast, the *SCN5A* H558R polymorphism was not associated with fibrillatory rate (Table 2).

There were no significant associations between fibrillatory rate and clinical (age, gender, AF duration, drug treatment) or echocardiographic (left atrial diameter, left ventricular ejection fraction) variables. In particular, the use of digoxin (426±67 versus 409±42 fpm, \( P=0.454 \)) or beta blockers (394±52 versus 418±47 fpm, \( P=0.319 \)) did not affect fibrillatory rate.

In multivariable regression analysis, the *KCNE1* S38G genotype (SS/1 GS coded 0, GG coded 1) was the only independent predictor of fibrillatory rate (\( \beta=-0.437, P=0.006 \)) with a SE of 44 fpm.

**Discussion**

**Main Finding**

To our knowledge, this study is the first in patients with persistent lone AF to assess possible genotype-phenotype correlations using atrial fibrillatory rate of the surface ECG. In contrast to clinical and echocardiographic variables, *KCNE1* (S38G) but not *SCN5A* (H558R) genotype was associated with fibrillatory rate. It was demonstrated that carriers of the 38GG *KCNE1* genotype had significantly lower rates than those with the GS or SS genotype. Of interest, in none of the patients with the GG genotype did fibrillatory rate exceed 450 fpm.

**Modulation of Atrial Electrophysiology by Gene Variants**

Few previous studies\(^4,5,10\) have assessed in vitro modulatory effects of gene variants on atrial electrophysiological properties such as atrial refractoriness or conduction velocity. Of special importance for our study are findings on *KCNE1* (S38G) and *SCN5A* (H558R) polymorphisms. Ehrlich et al found that the *KCNE1* 38G isoform is associated with reduced IKs likely due to decreased KvLQT1 membrane expression. This in turn leads to longer atrial action potential duration and refractoriness. Because longer refractory periods are associated with lower fibrillatory rates,\(^11\) our observation that lower rates not exceeding 450 fpm are present in patients with the GG genotype is in agreement with these findings. It needs to be pointed out that the increased risk for AF initiation with this genotype due to early afterdepolarizations is not in conflict with our observations that refer to AF persistence.

Although the *SCN5A* H558R polymorphism has been suggested to be associated with nonfunctioning or poorly
functioning sodium channels and a subsequently reduced conduction velocity, we have found no association between this genotype and slower fibrillatory rates. On the one hand, it needs to be emphasized, however, that atrial refractoriness is the main determinant of fibrillatory rate, whereas conduction velocity seems to be similar in a narrow range among patients with persistent AF. On the other hand, the sodium channel function is also affected by the amino acid splice variant that is unknown in the clinical setting.

Very limited in vivo data are available showing that certain gene variants may indeed exert functional effects on atrial electrophysiology. For instance, the promoter polymorphism −44G>A of the connexin 40 (Cx40) gene is associated with reduced transcriptional activity thereby influencing atrial Cx40 expression. Conceptually similar to our study, Firouzi et al have shown that this Cx40 polymorphism was associated with atrial refractoriness dispersion. In their study, the prevalence of the minor Cx40 allele (−44A) and −44AA genotype was significantly higher in subjects with increased dispersion. Interestingly, as with our study, this difference was revealed already in a small population (n = 30).

Previous studies have shown that a lower fibrillatory rate is associated with a better response to antiarrhythmic drugs and less AF recurrence after cardioversion. Similarly, certain genotypes such as the ACE ID polymorphism may modulate the response to antiarrhythmic therapy via increased ACE and consequently angiotensin II levels. The latter is known to promote atrial fibrosis and electrophysiological remodeling. In consequence, the presence of the ACE ID or DD polymorphisms may indicate a more severe remodeling process in AF that is refractory to class I and III antiarrhythmics.

In summary, only limited data are available on few polymorphisms that point to a variety of mechanisms and pathways involved in the electrical and structural remodeling during AF. The elaboration of their individual contribution that may, moreover, vary over time is in its infancy. Nevertheless, the findings of our study are hypothesis generating and suggest that fibrillatory rate is an intermediate genotype-dependent ECG phenotype, which—together with its underlying genotype—may be useful for predicting response to therapy.

Limitations
This study is limited by a small but homogenous patient population. However, in agreement with a previous study our current approach assessing genotype-ECG phenotype correlations among patients with AF requires a much smaller sample size than classic association studies. Nevertheless, certain genotypes (e.g., KCNE1 38SS, SCN5A 588RR) were underrepresented in this population and require further evaluation.

Using the candidate gene approach, this study was limited to the investigation of 2 single-nucleotide polymorphisms of 2 cardiac ion channel genes. However, as discussed earlier, other genes may also influence atrial electrophysiology and consequently the ECG phenotype.

This study was limited to the analysis of ECG lead V1. It can be argued that this is a closer reflection of right atrial but not left atrial activity. However, fibrillatory rates are similar among different sites in patients with persistent AF as in our population. Consequently, it is not surprising that ECG lead V1 closely reflects right atrial, but is also related to pulmonary venous/left atrial rates, especially when AF is persistent and the left to right atrial frequency gradient diminishes.

Aside from P-wave parameters and ventricular rate, fibrillatory rate during AF can be considered as 1 specific ECG phenotype. Although there are several theories about AF susceotm including multiple wavelets, focal activation, spiral wave; in the individual patient, the underlying mechanism is currently difficult (if not impossible) to assess. Consequently, the association between fibrillatory rate and the dominant underlying AF mechanisms has not been explored. But even with this limited knowledge, fibrillatory rate of ECG lead V1 can be considered as a general marker of atrial remodeling as it is also associated with spontaneous and drug-induced AF termination and recidivism after cardioversion.

ECG recordings in this study were limited to 10 seconds and variability over time was not assessed. However, previous studies have shown that fibrillatory rate obtained from the surface ECG is reproducible over 24 hours in clinically stable patients with persistent AF.

Finally, although we did not invasively assess ERP in our population, previous studies have shown the association between the KCNE1 (S38G) genotype and atrial refractoriness as well as between atrial refractoriness and fibrillatory rate.

Conclusions
This study suggests that atrial fibrillatory rate obtained from the surface ECG is at least in part determined by KCNE1 (S38G) genotype, implying that this variant exerts functional effects on atrial electrophysiology. This intermediate ECG phenotype may be useful for elaborating genetic influences on AF mechanisms and identifying subsets of patients for variability in AF susceptibility or response to therapies.

Acknowledgments
The authors thank Janey Wang, Christie Ingram, Shannon Carter, Vanderbilt University, and Andreu Climent, Polytechnic University of Valencia, Spain, for their help with this study.

Sources of Funding
Supported by the Volkswagen Foundation, Germany (to D.H. and M.S.); Riksbanken Jubileumsfond, Sweden through the Nils-Eric Svenssons Award and research grants (HU 1679/1-1, Deutsche Forschungsgemeinschaft [German Research Foundation] and Formel.I-109, University Leipzig) (to D.H.); and VOI HL65962, The Pharmacogenomics of Arrhythmia Therapy; and United States Public Health Service (HL075266) and (HL085690) (to D.D.).

Disclosures
None.

References


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*Circ Arrhythm Electrophysiol.* 2009;2:24-28; originally published online February 10, 2009; doi: 10.1161/CIRCEP.108.799098

*Circulation: Arrhythmia and Electrophysiology* is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231
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Print ISSN: 1941-3149. Online ISSN: 1941-3084

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