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Reference values of electrocardiogram repolarization variables in a healthy population☆

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Abstract

Introduction: Reference values for T-wave morphology analysis and evaluation of the relationship with age, sex, and heart rate are lacking in the literature. In this study, we characterized T-wave morphology in a large sample of healthy individuals.

Method: A total of 1081 healthy subjects (83% men; range, 17-81 years) were included. T-wave morphology variables describing the duration, area, slopes, amplitude, and distribution were calculated using 10-second digital electrocardiogram recordings. Multivariate regression was used to test for dependence of T-wave variables with the subject age, sex, and heart rate.

Results: Lead V5 (men vs women) T-wave variables were as follows: amplitude, 444 versus 317 μV; area, 48.4 versus 33.2 ms $*$ mV; Tpeak-Tend interval, 94 versus 92 milliseconds; maximal descending slope, −5.15 versus −3.69 μV/ms; skewness, −0.24 versus −0.22; and kurtosis, −0.36 versus −0.35. Tpeak-Tend interval, skewness, and kurtosis were independent of age, sex, and heart rate ($r^2 < 0.05$), whereas Bazett-corrected QT-interval was more dependent ($r^2 = 0.40$).

Conclusion: A selection of T-wave morphology variables is found to be clinically independent of age, sex, and heart rate, including Tpeak-Tend interval, skewness, and kurtosis.

Keywords: Electrocardiography; Electrophysiology; QT-interval; T_pT_e interval; Repolarization

Introduction

The T-wave in the electrocardiogram (ECG) reflects repolarization of the ventricular myocytes. The typical T-wave is due to the dispersion of repolarization of myocytes, which includes a complex mixture of transmural dispersion, differences in repolarization between the right and the left ventricle, and a repolarization gradient between the apex and the basis of the heart.[1]

In clinical ECG analysis, the only routinely used measure of repolarization is the duration of the QT-interval, although this is a surrogate measure because it includes the ventricular depolarization in the form of the QRS complex as well. Because the QT-interval is inversely correlated to the heart rate, it is routinely transformed into a more rate-independent "corrected" QT-interval (QTc).[2] Manual assessment of the QT-interval shows considerable intraobserver and interobserver variations, which may limit its clinical utility.[2] Therefore, there is an ongoing search for other ECG indices of repolarization, for example, by analysis of the T-wave.[3-9]

Several approaches for analysis of the T-wave morphology have been proposed, some being based on relatively complex mathematical methods.[3,5,8] The notion that variations of such T-wave–derived parameters result from

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underlying repolarization abnormalities is supported by computer simulations, experimental models, and clinical studies. These studies indicate usefulness in predicting adverse prognosis, for example, in healthy humans or in patients after acute myocardial infarction.[4-6,10,11] Moreover, T-wave morphology has been thoroughly examined in patients with long QT syndrome (LQTS), where mutations in cardiac ion channels lead to QT/QTc prolongation and alterations of the T-wave.[3,6,8] In addition, simple measurement of the T-wave amplitude allows for cardiovascular risk stratification both in a general medical population and in healthy individuals.[12] Hence, a relatively simple descriptive analysis of the T-wave morphology in the standard ECG, with assessment of readily apparent characteristics, for example, duration, area, amplitude, and slopes, seems to be an interesting method of addressing repolarization abnormalities.[3,4,7,8,11] Reference data for T-wave–derived repolarization measures in a healthy population is still limited, and the influence of age, sex, and heart rate remains to be evaluated. The aim of the present study was to characterize and quantify the T-wave amplitude, slope, area, duration, and distribution in a large population of healthy individuals.

Methods

Population

The data were collected from the Marquette Electronics (Milwaukee, WI) ECG database established in 1987. The study population consisted of company employees with no history of cardiovascular disease, including hypertension. Individual health status was confirmed by a normal medical history, a normal physical examination by a cardiologist including normotension, and absence of concurrent medication. A total of 1081 individuals (899 men, 182 women; mean age, 33 years; range, 17-81 years) had a digitally recorded 12-lead ECG performed. However, even in healthy subjects, diagnostic ECG abnormalities may exist. To investigate the impact of these ECG abnormalities in a healthy population, 102 subjects were analyzed separately according to their Minnesota coding (see below).

ECG acquisition

The ECG was recorded in the supine position after 5 minutes of rest on a MAC15 digital ECG recorder (GE Medical Systems, Milwaukee, WI), with a standard 12-lead system at a sampling rate of 500 Hz and an amplitude resolution of 1.22 μV.

ECG preprocessing

All ECGs were transferred to a personal computer for processing; ST-T segments were extracted and filtered by a low-pass Kaiser Window FIR filter with a cutoff frequency of 20 Hz. For each ECG, a mean RR- and QT-interval was calculated, and for each of the 12 leads, the following fiducial points were obtained using the Magellan Workstation (GE Medical Systems):

T_o, the time of T-wave onset, was determined by use of a modified Laguna algorithm.[8]
T_e, the time of T-wave end, was determined by use of the GE 12SL algorithm (GE Medical Systems) as described by Hnatkova et al.[13]
T_p, the time of T-wave peak, was defined at the moment of maximum T-wave amplitude.
Q_o, the beginning of the QRS complex.

All measurements were done in a fully automated fashion as described below and in detail elsewhere.[8]

Minnesota coding

The Minnesota coding[14] was performed using the Magellan workstation (GE Medical Systems) automatically coding the ECG with all appropriate Minnesota codes (MCs). The following MCs were regarded as diagnostic significant and used to define subjects in the subpopulation with diagnostic ECG abnormalities: diagnostic Q-wave patterns (MCs 1.1.1-1.2.5 plus 1.2.7), T-wave abnormalities (MCs 5.1-5.5), ST-segment elevation (MC 9.2), ST-segment depression (MCs 4.1-4.4), and left bundle branch block (MC 7.7.1).

T-wave parameters

The above preprocessing was followed by measurement and calculation of 9 variables describing the T-wave morphology and 3 variables related to the RR- and QT-intervals, respectively, which were further divided into the following 5 categories: (1) duration variables, (2) amplitude variables, (3) area variables, (4) slope variables, and (5) distribution variables. The variables are illustrated in Fig. 1A-F and described in details below. These variables were obtained for each of the 12 leads in the ECG. Due to the large amount of data, only results from lead V5 are presented. Results from the other leads are available online (see Appendix A for supplemental data).

Duration variables

RR-interval: time between 2 consecutive R-waves, averaged over all beats in the 10-second ECG, measured in milliseconds.

QT-interval: uncorrected interval between the beginning of the Q-wave and the end of the T-wave, measured globally in milliseconds based on the generation of a superlead (12SL algorithm; GE Medical Systems).[13]

QTcB: corrected QT-interval using Bazett correction,[15] measured in milliseconds.

QTcF: corrected QT-interval using Fridericia correction,[15] measured in milliseconds.

QTcL: linear heart rate–adjusted QT-interval, based on the Framingham adjustment,[15] measured in milliseconds.

T_oT_e: duration of the T-wave, from T_o to T_e, measured in milliseconds.

T_pT_e: time from T_p to T_e, measured in milliseconds.