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Circulation: Genomic and Precision Medicine

ORIGINAL ARTICLE

Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation

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BACKGROUND: The P-wave duration (PWD) is an electrocardiographic measurement that represents cardiac conduction in the atria. Shortened or prolonged PWD is associated with atrial fibrillation (AF). We used exome-chip data to examine the associations between common and rare variants with PWD.

METHODS: Fifteen studies comprising 64 440 individuals (56 943 European, 5681 African, 1186 Hispanic, 630 Asian) and ≈230 000 variants were used to examine associations with maximum PWD across the 12-lead ECG. Meta-analyses summarized association results for common variants; gene-based burden and sequence kernel association tests examined low-frequency variant-PWD associations. Additionally, we examined the associations between PWD loci and AF using previous AF genome-wide association studies.

RESULTS: We identified 21 common and low-frequency genetic loci (14 novel) associated with maximum PWD, including several AF loci (*TTN*, *CAND2*, *SCN10A*, *PITX2*, *CAV1*, *SYNPO2L*, *SOX5*, *TBX5, MYH6, RPL3L*). The top variants at known sarcomere genes (*TTN, MYH6*) were associated with longer PWD and increased AF risk. However, top variants at other loci (eg, *PITX2* and *SCN10A*) were associated with longer PWD but lower AF risk.

CONCLUSIONS: Our results highlight multiple novel genetic loci associated with PWD, and underscore the shared mechanisms of atrial conduction and AF. Prolonged PWD may be an endophenotype for several different genetic mechanisms of AF.

Key Words: atrial fibrillation ■ electrophysiology ■ exome ■ genetic ■ genome-wide association studies ■ population

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The Data Supplement is available at https://www.ahajournals.org/doi/suppl/10.1161/CIRCGEN.119.002874.

For Sources of Funding and Disclosures, see page 394.

Circulation: Genomic and Precision Medicine is available at www.ahajournals.org/journal/circgen

Nonstandard Abbreviations and Acronyms

AF	atrial fibrillation
LV	left ventricle
MAF	minor allele frequency
PWD	P-wave duration
RAA	right atrial appendage

P-wave duration (PWD) is an electrocardiographic measurement that reflects cardiac conduction through the atria. PWD variability may implicate intrinsic or acquired properties in the function and structure of atrial conductivity.[1] Shortened and prolonged PWD have been repeatedly associated with atrial fibrillation (AF),[2,3] a common and heritable[4] arrhythmia that predisposes to stroke, heart failure, and increased mortality.[5–7]

Although PWD is heritable[8, 9] only 2 genome-wide association studies have been conducted.[10,11] Given the relationship between PWD and AF, examining the genetic determinants of PWD may provide insights into the pathophysiology of AF. Moreover, assessment of coding variation may facilitate identification of AF-specific genes. Therefore, we conducted an exome-chip based analysis focused on rare and common genetic determinants of PWD.

METHODS

Each study was reviewed and approved by the local or institutional IRB, and each participant provided consent. Study-specific details are provided in Data Supplement, under Description of participating studies and in Table I in the Data Supplement. In our primary analysis, we considered loci/genes significantly associated with PWD if a common variant (minor allele frequency [MAF] ≥5%) or a gene-based test, including burden or sequence kernel association test[12] comprising low-frequency variants (MAF <5% or MAF <1%) exceeded exome-wide significance in meta-analyses, after Bonferroni correction. We reported low-frequency variants that exceeded exome-wide significance at significant loci identified in gene-based analyses. The full Methods section is available in the Data Supplement (under Methods). Data supporting the findings of this study can be made available, following reasonable request to the corresponding author.

Table 1. Study Participant Characteristics*

Study	Ancestry	N	Age, y, Mean±SD	Sex, Women, %	P-Wave Duration, ms, Mean±SD	RR Interval, ms, Mean±SD
ARIC	European	8861	53.9±5.7	54.1	106.0±11.8	920.5±133.8
	African	2922	53.3±5.8	62.2	111.5±11.9	924.2±148.6
BRIGHT	European	195	60.5±8.9	57.4	121.1±19.4	976.1±186.0
CAMP	European	1887	59.9±10.4	37.4	106.0±15.8	936.8±171.3
CHS	European	2648	72.3±5.4	60.7	109.9±13.0	950.0±145.8
	African	445	72.6±5.6	64.5	112.2±13.1	912.8±156.4
ERF	European	514	49.0±14.3	54.1	111.2±12.4	963.4±152.9
FHS	European	5677	47.2±13.3	55.0	105.0±12.0	973.7±155.9
INTER99	European	5872	46.2±7.9	51.6	104.3±12.5	920.4±150.5
KORA	European	2435	47.1±12.8	51.9	108.0±11.1	939.7±147.7
LIFELINES	European	1914	45.2±13.0	59.8	112.1±12.4	897.3±144.5
UHP	European	1657	38.5±12.5	55.8	109.1±14.6	956.5±152.4
MESA	European	2083	61.8±10.1	51.8	104.4±12.9	1054.5±158.9
	African	1131	61.3±10.3	52.9	107.9±12.3	1054.4±170.2
	Hispanic	1186	60.6±10.3	50.1	105.2±12.0	1061.0±154.5
	Asian	630	61.3±10.3	50.2	101.7±11.7	1059.0±140.3
NEO	European	5119	55.6±6.0	51.9	114.2±13.9	933.8±150.5
RS	European	1740	69.5±8.4	51.4	120.1±12.4	859.8±140.6
SHIP-0	European	2653	46.5±15.4	51.8	109.5±11.2	853.6±147.8
SHIP-Trend	European	2922	47.9±14.6	52.5	113.1±11.9	911.3±134.5
WHI	European	10766	65.8±6.6	100	107.2±11.9	914.3±134.2
	African	1183	64.3±6.5	100	110.6±11.5	920.2±143.7

ARIC indicates Atherosclerosis Risk in Communities study; BRIGHT, British Genetics of Hypertension; CAMP, MGH Cardiology and Metabolic Patient cohort; CHS, Cardiovascular Health Study; ERF, Erasmus Rucphen Family; FHS, Framingham Heart Study; INTER99, https://clinicaltrials.gov/ct2/show/NCT00289237; KORA, Kooperative Gesundheitsforschung in der Region Augsburg; LIFELINES, Lifelines Cohort Study; MESA, Multi-Ethnic Study of Atherosclerosis; NEO, Netherlands Epidemiology of Obesity study; RS, Rotterdam Study; SHIP, Study of Health in Pomerania; UHP, the Utrecht Health Project; and WHI, the Women's Health Initiative.

*N: sample size.

RESULTS

A total of 64 440 individuals from 4 ethnic groups (56 943 European, 5681 African, 630 Asian, 1186 Hispanic), and 15 studies were included in our meta-analysis. The per-study mean age ranged from 46.2 to 72.6 years; roughly 60% of participants were women (Table 1). For the multiethnic single variant analyses, we tested ≈26 000 common variants (see Table III in the Data Supplement for the exact number of variants included in each analysis). The Quantile-Quantile plots show a small degree of inflation for both PWD residuals (λ=1.10) and inverse normal transformed PWD residuals (λ=1.13; Figure IA and IB in the Data Supplement). We performed meta-analyses in ethnicity-specific groups (European: λ=1.10–1.13; African: λ=1.03; Figure IC through IF in the Data Supplement). Linkage disequilibrium score regression intercepts were 1 (multiethnic analyses) and 0.95 (European-specific analyses), suggesting the inflation was mainly due to polygenicity. Meta-analysis results from PWD residuals and inverse normal transformed PWD residuals were highly correlated across analyses (Pearson ρ≥0.99, $P<2.2\times10^{-16}$; Figure II in the Data Supplement).

COMMON VARIANT ANALYSES

We identified 41 exome-wide significant variants at 18 loci ($P<1.9\times10^{-6}$; Figure III in the Data Supplement) in our multiethnic meta-analysis of PWD residuals (Table 2). Eleven of the 18 PWD loci are novel, representing the following nearest genes: *PKP1* (rs1626370, $P=2\times10^{-6}$), *TTN* (rs2042995, $P=4\times10^{-7}$), *PITX2* (rs17042171, $P=8\times10^{-11}$), *ARHGAP10* (rs6845865, $P=2\times10^{-10}$), *TCF21* (rs2327429, $P=2\times10^{-7}$), *CDK6* (rs2282978, $P=2\times10^{-8}$), *SYNPO2L* (rs3812629, $P=4\times10^{-7}$), *SOX5* (rs17287293, $P=3\times10^{-7}$), *HMGA2* (rs8756, $P=7\times10^{-7}$), *GORS4* (rs17608766, $P=9\times10^{-15}$), and *MC4R* (rs12970134, $P=1\times10^{-6}$). Another novel locus was associated only with the inverse normal transformed PWD

Table 2. Top Exome-Wide Significant Variants for P-Wave Duration In Multiethnic Meta-Analysis

								Residuals					Inverse Normal Transformed Residuals				
Locus	Closest Gene	Location	rsID	EA	Function	N	EAF	Beta	SE	*P* Value	h^2, %	I^2, %	Beta	SE	*P* Value	h^2, %	I^2, %
Novel loci																	
1	*PKP1*	1q32.1	rs1626370	A	Missense	64 431	0.2	0.39	0.08	2×10^{-6}*	0.04	2	0.03	0.01	2×10^{-6}*	0.04	0
2	*TTN*†	2q31.2	rs2042995	C	Intron	64 410	0.3	0.41	0.08	4×10^{-7}*	0.04	8	0.03	0.01	5×10^{-7}*	0.04	12
3	*DLEC1*‡	3p22.2	rs116202356	G	Missense	64 331	0.98	1.72	0.27	2×10^{-10}*	0.06	20	0.14	0.02	2×10^{-10}*	0.06	19
4	*PITX2*	4q25	rs17042171	C	Intergenic	64 399	0.9	0.64	0.10	8×10^{-11}*	0.07	45	0.06	0.01	2×10^{-11}*	0.07	50
5	*ARHGAP10*	4q31.23	rs6845865	C	Intron	64 437	0.2	0.54	0.09	2×10^{-10}*	0.06	0	0.05	0.01	9×10^{-11}*	0.07	0
6	*TCF21*/ *TARID*	6q23.2	rs2327429	C	Upstream	64 434	0.3	0.39	0.07	2×10^{-7}*	0.04	13	0.03	0.01	1×10^{-7}*	0.04	9
7	*JAZF1*	7p15.1	rs864745	C	Intron	64 388	0.5	0.32	0.07	2×10^{-6}	0.04	0	0.03	0.01	1×10^{-6}*	0.04	0
8	*CDK6*	7q21.2	rs2282978	C	Intron	64 424	0.4	0.39	0.07	2×10^{-8}*	0.05	0	0.03	0.01	5×10^{-8}*	0.05	6
9	*SYNPO2L*	10q22.2	rs3812629	A	Missense	64 423	0.2	0.47	0.09	4×10^{-7}*	0.04	0	0.04	0.01	7×10^{-7}*	0.04	0
10	*SOX5*	12p12.1	rs17287293	A	Intergenic	64 429	0.9	0.49	0.10	3×10^{-7}*	0.04	0	0.04	0.01	3×10^{-7}*	0.04	0
11	*HMGA2*	12q14.3	rs8756	C	3′-UTR	64 418	0.5	0.33	0.07	7×10^{-7}*	0.04	0	0.03	0.01	5×10^{-7}*	0.04	0
12	*RPL3L*‡	16p13.3	rs113956264	C	Missense	64 403	0.97	0.99	0.20	1×10^{-6}*	0.04	0	0.08	0.02	4×10^{-6}	0.03	10
13	*GOSR2*	17q21.32	rs17608766	C	Intron	64 435	0.1	0.80	0.10	9×10^{-15}*	0.09	0	0.07	0.01	1×10^{-15}*	0.10	0
14	*MC4R*	18q21.32	rs12970134	A	Intergenic	64 430	0.3	0.38	0.08	1×10^{-6}*	0.04	0	0.03	0.01	7×10^{-6}	0.03	0
Previously reported loci																	
15	*CAND2*	3p25.2	rs11718898	T	Missense	52 472	0.3	0.39	0.08	9×10^{-7}*	0.05	0	0.03	0.01	8×10^{-7}	0.05	0
	CAND2	3p25.2	rs3732675	T	Missense	64 395	0.4	0.34	0.07	1×10^{-6}	0.04	0	0.03	0.01	3×10^{-7}*	0.04	0
16	*SCN10A*	3p22.2	rs6800541	C	Intron	64 423	0.4	1.18	0.07	4×10^{-63}*	0.44	51	0.10	0.01	2×10^{-65}*	0.45	45
17	*HCN1*	5p12	rs6892594	T	Intron	64 427	0.4	0.43	0.07	2×10^{-10}*	0.06	0	0.04	0.01	3×10^{-10}*	0.06	0
18	*CAV1*	7q31.2	rs3807989	A	Intron	64 430	0.4	0.47	0.07	2×10^{-12}*	0.08	0	0.04	0.01	8×10^{-13}*	0.08	0
19	*FADS1*	11q12.2	rs174546	C	3′-UTR	64 430	0.7	0.50	0.07	2×10^{-11}*	0.07	9	0.04	0.01	6×10^{-12}*	0.07	9
20	*TBX5*	12q24.21	rs883079	C	3′-UTR	64 435	0.3	0.80	0.07	9×10^{-28}*	0.19	17	0.07	0.01	6×10^{-29}*	0.19	11
21	*MYH6*	14q11.2	rs452036	A	Intron	64 422	0.4	0.68	0.07	8×10^{-23}*	0.15	0	0.06	0.01	1×10^{-23}*	0.16	0

Beta indicates the changes of (inverse normal transformed) P-wave duration residuals per 1 effect allele increment; EA, effect allele; EAF, effect allele frequency; h^2, SNP heritability estimate; N, sample size; and UTR, untranslated region.

*P values at exome-wide significance.

†Locus with minor allele frequency <5% is also identified from gene-based analysis.

‡Locus with minor allele frequency <5% identified from gene-based analysis.

(*JAZF1*, $P=1\times10^{-6}$; Table 2; Table IV in the Data Supplement). The PWD variance explained by each of the top variants ranged from 0.04% to 0.44%; the top variants in aggregate explained ≈1.6% of the phenotypic variance. Associations for *SCN10A* and *PITX2* regions were moderately heterogeneous across individual studies (I^2 ≥45%; Table 2). Of these 19 multiethnic significantly associated loci, 13 were significantly associated with PWD residuals in the European ancestry subset, and one (*SCN10A*) was observed in individuals of African ancestry (Table IV in the Data Supplement). No additional loci were observed in analyses restricted to either European or African ancestry (Figure IV in the Data Supplement for Manhattan plots).

In conditional analyses, we identified additional signals from *SCN5A* and *SCN10A* (Table V in the Data Supplement). For inverse normal transformed PWD residuals, an additional signal (rs10033464, $P=2\times10^{-7}$) was observed in the *PITX2* region. In addition to the 7 previously known loci that exceeded exome-wide significance, we observed 2 nominally significant associations with PWD at *SSBP3* and *EPAS1* ($P<0.001$; Table VI in the Data Supplement).[10]

GENE-BASED ANALYSES

We performed burden and sequence kernel association tests for associations with PWD for 16949 genes with a cumulative minor allele count ≥10, including 192455 low-frequency and rare variants, in the multiethnic sample. We identified 4 genes associated with PWD using sequence kernel association tests aggregating functional variants with MAF <5% (*TTN*, $P=6\times10^{-27}$; *DLEC1*, $P=2\times10^{-13}$; *SCN10A*, $P=7\times10^{-8}$; and *RPL3L*, $P=9\times10^{-7}$; Table 3). We identified an additional association (*TTC21A*, $P=1\times10^{-6}$) using inverse normal transformed PWD residuals in the European-specific analysis. Using burden tests, we identified *TTN* and *MUC5B* as PWD-associated genes in the multiethnic and European-specific analyses. We did not observe any significant associations for variants with MAF <1%, suggesting that identified associations were mainly driven by low-frequency, not rare, variants. Among these significant genes, we identified 2 additional low-frequency missense variants exceeding exome-wide significance for association (*DLEC1*, rs116202356, Glu264Lys, $P=2\times10^{-10}$; *RPL3L*, rs113956264, Val262Met, $P=1\times10^{-6}$; Table 2), which were not reported in our single variant tests.

EXPRESSION QUANTITATIVE TRAIT LOCUS ANALYSES BETWEEN GENES AT PWD LOCI AND GENE EXPRESSION

We assessed expression quantitative trait locus associations for top variants and proxies (linkage disequilibrium: $r^2>0.8$; 1000 Genomes: phase 3 version 5, all individuals from LDlink[13]) in 2 heart tissues from GTEx version 7 (right atrial appendage [RAA] and left ventricle [LV]; Table VII in the Data Supplement).[14] Six loci were associated with significant changes in gene expression, especially in the RAA, including 2 known PWD loci (*HCN1*, *FADS1)* and 4 novel loci (*TTN, TCF21*, *JAZF1*, *SYNPO2L*; Table VII in the Data Supplement). The alleles associated with longer PWD at *HCN1* and *SYNPO2L* had lower expression of these genes in RAA tissues. In contrast, alleles at the *JAZF1* and *FADS1* loci were associated with higher gene expression in the RAA and LV, respectively. Gene expression directionality was consistent across RAA and LV tissues. Expression level changes of *JAZF1* and *MYOZ1* per allele in RAA tissue were significantly higher than in the LV. We observed more significant

Table 3. Top Gene in Low-Frequency Variant Gene-Based Analyses of P-Wave Duration Stratified by Ancestral Group

	Multiethnic				European				African			
			Residuals	Inverse Normal Transformed Residuals			Residuals	Inverse Normal Transformed Residuals			Residuals	Inverse Normal Transformed Residuals
Gene	Var No.	cMAC	*P* Value	*P* Value	Var No.	cMAC	*P* Value	*P* Value	Var No.	cMAC	*P* Value	*P* Value
SKAT												
TTN	775	276986	5×10^{-27}*	5×10^{-26}*	704	215801	5×10^{-27}*	1×10^{-26}*	536	23041	0.59	0.71
DLEC1	57	10419	2×10^{-13}*	2×10^{-13}*	55	6937	2×10^{-12}*	3×10^{-12}*	39	2568	0.70	0.73
TTC21A	37	12207	1×10^{-5}	5×10^{-6}	32	10900	4×10^{-6}	1×10^{-6}*	28	1250	0.98	0.98
SCN10A	61	16550	7×10^{-8}*	9×10^{-9}*	47	12804	2×10^{-7}*	4×10^{-8}*	34	524	0.84	0.81
RPL3L	26	8510	1×10^{-6}*	4×10^{-6}	25	6742	2×10^{-6}*	1×10^{-5}	18	265	0.33	0.21
Burden												
TTN	775	276986	1×10^{-14}*	8×10^{-14}*	704	215801	1×10^{-20}*	4×10^{-18}*	536	23041	0.26	0.27
MUC5B	68	36414	7×10^{-6}*	1×10^{-5}	63	25110	3×10^{-6}*	6×10^{-6}	58	2846	0.59	0.56

cMAC indicates cumulative minor allele count; SKAT, sequence kernel association test; and Var no., number of variants included in the gene set.

*P values that exceed the exome-wide significance threshold ($P<3.0\times10^{-6}$, 3.1×10^{-6}, and 3.5×10^{-6} for individuals of multiethnic, European, and African ancestries, respectively).

expressions quantitative trait locus in the RAA than the LV, as expected, because PWD reflects atrial conduction.

RELATION OF THE PWD WITH ECG TRAITS IDENTIFIES 4 NOVEL AND 5 KNOWN LOCI

We examined associations between PWD loci and other ECG measurements from large-scale association studies (Table VIII in the Data Supplement). We identified 8 novel (*TTN*, *DLEC1*, *ARHGAP10*, *JAZF1*, *SYNPO2L*, *SOX5*, *HMGA2*, *GOSR2*) and 5 known (*SCN10A*, *CAV1*, *FADS1*, *TBX5, MYH6)* PWD loci, all previously reported to be associated with PR interval, PR segment, QRS duration, QT interval, or RR interval. Variants at *TCF21*, *SYNPO2L*, and *MYH6* were associated with PR interval in recent large-scale genetic association studies,[15–17] but the top variants in our PWD analysis were in low to moderate linkage disequilibrium with top variants from these earlier analyses (linkage disequilibrium, r^2<0.8; 1000 Genomes: phase 3 version 5, all individuals).

OVERLAP BETWEEN PWD LOCI AND AF

Fourteen PWD loci were associated with AF risk in a recent AF genome-wide association studies[18] (P<0.0024=0.05/21 loci; Figure 1 and Table VIII in the Data Supplement). Two loci in well-known AF gene regions, *PITX2* and *TTN,* were novel PWD loci. Among these 14 loci, 6 were associated with longer PWD and higher AF risk (*TTN*, *TCF21*, *SOX5*, *GOSR2*, *MC4R*, *MYH6*), whereas 8 were associated with longer PWD but lower AF risk (*DLEC1*, *PITX2*, *CDK6*, *SYNPO2L*, *CAND2*, *SCN10A*, *CAV1*, *TBX5*).

DISCUSSION

In a multiancestry study comprising ≈65 000 individuals, we identified 12 novel and 7 previously reported loci related to PWD in a meta-analysis of common exome-chip variants. After aggregating rare and low-frequency exonic variants, we identified 6 genes, including 2 additional low-frequency variants potentially related to PWD, and loci with specific patterns of association for PWD and AF risk. These findings suggest that AF may result from multiple genetic mechanisms, and PWD may be an endophenotype for these mechanisms.

Our study extends the literature on the genetic components underlying atrial conduction, and the relationship between PWD and AF risk. In comparison to earlier genetic association studies of PWD,[10,11] we predominantly focused on genetic variants in coding regions (Table 2). In total, we identified 21 common variant loci related to PWD. The top common variants explain ≈1.6% of the phenotypic variance in PWD. Our gene-based

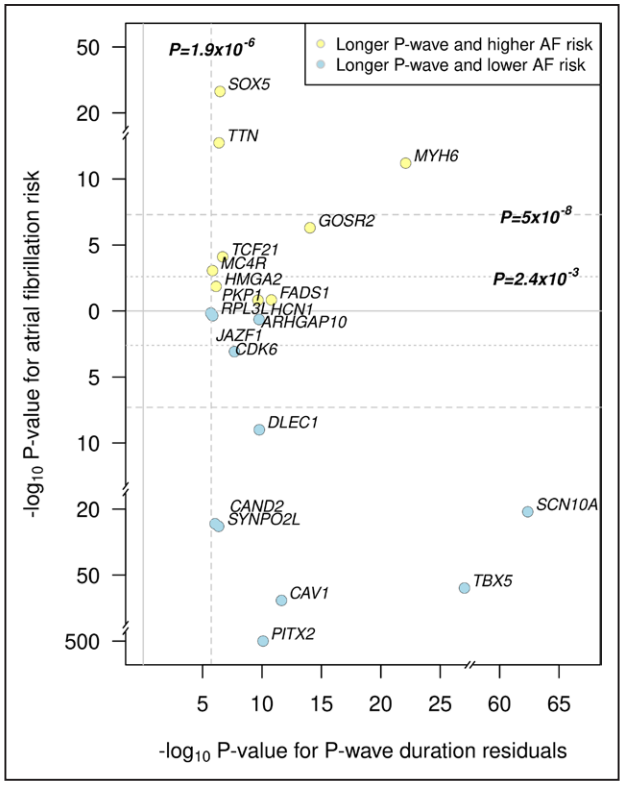

Figure 1. P-wave duration (PWD) loci and atrial fibrillation (AF) risk.
The *x* axis represents the association between the top PWD loci and PWD in $-\log_{10}$ scale. The *y* axis represents the association *P* value between the top PWD loci and AF risk ($-\log_{10}$ scale). Variants above y=0 refer to loci associated with longer PWD and higher AF risk (colored in yellow). Variants below *y*=0 refer to loci associated with longer PWD but lower AF risk (colored in blue). Displayed results are from the multiethnic meta-analysis of PWD residuals. Associations with AF were derived from a recent AF genome-wide association studies.[18] Dashed lines show the significance threshold for the current exome-wide analysis (vertical; $P<1.9\times10^{-6}$) and for prior genome-wide analyses of AF (horizontal; $P<5\times10^{-8}$). The dotted line represents the significance cutoff after Bonferroni correction (horizontal; $P<2.4\times10^{-3}$=0.05/21 PWD loci).

analyses also highlight the importance of low-frequency variants contributing to PWD in genes, such as *TTN*, *SCN10A*, and *RPL3L.*

Our findings have 2 major implications. First, associated loci span genes involved in the development and maintenance of adult cardiac tissue (*PITX2*, *TCF21*, *HMGA2*, *NKX2-5*, *TBX5, CAND2*, *CDK6*), muscle and sarcomere structure (*TTN*, *SYNPO2L*, *SOX5*, *MYH6, RPL3L*), ion channel function (*HCN1, SCN10A*), and cell-cell contact (*PKP1*, *ARHGAP10*, *CAV1*). We additionally noted several genes with a role in metabolism (*JAZF1*, *CDK6*, *HMGA2*, *MC4R*) though the connection to AF is less clear.[19–22] The transcription factor *PITX2* is the top susceptibility locus for AF. Decreased *Pitx2* expression in the adult left atrium is associated with AF in humans,[23] and abnormal cardiac conduction, and low-voltage P-waves in knockout mice.[24] *PITX2* is activated

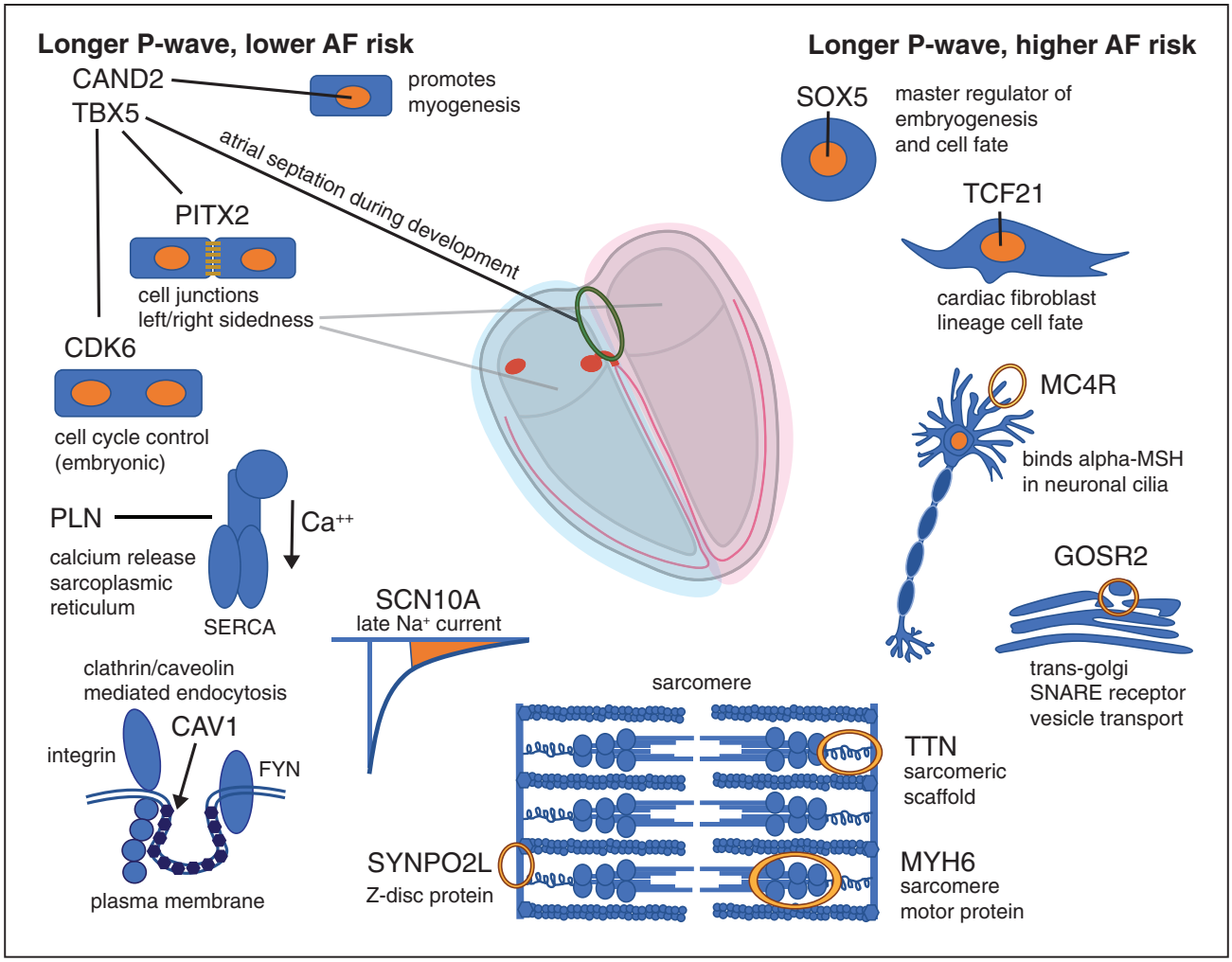

Figure 2. Identified P-wave duration (PWD) associated genes highlight multiple biological pathways for atrial fibrillation (AF) risk.

Genes with increasing risk of AF coupled with prolonged PWD are listed at the **right**. Genes with decreasing risk of AF coupled with prolonged PWD are listed at the **left**. Each gene is accompanied by a diagram representing the biological function of the gene, indicating how the gene may affect PWD.

by *TBX5* to coregulate many membrane effector genes (such as *SCN5A*, *GJA5*, and *RYR2*). Reduction of *Tbx5* expression in a mouse model decreased myocardial automaticity.[25] *TCF21* is a transcription factor required during embryogenesis for formation of heart tissue and is involved in fibroblast generation after injury in adults.[26] The nuclear scaffolding protein *HMGA2* trans-activates the heart-specific transcription factor *NKX2-5*.[27] *HMGA* overexpression in mice mediates the response to pressure-overload induced cardiac remodeling.[28] *CAND2* suppresses myogenin degradation and directs cardiac progenitor cells towards a myocyte fate.[29]

Titin (*TTN*) is a major structural component of the sarcomere, required for contractile function in cardiomyocytes. Loss of function mutations in *TTN* are associated with early-onset AF[30] and dilated cardiomyopathy.[31] cytoskeletal heart-enriched actin-associated protein; aka *SYNPO2L* is a Z-disc protein; zebrafish knockdown models display hypertrophy and delayed conduction,[32] and the locus has been associated with AF in genome-wide association studies.[18] *SOX5* is a master regulator of cell fate in embryonic development.[33] In drosophila, *SOX5* knockdown results in decreased heart rate and increased cardiac wall thickness.[34] *MYH6*, specifically expressed in the atria, forms the thick filament in cardiac smooth muscle; mutations are associated with cardiomyopathies,[35] sinus node dysfunction,[36] and congenital heart disease.[37] Some identified genes are important for atrial conduction, including *HCN1*[38] and *SCN10A*[39] which govern potassium, and late sodium channel currents, respectively. The proteins *ARHGAP10*,[40] *PKP1*,[41] and *CAV1*,[42] are involved in cell-cell contact and are necessary for efficient signal conduction. The ribosomal protein RPL3L is specifically expressed in skeletal muscle and heart; coding variants in this gene are associated with AF.[43]

Second, our study implicates PWD as a powerful endophenotype for understanding the biological mechanisms of AF. Fifteen loci identified in our study were associated

with AF risk in a recent AF genome-wide association studies,[18] underscoring the genetic correlation between atrial conduction and AF risk. Epidemiological data indicate that PWD variability is associated with AF risk,[2,3] AF recurrence after cardioversion,[44] and ablation,[45] as well as ischemic stroke.[46] Generally, we observed that top variants at known sarcomere genes (eg, *TTN, MYH6*) were associated with increased PWD and increased AF risk, implicating atrial myopathic pathways in AF susceptibility. We speculate that myopathic pathways predispose individuals to AF via delayed conduction velocity, increased propensity for reentry, and susceptibility to ectopic atrial activity. Similarly, *TCF21* and *SOX5* are 2 transcription factors associated with increased PWD and increased AF risk.

In contrast, top variants at *SCN10A* were associated with increased PWD but reduced AF risk. Other PWD-associated genes, such as *PITX2*, *CAND2, TBX5*, and *CDK6*, contained variants associated with longer PWD and reduced AF risk. The directionality of gene associations observed for PWD and AF risk underscore the complexity of AF susceptibility while highlighting the potential to leverage PWD to elucidate AF-specific pathways (Figure 2). Whether studying PWD can lead to insights relevant to therapeutic targeting remains unclear.

Our results should be interpreted within the context of our study design. First, the majority of our sample consisted of individuals of European ancestry and may have limited generalizability to non-European ancestries. Studies with broader ethnic/racial diversity are warranted. Second, top variants identified in our study may not directly modulate PWD, a limitation of most genetic association studies. Biological characterization of loci is needed to conclusively link variants to function. Third, ascertainment of rare variation is limited using the exome-chip, and future analyses of sequence data are warranted. Fourth, despite a relatively large sample, our findings explained a small proportion of phenotypic variance. Because the additive SNP-based heritability of PWD has been estimated to be as high as 19%,[8] our results highlight the fact that much of the genetic susceptibility to PWD remains unexplained. Larger samples, genome-wide assessments, and examination of rare variation may be necessary to identify additional loci for PWD.

In conclusion, we identified 14 novel loci in common and low-frequency variant analyses and 6 gene regions in a low-frequency variant analysis for PWD. Our findings highlight the shared genetic components of atrial conduction and AF risk and illustrate the diverse biological pathways affecting atrial conduction and mechanisms leading to AF.

ARTICLE INFORMATION

Received December 5, 2019; accepted July 27, 2020.

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Acknowledgments

Complete acknowledgments by study are available in the Data Supplement. The Genotype-Tissue Expression (GTEx) Project was supported by the Common Fund of the Office of the Director of the National Institutes of Health, and by National Cancer Institute, National Human Genome Research Institute, National Heart, Lung, and Blood Institute, National Institute on Drug Abuse, National Institute of Mental Health, and National Institute of Neurological Disorders and Stroke. The data used for the analyses described in this article were obtained from the GTEx Portal on October 05, 2018 and January 25, 2020.

Sources of Funding

Dr Weng is supported by an American Heart Association (AHA) Postdoctoral Fellowship Award (17POST33660226). This work was supported by an AHA Strategically Focused Research Networks (SFRN) postdoctoral fellowship to Drs. Weng and Hall (18SFRN34110082). Funded in part by training grant (National Institute of General Medical Sciences) 5T32GM07814 (Dr Bihlmeyer) and R01HL116747 (Drs Arking and Bihlmeyer), and R01 HL111089 (Dr Arking). This material is based on work supported by the National Science Foundation Graduate Research Fellowship under Grant No. DGE-1232825 (Dr Bihlmeyer). Any opinion, findings, and conclusions or recommendations expressed in this material are those of the authors(s) and do not necessarily reflect the views of the National Science Foundation. Additional support was provided by AHA grant 16EIA26410001 (Dr Alonso) and National, Heart, Lung and Blood Institute grant K24HL148521 (Dr Alonso). Dr Ramírez was supported by Medical Research Council grant MR/N025083/1, by the People Programme (Marie Curie Actions) of the European Union's Seventh Framework Programme (FP7/2007-2013) under REA grant agreement no. 608765 and from the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement No 786833. Dr Sotoodehnia is supported by the following grants from the National Institutes of Health (NIH): R01HL141989, HL116747, and R01 HL111089, and by the Laughlin Family Fund. Dr Kornej was supported by the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement No 838259. Dr Benjamin is supported by NIH grants HHSN26818HV00006R; 75N92019D00031; R01HL092577; 1R01HL128914; and American Heart Association 18SFRN34110082. Dr Lunetta is supported by R01 HL092577, AHA 18SFRN34230127, and 18SFRN34150007. Dr Ellinor is supported by the Fondation Leducq (14CVD01), by grants from the NIH (1RO1HL092577, R01HL128914, K24HL105780), and by a grant from the AHA (18SFRN34110082). Dr Lubitz is supported by NIH grant 1R01HL139731 and AHA 18SFRN34250007. Additional funding and acknowledgments for each participating study are provided in the Data Supplement.

Disclosures

Dr Lubitz receives sponsored research support from Bristol-Myers Squibb / Pfizer, Bayer AG, and Boehringer Ingelheim, and has consulted for Bristol Myers Squibb / Pfizer and Bayer AG. Dr Ellinor is supported by a grant from Bayer AG to the Broad Institute focused on the genetics and therapeutics of cardiovascular diseases. Dr Ellinor has also served on advisory boards or consulted for Bayer AG, Quest Diagnostics, Novartis, and MyoKardia. Dr Mook-Kanamori is a part-time clinical research consultant for Metabolon, Inc. The UMCG, which employs Dr de Boer, has received research grants or fees from AstraZeneca, Abbott, Bristol-Myers Squibb, Novartis, Novo Nordisk, and Roche. Dr de Boer received personal fees from Abbott, AstraZeneca, MandalMed, Inc, Novartis, and Roche. Psaty serves on the Steering Committee of the Yale Open Data Access Project funded by Johnson & Johnson.

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