**NET silencing by let-7i in postural tachycardia syndrome**

Abdul Waheed Khan,1,2,3 Mark Ziemann,1,2 Susan J. Corcoran,2 Harikrishnan K.N.,1,2,3 Jun Okabe,1,2 Haloom Rafehi,1,2 Scott S. Maxwell,1,2 Murray D. Esler,2 and Assam El-Osta1,2,3,4

1Central Clinical School, Faculty of Medicine, Monash University, Victoria, Australia. 2Baker IDI Heart and Diabetes Institute, The Alfred Medical Research and Education Precinct, Melbourne, Victoria, Australia. 3Department of Pathology, The University of Melbourne, Parkville, Victoria, Australia. 4Hong Kong Institute of Diabetes and Obesity, Prince of Wales Hospital, The Chinese University of Hong Kong, Hong Kong, China.

**Introduction**

Postural tachycardia syndrome (POTS) is an autonomic disorder that presents with tachycardia, lightheadedness, and sometimes syncope on standing. While the etiology remains largely unknown, faulty neuronal reuptake of the sympathetic nervous system signaling neurotransmitter norepinephrine (NE) has been implicated (1). Augmented NE signaling due to impaired transmitter reuptake has been reported not only in POTS, but additionally in anxiety disorders (2), depression (3), and essential hypertension (4).

The action of NE is terminated, in part, by its uptake into presynaptic noradrenergic neurons by the plasma-membrane NE transporter (NET), which is encoded by the \( \text{SLC6A2} \) gene, abbreviated as \( \text{NET} \). The effectiveness of NE reuptake relies on the capacity of the NET to tightly recapture NE released by sympathetic nerves, this being approximately 90% for the heart (5). While the dramatic phenotypic effects observed in one kindred family has been located to a specific point mutation in the \( \text{NET} \) gene responsible for impaired NET function (1), extensive genotyping studies have found nominal single-nucleotide polymorphism association with POTS (6). A likely explanation is that interindividual variation in \( \text{NET} \) function is common, and in light of the clinical importance of the transporter’s central role in NE regulation, rather than querying genetic variation, we investigated gene-environment interactions, asking which biological processes might be prime targets for \( \text{NET} \) gene regulation.

The first glimpse into epigenetic regulation of the \( \text{NET} \) came from ex vivo studies in depolarized neuronal cortical cells (7). Activation of \( \text{NET} \) expression in depolarized cells is tightly linked with the dissociation of the SMARCA2-methyl-CpG-binding protein 2 (MeCP2) corepressor complex (8). In a search for a molecular basis of regulation, extensive CpG methylation analyses using bisulfite sequencing confirm that \( \text{NET} \) gene methylation is unremarkable (7). \( \text{NET} \) activation involves hyperacetylation of histone H3 lysines 9 and 14 (H3K9/14ac) and is correlated with methylation of histone H3 lysine 9 (H3K9me3). Furthermore, dissociation of the MeCP2 corepressor complex is inversely correlated with increased histone acetylation. Subsequent human studies revealed that \( \text{NET} \) expression was indeed subject to epigenetic modification in POTS (6). While we are beginning to understand the epigenetic modifications that regulate gene expression, we still do not know the molecular machineries that target \( \text{NET} \) for reactivation. Given the biological complexity of transcriptional control, we hypothesized that the chromatin state relates to the ability of the \( \text{NET} \) promoter to perceive MeCP2 binding (9). In this context, we developed a potentially novel RNA of isolated chromatin (RICh) assay using locked nucleic acid (LNA) probes designed to target the human \( \text{NET} \) promoter. The purpose of this study was to investigate \( \text{NET} \) gene silencing with the specific aim to...
reactivate expression. We show that MeCP2 binding on the NET gene is mediated by the noncoding RNA (ncRNA), let-7i, and that NET expression is subject to pharmacological histone deacetylase (HDAC) inhibition, restoring specific epigenetic modifications associated with expression in POTS participants.

**Results**

Disambigous capture of NET-interacting RNAs. To investigate the altered chromatin state of the NET we developed a RICH assay followed by massive parallel sequencing (RICH-seq) method to isolate interacting RNAs (Figure 1A). Three specific LNA probes were designed against the human NET promoter aided by the ENCODE project dataset including transcription factor binding sites, chromatin accessibility, and active histone marks (Supplemental Figure 1; supplemental material available online with this article; https://doi.org/10.1172/jci.insight.90183DS1). LNA probes were designed to capture an almost 1.2-kbp region of the human NET promoter (Figure 1B). In experiments used to optimize assay conditions, single-strand LNA probes were assessed for soluble-chromatin pulldown (Figure 1C). Scrambled-sequence probes were used to assess the specificity of LNA-chromatin hybrids. NET-associated RNAs were captured using streptavidin beads and purified RNA was used in the library constructions for massive parallel sequencing. Detection of the NET promoter using quantitative PCR (qPCR) from RICH-captured DNA shows the specificity of the LNA probes (Figure 1, D–F) as well as regional specificity of the probe against exon 5 of the NET gene (Figure 1G). RICH-seq generated 1.2 million reads for the specific NET probes, 2.5 million reads for input control, and 0.5 million for the scrambled control (Supplemental Table 1). RNA species enriched by the NET probes were determined for 2 control groups: (a) total chromatin RNAs, and (b) scrambled-sequence probe–bound RNAs. We identified 18 RNAs at the NET promoter compared with the input control, and 9 enriched RNAs when compared with the scrambled-probe control (Figure 2A). RNA species interacting with the NET promoter include protein-coding and ncRNAs such as miRNA, small nucleolar RNA (snoRNA), and small nuclear RNA (snRNA) (Figure 2B). K-means clustering of RNAs associated with the NET promoter identified 6 strongly enriched genes (see cluster 2, Figure 2C). Of the 6, five RNAs (MIRLET7I [let-7i], SCARN4A, SNORA66, SNORD96, and TUFM) were significantly enriched using the NET probe in both groups (FDR < 0.05, as shown in cluster 2 of Figure 2C and summarized in Supplemental Table 2). Taken together, these results suggest that the RICH technique using LNA probes can selectively capture chromatinized NET-associated RNAs.

Chromatinization of NET involves MeCP2 and let-7i interactions in POTS. Having identified NET-interacting transcripts, we investigated the expression of specific RNAs in a case and control cohort. The case group included 12 participants with POTS (9 females, 3 males) that underwent exhaustive medical evaluation to exclude any other relevant medical condition. They share the common clinical characteristics central to the diagnosis: recurrent episodes of presyncope while standing, freedom from postural hypotension despite the presence of postural dizziness, and the presence of posture-related tachycardia (10). The healthy reference group had none of these symptoms in the 12 participants (9 females, 3 males). The characteristics of these 24 participants are summarized in Table 1.

Since the NET gene has been implicated in the pathophysiology of participants matched with POTS, we assessed expression in leukocytes compared with other cell types. Interestingly, NET gene expression was inversely regulated with let-7i RNA expression (Supplemental Figure 2). Of the 5 RNA transcripts detected by RICH-seq, let-7i was significantly increased (P < 0.01) in the POTS group (Figure 3A). RNA hybrid prediction identified 3 let-7i consensus binding sites, which were validated by RICH at the NET promoter (Supplemental Figure 3). To exclude the possibility that the let-7i interaction is a result of nonspecific binding, we assessed LNA probes with scrambled sequences using the RICH protocol. We observed no change in let-7i binding at the NET promoter using scrambled LNA probes. Chromatin from the POTS group was significantly enriched for let-7i (P < 0.01), consistent with binding at the NET promoter (Figure 3B). These experimental results indicate that in leukocytes the NET promoter is subject to let-7i–mediated chromatin interaction.

Because MeCP2 is implicated in NET silencing but of unknown binding function (6), we next assessed physical interaction with let-7i. Soluble chromatin fractions were prepared from healthy and POTS participants and RNA immunopurifications (RIPs) were performed with an antibody that specifically recognizes the MeCP2 epitope. To exclude the possibility of indirect MeCP2 binding, RIPs were performed with IgG control antibody. Chromatin derived from POTS participants was significantly enriched for let-7i with MeCP2 (P < 0.01, Figure 3C). Furthermore, ChIP experiments confirm that MeCP2 interacts with the NET promoter at the same sites the LNA probes were designed to capture.
Supplemental Figure 4, A–C). Taken together, these results show increased MeCP2 and let-7i chromatin interaction in leukocytes derived from POTS participants.

RNA-dependent MeCP2 binding on NET. Having demonstrated that MeCP2 and let-7i are associated with NET, we investigated the effect of MeCP2 loss on NET-mediated transcription using lentivirus shRNA. Because lentiviral transduction of primary untransformed leukocytes is notoriously difficult (11), we performed MeCP2 knockdown (KD) using nonprimary immortalized cells (Figure 4A). NET expression was significantly increased in MeCP2 KD cells ($P < 0.01$ Figure 4B). Since MeCP2 interacts with chromatin...
and also RNA-dependent protein complexes with high affinity (12), we hypothesized that NET silencing by MeCP2 is mediated by chromatin interaction with let-7i. To assess the specificity of MeCP2 binding to the NET promoter, ChIP assays were performed with MeCP2 antibody and association with the NET promoter assessed by qPCR. As shown in Figure 4C, chromatin was significantly enriched for MeCP2. To address the possibility that recruitment of MeCP2 on NET is subject to RNA-mediated interactions we devised a ChIP-RNase technique (Figure 4D). In this assay, soluble MeCP2-associated chromatin was subject to endoribonuclease A (RNase A), which catalyzes the cleavage of single-strand RNA molecules. Soluble chromatin not exposed to RNase A degradation was significantly enriched for MeCP2 on the NET promoter when compared with IgG antibody controls. Furthermore, MeCP2 binding at the NET promoter was significantly reduced in RNase-treated chromatin (Figure 4E). The ChIP-RNase results support the notion that MeCP2 localization on NET chromatin is dependent on RNA. To confirm that the loss of MeCP2 binding following RNAse was specific for the NET promoter, we assessed known MeCP2 target genes such as IL-6 (IL6), which is suppressed by MeCP2 binding (13). In ChIP assays we recovered IL6 DNA equally well from –RNAse and +RNAse chromatin isolates using MeCP2 antibody (Figure 4F). These results suggest that NET is subject to RNA-dependent MeCP2 interactions.

Vorinostat restores let-7i–mediated NET silencing. MeCP2 resides in a co-repressor complex with HDAC activity (14), and vorinostat (suberoylanilide hydroxamic acid or SAHA) has been approved by the FDA for the treatment of hematological malignancies and is currently being evaluated for other diseases (15). Using human leukocytes isolated from healthy and POTS participants, we developed an experimental assay to test NET reactivation because there are no comparative ex vivo models or human studies to assess the efficacy of therapies directly in POTS. Leukocytes stimulated with the paradigmatic HDAC inhibitor trichostatin A (TSA) show increased NET expression when assessed by quantitative reverse transcription PCR (qRT-PCR) (Supplemental Figure 5, A–C). Next, we investigated whether ex vivo treatment using single-dose exposure to 2 μM vorinostat could reactivate NET expression. Treatment of leukocytes derived from POTS participants with vorinostat caused a dramatic upregulation of NET expression (Figure 5A). To exclude the possibility that increased NET expression occurs as a result of ex vivo maintenance of human leukocytes in primary conditions, we examined genes that are relevant to leukocyte response and regulated by vorinostat. TNFSF9 is a member of the TNF (ligand) superfamily and is induced by pharmacological HDAC inhibition (16). TP53

![Figure 2. RICH-seq identifies NET promoter–specific RNAs.](http://insight.jci.org)
Table 1. Demographic data of healthy and postural tachycardia syndrome (POTS) groups, and head-up tilt (HUT)\(^a\) results for the POTS cohort

<table>
<thead>
<tr>
<th></th>
<th>Controls</th>
<th>POTS</th>
<th>(P)</th>
</tr>
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<tbody>
<tr>
<td>Sex, F/M</td>
<td>9/3</td>
<td>9/3</td>
<td>0.84</td>
</tr>
<tr>
<td>Age, y</td>
<td>32 ± 3</td>
<td>32 ± 3</td>
<td>0.93</td>
</tr>
<tr>
<td>Height, m</td>
<td>1.72 ± 0.06</td>
<td>1.72 ± 0.04</td>
<td>0.93</td>
</tr>
<tr>
<td>Weight, kg</td>
<td>62 ± 3</td>
<td>81 ± 7</td>
<td>0.001</td>
</tr>
<tr>
<td>BMI</td>
<td>21 ± 1</td>
<td>26 ± 2</td>
<td>0.006</td>
</tr>
<tr>
<td>Supine SBP, mmHg</td>
<td>127 ± 3</td>
<td></td>
<td></td>
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<tr>
<td>Supine DBP, mmHg</td>
<td>67 ± 2</td>
<td></td>
<td></td>
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<tr>
<td>Supine HR, bpm</td>
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<tr>
<td>End HUT SBP, mmHg</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>End HUT DBP, mmHg</td>
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<td></td>
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<tr>
<td>End HUT HR, bpm</td>
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<tr>
<td>(\Delta)HR, bpm</td>
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<tr>
<td>Supine Total NE spillover, ng/min</td>
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<tr>
<td>Supine MSNA, bursts per min (n = 7)</td>
<td>21 ± 4</td>
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<tr>
<td>End HUT Total NE spillover, ng/min</td>
<td>801 ± 79</td>
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<tr>
<td>End HUT MSNA, bursts per min (n = 4)</td>
<td>35 ± 6</td>
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\(^{a}\)The healthy reference population did not undergo HUT testing. \(P\) values determined by Student’s \(t\) test. SBP, systolic blood pressure; DBP, diastolic blood pressure; HR, heart rate; NE, norepinephrine; MSNA, muscle sympathetic nerve activity; bpm, beats per minute; F, female; M, male; y, years. All results expressed as mean ± SEM.

is a protein-coding gene that acts as a tumor suppressor and is suppressed by vorinostat treatment (17). The expression of \(TNFSF9\) increased (Figure 5B) and \(TP53\) decreased (Figure 5C) in cells stimulated by vorinostat. Taken together, the results of our preclinical investigation of an epigenetic mechanism indicate \(NET\) reactivation using pharmacological HDAC inhibitors in leukocytes derived from POTS participants.

**Discussion**

It is probable that the faulty neuronal reuptake of the sympathetic transmitter we describe is responsible for key clinical manifestations of POTS. The diagnostic supranormal increase in heart rate with standing most probably derives from augmentation of the reflex increase in the sympathetic outflow to the heart with standing. The disposition of NE after release from sympathetic nerves is more dependent on neuronal reuptake in the heart than in all other organs. Persistence of NE in the synaptic space of the cardiac sympathetic nerves, and inappropriate tachycardia, would be a consequence of a neuronal NE reuptake defect.

POTS is characterized by postural syncope, but surprisingly without postural hypotension. The mechanism of the syncope is a pronounced reflex fall in cerebral blood flow on standing (18). As for the postural tachycardia, the probable cause is augmentation of a reflex sympathetic response to posture, this time in the cerebral blood vessels, by impaired neuronal reuptake of NE in POTS patients. Despite previous disagreement on this point, the human cerebral blood vessels have been demonstrated to have a functional sympathetic innervation (19). The cerebrovascular sympathetic nerves in healthy subjects have demonstrable capacity for NE reuptake, and are subject to CNS regulatory control.

Recent reports suggest that ncRNA interactions can induce significant structural changes to chromatin and regulate gene transcription (20). Demonstrable evidence indicates that MeCP2 coexists with regulatory determinants that recruit HDAC activity and is thought to be functionally important in gene silencing (21). The experimental results presented here suggest that \(NET\) silencing involves an HDAC complex that is subject to pharmacological inhibition (7, 22). Indeed, this is consistent with a model in which \(NET\) chromatinization is probably mediated by MeCP2 (6). In this study, we did not observe demonstrable epigenetic changes influenced by age or gender in POTS and healthy participants.

The findings presented are potentially novel for 2 reasons. First, to our knowledge there are no reports of MeCP2 binding at unmethylated loci altering gene expression in human disease. It is commonly assumed that the dominant role of MeCP2 as a silencing determinant at CpG sites is dependent on methylation (23). While recent studies have shown that the binding preferences of MeCP2 are broader than previously described (24) and can be associated with transcriptional activation (9), no studies have implicated gene silencing with \(let-7i\). Whereas MeCP2 has been associated with silencing at unmethylated genes, the molecular connection to form that inactive chromatin conformation has been missing (25, 26). Second, and most relevant clinically, to our knowledge our study is the first to demonstrate that pharmacological HDAC inhibition can partly attenuate \(let-7i\)-mediated gene silencing by MeCP2 to reactivate \(NET\) expression.

The combination of agents often used to manage symptoms may not necessarily lend itself to accurate interpretation and influence of distinct epigenetic properties underlying chromatin modifications subject to \(let-7i\) regulation. While propranolol has been proposed to alter the expression of several miRNAs, this proposition is largely supported in small animal studies (27) and our preclinical results based on the cohort size do not support the pharmacological function of propranolol as a regulator of \(let-7i\). Neither propranolol nor atenolol predicted \(let-7i\) expression and such observations should be tested independently. While a combination of pharmacological agents is often used to treat the symptoms of POTS, which may offer yet
unforeseen synergistic benefit, further studies are warranted to better understand the underlying drug interactions that confer transcriptional control of *NET*. With the identification of miRNAs such as let-7i that participate in regulatory control with MeCP2, the challenge is now to understand their biological function and signaling interactions with specific pharmacological therapies. This remains an important area of clinical-epigenetic investigation.

MeCP2 can bind double-stranded RNA molecules (28) and a protein interaction screen has identified an RNA-dependent class of spliceosome determinants (29). The screen also identified MeCP2-associated RNA including MALAT1, a long ncRNA implicated in regulating blood vessel growth (30, 31), as well as RNCR3, which is thought to be atheroprotective (32). MeCP2 coexists in distinct complexes that support a functional role in RNA processing and transcriptional suppression (33). This lends further support to the concept that one possible role for let-7i interaction with chromatin is to lock *NET* into a silent chromatin state. Consistent with our findings, vorinostat alone does not fully reactivate silent alleles, which is in contrast to promoters that are open to histone acetylation at consensus binding sites (34). Indeed, in that same study a survey of human loci by massive parallel sequencing indicated that vorinostat significantly altered their biological function and signaling interactions with specific pharmacological therapies. This remains an important area of clinical-epigenetic investigation.

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While other transcriptional factors need to be considered with respect to regulation, our data suggest a 3-way connection with chromatin mediated by HDAC activity accompanied by let-7i and MeCP2 interaction on the *NET* gene. In this context, we posit that let-7i silencing of *NET* by MeCP2 is amenable to consequent inhibition of HDAC activity. To maximally achieve gene reactivation, it may be necessary to simultaneously block the events that are essential to the formation and maintenance of silent *NET* chromatin.
Taken together, our results indicate that pharmacological HDAC inhibition by vorinostat may represent a therapeutic strategy that merits ongoing effort to develop novel chromatin-based treatments for POTS. Furthermore, because we observe an impaired neuronal NE reuptake phenotype in essential hypertension, panic disorder, and depressive illness, clinical epigenomic studies in essential hypertension have commenced.

**Methods**

Rich-seq and LNA probe design. The NET promoter region was selected by analyzing the ENCODE data for chromatin accessibility, binding sites of transcription factors, and active histone marks (41) as illustrated in Supplemental Figure 1. Three probes were designed at Chr16 (q12.2): 55689225-55691050 (GRCh37/hg19) using Stellaris probe designer version 4.1. Replacing almost 50% of DNA nucleotides with LNA residues increased probe-chromatin interaction stability. These DNA-LNA probes were modified at their 5’ end by a Biotin-TEG-iSP18 spacer using LNA Oligo design tools; these probes were manufactured by Exiqon. A mixture of equal amounts of all 3 probes was used to capture the chromatin of interest. To verify that the NET promoter was captured specifically by NET probes, a probe with a scrambled sequence at equal concentration was included.
Probe sequences are as follows (+ represents LNA nucleotide): NET-1, 5′-A+GT+GA+CA+GACT+C TC+CAGAAC-3′; NET-2, 5′-T+GCA+CTA+CAAA+CTC+GCTA+GC-3′; NET-3, 5′-A+CA+GCA+GGAA+GT+CGAT+CTTC-3′; Scrambled, 5′-GC+GA+CA+CC+GCAA+CTA+GATTA-3′.

Soluble chromatin preparation. HeLa cells (3 × 10⁷) were crosslinked with 1% formaldehyde for 10 minutes at room temperature. Collected cell pellets were lysed in lysis buffer (1% SDS, 10 mM EDTA, and 50 mM Tris-HCl pH 8.0). Cell lysates were sonicated using a Bioruptor (Diagenode) with constant power settings. Soluble chromatin was 5-fold diluted in chromatin dilution buffer (0.01% SDS, 1.1% Triton X-100, 1.2 mM EDTA, 1 mM EGTA, 167 mM NaCl, 16.7 mM Tris-HCl pH 8.0).

Chromatin capture. M-270 streptavidin Dynabeads were washed and blocked with salmon sperm DNA in binding buffer (10 mM Tris pH 7.5, 1 mM EDTA, 1 M NaCl, 0.1% Tween 20). NET probes and scrambled probes (100 pmol) were added to 3 μg of diluted crosslinked chromatin and incubated at 95°C for 5 minutes, 37°C for 30 minutes, 72°C for 2 minutes, 37°C for 30 minutes, 72°C for 2 minutes, and 37°C for 30 minutes using a thermal cycler. Multiple reactions were performed and the captured chromatin was pooled. Hybridized biotin probe/chromatin isolates were captured with blocked streptavidin Dynabeads and reverse crosslinked with proteinase K at 62°C for 45 minutes before RNA purification. The RNAs associated with captured chromatin and input (total chromatin-bound RNA) underwent small RNA-seq library preparation with the NEBNext Small RNA Library Prep Set for Illumina and sequenced with Illumina MiSeq sequencing platform for 36 cycles with version 2 reagents.

Validation of let-7i and NET promoter interaction was performed using qRT-PCR and miScript II RT kits from Qiagen.

Bioinformatic analysis. Short reads underwent quality trimming using a quality threshold of 10 and minimum length of 18 nucleotides followed by clipping the adapter sequence with Fastx-Toolkit. Filtered reads were mapped to the human genome using STAR aligner (42). Human genome sequence and version 78 annotations were obtained from the Ensembl FTP site (43). FeatureCounts was used to count reads mapped to exons and generate the expression count matrix (44). Differential analysis was undertaken using edgeR correcting for batch variation (45). A Benjamini-Hochberg FDR-adjusted P value of less than or equal to 0.05 was considered significant. Two comparisons were undertaken: (a) NET-probe-bound versus scrambled-probe-bound and (b) NET-probe-bound versus total input RNA. The intersection of these 2 gene lists was considered candidate binders to the NET promoter. The RICH-seq results were deposited in the NCBI’s Gene Expression Omnibus (GEO GSE93235).

RIP. Soluble chromatin was prepared using micrococcal nuclease enzyme in human leukocytes. To ensure RNA integrity, only freshly prepared buffers containing RNase inhibitors were used. An antibody that recognizes the MeCP2 epitope (Sigma-Aldrich, 9317) was used in immunoprecipitation (4°C for 4 hours) to purify RNA associated with MeCP2. RNA was purified from conjugates using a Qiagen RNeasy kit. qRT-PCR and miScript II RT were used for let-7i and MeCP2 interactions.

Figure 5. Vorinostat reactivates NET expression in POTS-derived leukocytes. (A) Norepinephrine transporter (NET) expression following vorinostat stimulation of leukocytes derived from healthy and postural tachycardia syndrome (POTS) participants (n = 9). Relative expression was measured against ACTB using quantitative reverse transcription PCR (qRT-PCR). (B) TNFSF9 expression following vorinostat stimulation of leukocytes derived from healthy and POTS participants (n = 9). Relative expression was measured against ACTB using qRT-PCR. (C) TP53 expression following vorinostat stimulation of leukocytes derived from healthy and POTS participants (n = 9). Relative expression was measured against ACTB using qRT-PCR. Data are the mean ± SEM. *P ≤ 0.05 by Student’s t test.
shRNA-mediated KD strategies. The KD of MeCP2 protein in HeLa cells was achieved by MISSION shRNA-expressing lentiviral vectors (Sigma-Aldrich) specifically targeting human MeCP2 (RefSeq sequence NM_001110792). The target sequence for MeCP2 was 5'-CGTCTGCAAGGAGAGAGAT-3'. MeCP2 KD in the cells was verified by qRT-PCR with MECP2-specific primers. Cells transduced with MISSION nontarget shRNA vector served as controls.

RNase treatment of immunopurified chromatin (ChiP-RNase). Soluble chromatin was prepared with 1% formaldehyde and sonication using the Bioruptor. Immunoprecipitation was performed by incubating cross-linked chromatin with anti-MeCP2 antibody at 4°C for 4 hours. The immunopurified chromatin was subject to RNase A treatment (20 μg) in 100 μl of 1 M NaCl in Tris-EDTA (TE). Input and antibody-bound isolates were heated at 62°C for 45 minutes in elution buffer containing proteinase K and reversed crosslinked DNA was purified with a NucleoSpin Extract II Kit (Macherey-Nagel). ChiP enriched DNA sequences (± RNase A) were detected by amplification with qRT-PCR using NET-specific primers. Percentage input was calculated and results are presented as relative fold change for the target sequence compared with IgG control.

Primers used in RIch, ChiP-RNase, MeCP-KD, and RIP experiments were: NET (region 1) forward GTGCTGGGCTGTCCTGTA and reverse GGAGATGTCGGCAGGG; NET (region 2) forward GCCCTAGAGCCTGGCAAG and reverse GCCGAGTTGGCAACAGCAGCG; NET (region 3) forward AGCTGTCTGTGGTGAAGG and reverse CGACTCAGGACAGCGAGGAAG; NET (exon 5) forward AGGAAAGGTGGGAAAGAGCAT and reverse GCACAGAACACGCTGAAGTAA; IL6 forward TGCACCTTTCCCCCTAGGTT and reverse TCATGGGAAAATCCACACACCC; MECP2 mRNA forward ACTCCAGAATACACCTTGTT and reverse TTAGGGCCCTGGAGGTCTCT; NET mRNA forward ATTCCTCGAGGGGCCGAGCT and reverse ATCACAGGGAGCCGCTTGGG; TNFSF9 mRNA forward AAAATGTCTTCTGATGCTGATG and reverse CGCAGCGCTCTGATGTTA; TP53 mRNA forward ACAAGCACCCTCAAGGGGTCA and reverse TGCTGGCATTTGCACCTACCT; TUFM mRNA forward GCTGCCGCAAGATTAGGTT and reverse TGTTCTCCCTGACTTGGGAC; SCARN4 mRNA forward CAGTGAAGGCTGCTCTCC and reverse CTGGACTCCTAATCCACACCC; MECP2 KD in the cells was verified by qRT-PCR with NET-specific primers. Cells transduced with MISSION shRNA expressing lentiviral vectors (Sigma-Aldrich) specifically targeting human MeCP2 (RefSeq sequence NM_001110792). The target sequence for MeCP2 was 5'-CGTCTGCAAGGAGAGAGAT-3'. MeCP2 KD in the cells was verified by qRT-PCR with MECP2-specific primers. Cells transduced with MISSION nontarget shRNA vector served as controls.

POTS recruitment. Patients with POTS sharing the common clinical characteristics were recruited through our orthostatic intolerance clinic. Participants with POTS were taking medications including fludrocortisone, midodrine, propranolol, atenolol, pyridostigmine, topiramate, cilanopram, thyrroxine, amitriptyline, benzotropine, and dihydroergotamine. Control participants were taking no medications other than fludrocortisone, midodrine, propranolol, atenolol, pyridostigmine, topiramate, citalopram, thyroxine, and AK.

Statistics. Data are presented as mean ± SEM or SD as indicated in each group. All data were evaluated with 1-tailed or 2-tailed, unpaired or paired (where appropriate) Student’s t test using QuickCals (Graphpad). A P value less than or equal to 0.05 was considered statistically significant.

Study approval. This study was approved by Alfred Hospital Ethics Committee (approval number 268/10). There was no clinical trial listing associated with this study. Written specific genetics consent for this study was received from the participants prior to inclusion.

Supplemental data. Further information can be found in the Supplemental Data.

Author contributions
AK and AE designed the study. AK developed RiCh and ChiP-RNase. AK and HK obtained leukocytes from human blood. MZ performed deep sequencing. AK, MZ, and HR analyzed sequencing data. JO and AK performed MeCP2 knockdown experiments. SC and ME recruited patients and collected blood. AE and AK prepared figures and cowrote the manuscript, which has been edited by AK, HR, MZ, ME, SM, and HK. All authors have read and approved the submitted manuscript.
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Address correspondence to: Assam El-Osta, Central Clinical School, Faculty of Medicine, Level 5, Epigenetics in Human Health and Disease Laboratory, 99 Commercial Road, Melbourne, Victoria 3004, Australia. Phone: 613.99030477; E-mail: sam.el-osta@monash.edu.


