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INSUFFICIENT SLEEP IS ASSOCIATED WITH A PROATHEROGENIC CIRCULATING microRNA SIGNATURE

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Abstract

Habitual short sleep duration (<7 hours/night) is associated with increased morbidity and mortality due, in large part, to increased inflammatory burden and endothelial dysfunction. microRNAs (miRNAs) play a key role in regulating vascular health and circulating levels are now recognized to be sensitive and specific biomarkers of cardiovascular function, inflammation and disease. The aim of this study was to determine whether the circulating expression of: miR-34a; miR-92a; miR-125a; miR-126; miR-145; miR-146a; and miR-150; are disrupted in adults who habitually sleep <7 h/night (short sleep). These were chosen based upon their well-established links with vascular inflammation, function and, in-turn, cardiovascular risk. Twenty-four adults were studied: 12 with normal nightly sleep duration (6M/6F; age: 55±3 y; sleep duration: ≥7.0 h/night) and 12 with short nightly sleep duration (7M/5F; 55 ± 2 y; sleep duration: <7.0 h/night) and circulating miRNA expression was assayed by RT-PCR. All subjects were non-smokers, normolipidemic, non-medicated and free of overt CVD. Circulating levels of miR-125a (3.07±1.98 vs 7.34±5.34 AU), miR-126 (1.28 (0.42 to 2.51) vs 1.78 (1.29 to 4.80) AU) and miR-146a (2.55 (1.00 to 4.80) vs 6.46 (1.50 to 11.44) AU) were significantly lower $(\sim 60\%$, 40% and 60%, respectively) in the short compared with the normal sleep group. However, there were no significant group differences in circulating levels of miR-34a, miR-92a, miR-145, and miR-150. In summary, chronic short sleep is associated with marked reduction in circulating levels of miR-125a, miR-126 and miR-146a. Dysregulation of these miRNAs may contribute to the increased inflammatory burden and endothelial dysfunction associated with habitual insufficient sleep.

Conflicts of Interest: The authors have no conflicts of interest to disclose.

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All experiments were performed at the University of Colorado Boulder. Conception and design of the work: JGH, KJD, JJG, BLS, CAD. Data acquisition, analysis and interpretation: JGH, VG, MVL, GML, KJD, CAD. All authors contributed to the drafting of work and the revision for critically important content. All authors approved the present manuscript and agree to be accountable for the work herein. All persons who qualify for authorship have been listed and all authors meet the criteria for authorship.

COMPETING INTERESTS

The authors have no conflicts of interest to disclose.

INTRODUCTION

Habitual insufficient nightly sleep, defined as <7 h/night, is associated with increased cardiovascular disease (CVD) risk, events and mortality (Cappuccio *et al.*, 2011; Liu, 2016; Yin *et al.*, 2017). The mechanisms underlying the detrimental cardiovascular effects of habitual short sleep duration are not fully understood. Heightened inflammation and impaired endothelial function are recognized as contributing factors to sleep-related CVD risk. We (Weil et al., 2010; Bain et al., 2017) and others (Calvin et al., 2014; Akinseye et al., 2015) have demonstrated profound endothelial vasomotor dysfunction and heightened systemic inflammation in adults who habitually sleep $\langle 7 \text{ h/night}$. The factors leading to this proinflammatory, endothelial dysfunction state are not well defined.

microRNA (miRNAs) are short non-coding RNAs which regulate gene expression on the post-transcriptional level by targeting mRNA and inhibiting translation. A specific subset of miRNA have been identified as critical regulators of vascular inflammation (i.e. miR-92a, miR-145, miR-146a, miR-150, miR-181b and miR-Let-7a), endothelial cell dysfunction (i.e. miR-126 and miR-34a) and vasoconstrictor tone (miR-125a)(Empel et al., 2012; Hao et al., 2014; Ma et al., 2016). For example, inhibition of miR-92a and over-expression of miR-146a, miR-181b, and miR-Let-7a is associated with suppressed endothelial inflammation and atherogenesis (Loyer et al., 2014; Bao et al., 2014; Ma et al., 2016). Both miR-145 and miR-150 limit immune cell activation, cytokine production, and vascular inflammation (Lovren & Verma, 2013; Sang et al., 2016). miR-34a has been identified as a key driver of endothelial senescence and apoptosis through the inhibition of the sirtuin system (Yamakuchi et al., 2008; Ito et al., 2010; Han et al., 2015). Conversely, miR-126 and miR-125a have been shown to be key, pleiotropic promotors of endothelial health and vasomotor function. Furthermore, altered circulating levels of these vascular-related miRNAs have been shown to be indicative of elevated vascular inflammation and endothelial dysfunction as well as predictive of cardiovascular morbidity and mortality (Empel et al., 2012; Sayed et al., 2014; Wronska et al., 2015). Currently, it is unknown if habitual short sleep is associated with altered circulating miRNA expression. Circulating miRNA desynchrony may contribute to the increased cardiovascular risk associated with short sleep.

Accordingly, the aim of the present study was to determine the influence of habitual short sleep on a subset of specific vascular-related miRNAs. Specifically, we tested the hypothesis that circulating miR-34a and miR-92a would be higher and miR-125a, miR-126, miR-145, miR-146a, and miR-150 would be lower in middle-aged adults who habitually sleep <7 h/ night compared with adults who sleep 7–9 h/night. The rational for focusing on these specific circulating miRNAs is based on their established regulatory links with endothelial cell function and inflammatory pathways and association with CVD risk.

METHODS

Ethical Approval

All subjects had the research study and its potential risks and benefits explained before providing written informed consent according to the guidelines of the University of Colorado Boulder. All aspects of this research study complied with the Declaration of

Helsinki, except for registration in a public database (clause 35) (World Medical Association, 2013). This study was approved by the University of Colorado Institutional Review Board (approval # B5079).

Subjects

Twenty-four sedentary middle-aged adults (age range: 44–62 years) were studied: 12 normal sleep duration (6M/6F; range: 7.0–8.5 h/night) and 12 short sleepers (7M/5F; range: 5.0–6.8) h/night). All subjects were sedentary, non-smokers, normolipidemic, non-medicated and free of overt cardiovascular, metabolic, renal, and hematologic disease, as assessed by medical history, resting and exercise electrocardiograms, and fasting blood chemistries. Female subjects were at least 1 year postmenopausal and had never taken or had discontinued use of hormone replacement therapy at least 1 year before the start of the study.

Sleep Duration

Sleep duration was self-reported as a component of the Stanford Physical Activity Questionnaire as previously described (Weil et al., 2010). Nightly mean reported sleep duration was calculated as the weighted mean of weeknight and weekend values as follows: $(5 \text{ X}$ weekday sleep duration) + $(2 \text{ X}$ weekend sleep duration)/7. Subjects were divided into 2 groups based upon their reported sleep duration: $7-9$ h/night = "normal sleep" and $\langle 7 \text{ h} /$ night = "insufficient or short sleep" (Bain *et al.*, 2017). These criteria were chosen based on reports that indicate that habitual sleep duration shorter than 7 h/night is associated with increased health risks (Cappuccio et al., 2011; Yin et al., 2017).

Body Composition and Metabolic Measures

Body mass was measured to the nearest 0.1 kg using a medical beam balance. Percent body fat was determined by dual energy X-ray absorptiometry (Lunar Corp., Madison, WI, USA). Body mass index (BMI), fasting plasma lipid, lipoprotein, glucose, and insulin concentrations were determined using standard techniques.

MicroRNA isolation and Reverse Transcription Quantitative Polymerase Chain Reaction Analysis (RT-qPCR)

Blood samples were collected from the antecubital vein between 8:00 and 10:00am following an overnight fast. Blood was centrifuged at $600 \times g$ for 20 minutes and the supernatant was centrifuged 1500 x g for 15 minutes at 4^oC to remove any additional cellular debris.

Total RNA was isolated from platelet poor plasma using the miRNeasy Serum/Plasma Kit (Qiagen, Hilden, Germany) (Hijmans et al., 2018). Briefly, RNA was isolated from 100μL of plasma using the QIAsol lysis reagent, washed and eluted in RNAse free water. To normalize between samples 3.5μL (1.6×10⁸ copies/μL) *Canorhabditis elegans* miR-39 (celmiR-39) was added to each sample. Immediately after RNA isolation, 12μL of RNA was reverse transcribed using the miScript Reverse Transcription Kit (Qiagen, Hilden, German). cDNA was PCR-amplified (BioRad CFX96 Touch Real Time System) using the miScript SYBR green PCR kit (Qiagen, Hilden, Germany) and miRNA specific primers for miR-34a, miR-92a, miR-125a, miR-126, miR-145, miR-146a and miR-150 (Qiagen, Hilden,

Germany). All samples were assayed in duplicate. Relative expression level for a given miR was normalized to cel-miR-39, calculated as $Ct = 2^{-(Ct[\text{miR}-Ct[\text{cel-miR}-39])}$ and expressed as arbitrary units (AU) (Hijmans et al., 2018).

Statistical Analysis

The distribution of the data was assessed by the Shapiro-Wilk test and the homogeneity of variances by the Levene test. Group differences in subject characteristics, circulating microparticles concentrations, cellular protein expression, miRNA expression, oxidative stress, and senescence were determined by independent Student t-test or Mann-Whitney U test. Data were presented as mean \pm standard deviation (SD) or normally distributed variables, and as the median (interquartile range [IQR]) for non-normally distributed variables. Pearson correlations were determined between variables of interest. Statistical significance was set a priori at P<0.05.

RESULTS

Selected subject characteristics are presented in the Table. There were no significant differences in any anthropometric, hemodynamic or metabolic variables between the groups, however, by design, nightly sleep was significantly lower $(\sim 20\%)$ in the short vs normal sleep group. Circulating levels of miR-125a ([short vs. normal sleep] 3.07 ± 1.98 vs 7.34±5.34 arbitrary units [AU]), (1.28 (0.42 to 2.51) vs 1.78 (1.29 to 4.80) AU) and miR-146a (2.55 (1.00 to 4.80) vs 6.46 (1.50 to 11.44) AU) were significantly lower (~60%, \sim 40%, and \sim 60% respectively) in the short sleep compared with normal sleep group (Figure 1). There were no significant group differences in circulating miR-34a ([short vs. normal sleep] 1.63±1.00 vs 1.70±1.23 AU), miR-92a (6.86 (1.95 to 9.51) AU), miR-145 (0.74 (0.10 to 2.02) vs 1.08 (0.21 to 2.17) AU) and miR-150 ([short vs. normal sleep] 0.91 ± 0.51 vs 1.35±1.20 AU) (Figure 2).

In the overall study population, miR-125a (r=0.59; P<0.05), miR-126 (r=0.43; P<0.05) and miR-146a levels ($r=0.41$; P<0.05) were each significantly related to average nightly sleep duration (Figure 3). No other miRNAs were associated with nightly sleep duration.

DISCUSSION

Interest in circulating miRNA profiles has intensified as their role as biomarkers and mediators of cardiovascular dysfunction and potential therapeutic targets has become increasingly established (Wronska *et al.*, 2015). The key finding of the present study is that habitual insufficient sleep (<7 h/night) is associated with disruption in circulating levels of miR-125a, miR-126 and miR-146a. Altered circulating profiles of these vascular-related miRNAs have been linked to vascular dysfunction and increased CVD risk and events (Zampetaki et al., 2010; Empel et al., 2012; Hao et al., 2014; Bao et al., 2015). To our knowledge this the first study to determine the influence of short sleep duration on circulating miRNA signatures.

A primary factor underlying the elevated incidence of myocardial infarction and stroke associated with habitual short sleep is endothelial dysfunction, specifically impaired

vasomotor function and reduced fibrinolytic capacity (Weil et al., 2010, 2013; Levy et al., 2012; Bain et al., 2017). For example, we have demonstrated that short sleep is associated with reduced nitric oxide-mediated endothelium-dependent vasodilation (Bain *et al.*, 2017). In a similar population to the present study, forearm blood flow responses to the endothelial agonist acetylcholine was significantly lower in adults who habitually slept less than 6.5 h/ night compared with their cohorts of similar age who slept >7 h/night. The co-administration of the endothelial nitric oxide synthase inhibitor, $L-N^G$ -monomethyl arginine, with acetylcholine demonstrated that the insufficient sleep-related loss in vasodilator function was due, in part, to reduced nitric oxide bioavailability (Bain et al., 2017). In addition, enhanced endothelin(ET)-1-mediated vasoconstrictor tone has been shown to be elevated with insufficient sleep, further compounding the vasomotor dysfunction and increasing CVD risk (Weil et al., 2010). In the present study, circulating concentrations of both miR-125a and miR-126 were significantly lower in the short sleep group. This finding is congruent with previous studies demonstrating impaired vasomotor function with insufficient sleep (Weil et al , 2010; Calvin et al., 2014; Bain et al., 2017). The endo-miR, miR-126, is critical for proper endothelial function and vascular homeostasis (Chistiakov et al., 2016). miR-126 promotes eNOS activation and endothelial cell survival by targeting the PI3K/AKT/eNOS pathway regulator PI3KRA as well as suppressing the proatherogenic proteins SPRED1 and CXCL12 (Jansen et al., 2013; Chen et al., 2016). Clinically, circulating miR-126 expression has been associated with endothelial vasodilatory capacity and function (Widmer *et al.*, 2014; Park et al., 2015; Chistiakov et al., 2016). Along with vasomotor function, miR-126 also regulates endothelial fibrinolytic function and diminished miR-126 is thought to result in a prothrombotic state (Gao *et al.*, 2017). Contrastingly, miR-125a directly targets the 3'UTR of ET-1 mRNA inhibiting translation and, in turn, ET-1 system activity. Thus, reduced expression of miR-125a is associated with greater ET-1 production and release (Li et al., 2010; Hao et al., 2014). Lower circulating miR-125a in the short vs normal sleepers observed herein is consistent with previous studies reporting increased ET-1 system activity with insufficient sleep (Palma et al., 2002; Weil et al., 2010). Collectively, reduced levels of miR-125a and miR-126 may be etiologically involved in the increased incidence of endothelial dysfunction and CVD with insufficient sleep.

A proinflammatory vascular environment is a common consequence of insufficient sleep and is thought to be a major contributor to insufficient sleep-related CVD risk (Hansson, 2005). It is well established that short sleep is associated with elevated levels of pro-inflammatory cytokines, such as IL-6 and IL-8, and markers of vascular inflammation, such as C-reactive protein (Grandner et al., 2013). In a seminal study, Aho and colleagues (2013) demonstrated that short sleep is associated with increased activation of the proinflammatory transcription factor, nuclear factor-κB (NF-κB) resulting in increased inflammatory gene expression and cytokine production (Aho et al., 2013). Dysregulation of miR-146a has been directly linked with increased NF-κB activation. Reduced miR-146a expression limits TRAF-6 and IRAK-1 suppression allowing unregulated NF-κB activation. Elevated NF-κB activation promotes increased cytokine production, endothelial dysfunction and atherogeneis (Ma et al., 2016; Paterson & Kriegel, 2017). Ma and colleagues (2016) demonstrated that low circulating levels of miR-146a is associated with increased vascular inflammation and atherosclerosis (Ma et al., 2016); whereas, exogenous restoration of circulating miR-146a

blunted vascular inflammation in mice (Ma et al., 2016). Thus, it is plausible that lower miR-146a levels may contribute to the increased inflammatory burden associated with habitual short nightly sleep (Aronica *et al.*, 2010). Moreover, considering lower circulating miR-146a levels have been shown to be predictive of atherosclerosis and coronary events (Ramkaran et al., 2014; Bao et al., 2015), the negative influence of insufficient sleep on miR-146a may have yet untold cardiovascular consequences.

In contrast to miR-125a, miR-126 and miR-146, there was no significant impact of nightly sleep duration on circulating miR-34a, miR-92a, miR-145 and miR-150 levels. Each of these miRs contribute to the regulation of vascular health and are associated with CVD risk (Zeller et al., 2014; Satoh et al., 2015). miR-34a promotes cellular senescence and dysfunction through the regulation of sirtuin-1 and the apoptotic protein BCL-2 (Boon *et al.*, 2013). Circulating miR-34a has been reported to be two-fold higher in adults with coronary artery disease compared with healthy controls (Han *et al.*, 2015) and to play contributing role in the development of heart failure and cardiac death (Boon et al., 2013; Han et al., 2015). miR-92a negatively regulates KLF-2 and KLF-4 proteins resulting in diminished endothelial repair capacity, eNOS expression and endothelial function (Daniel *et al.*, 2014; Shang *et al.*, 2017). Increased expression of miR-92a is associated with the progression of atherosclerotic lesions (Daniel et al., 2014). miR-145, on the other hand, interacts with vascular smooth muscle cells to drive differentiation from a proliferative state to a contractile phenotype and miR-145 mediated reduction in vascular smooth muscle cell proliferation has been shown to blunt atherosclerotic lesion progression (Lovren et al., 2012). miR-150 limits atherogenesis by moderating immune cell activation and secretion of cytokines and enhances vascular health by promoting endothelial and endothelial progenitor cell function (Desjarlais et al., 2017). Lower circulating levels of miR-145 and miR-150 have been linked with increased CVD risk and events (Rhodes et al., 2013; Dong et al., 2015). Lack of alteration in these miRNAs with insufficient sleep suggest a differential effect of sleep on circulating miRNA and demonstrate the complexity of the interaction of sleep and circadian physiology with miRNA regulation and, in turn, cellular function. In fact, it is possible that other sleep disorders such as insomnia or sleep apnea may influence the circulating profile of these miRNAs.

There are a few experimental considerations regarding the present study that deserve mention. Firstly, inherent with all cross-sectional studies involving humans it is possible that genetic, dietary or lifestyle factors may have influenced our results. However, to minimize the potential confounding effects of other lifestyle behaviors, besides habitual sleep duration, all subjects were similar in age, body composition and cardiorespiratory fitness; additionally they were sedentary, non-smokers, free of overt cardiometabolic diseases and not taking vitamins or medications that could influence circulating miRNAs. Secondly, we assessed habitual nightly sleep duration by self-report opening the possibility for bias and experimental error. Although we did not utilize more objective measures of sleep duration through actigraphic monitoring, previous studies have reported a strong correlation between self-report sleep duration and actigraphic data (Hauri & Wisbey, 1992; Lockley et al., 1999). Thirdly, we did not screen for sleep disorders such as sleep apnea. Considering that the study population was non-obese and cardiometabolically healthy, the risk of sleep apnea would be small. Finally, although we are ascribing the disruption in circulating miR-125a, miR-126

and miR-146a to insufficient sleep, we are unable to identify which cells or tissue are involved in the production, release or clearance of these miRNAs in the circulation. Thus, the mechanisms by which sleep may affect their circulating signature is outside the scope of this study. Nevertheless, circulating levels of miR-125a, miR-126 and miR-146a, regardless of cell of origin or mechanism of release, are correlated with disease and provide mechanistic insight into disease development and progression (Empel et al., 2012; Sayed et al., 2014).

In conclusion, the results of the present study suggest that habitual insufficient nightly sleep adversely affects the circulating profile of miR-125a, miR-126 and miR-146a. Sleep related changes in these miRNA may play a role in the aberrant vascular physiology and increased vascular risk associated with short sleep (Empel et al., 2012; Wronska et al., 2015). Indeed, lower circulating levels of miR-125a, miR-126 and miR-146a are consistent with, and can be linked to, the reduction in nitric oxide-mediated vasodilation, increased ET-1 vasoconstrictor tone, diminished fibrinolytic function and increased vascular inflammation associated with insufficient sleep (Weil et al., 2010, 2013; Hao et al., 2014; Chistiakov et al., 2016; Paterson & Kriegel, 2017 ; Bain *et al.*, 2017). Future studies are needed to establish whether circulating miRNAs may be used as biomarkers of sleep-related vascular risk.

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What is the central question of the study

• Is habitual short sleep associated with altered circulating levels of specific inflammation and vascular-related miRNAs?

What is the main finding and its importance?

• Circulating levels of miR-125a, miR-126 and miR-146a were significantly lower in the short compared with normal sleep group. Altered circulating profiles of these vascular-related miRNAs have been linked to vascular inflammation, dysfunction and increased CVD events. Sleep related changes in these miRNAs are consistent with, and may play a role in, the aberrant vascular physiology and increased vascular risk associated with short sleep

Figure 1.

Circulating miR-125a, miR-126, and miR-146a in the normal sleep and short sleep duration groups. Mean circulating level is denoted for miR-125a; median for miR-126 and miR-146a. *P<0.05

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Figure 2.

Circulating miR-34a, miR-92a, miR-145 and miR-150 in the normal sleep and short sleep duration groups. Mean circulating level is denoted for miR-34a and miR-150; median for miR-92a and miR-150.

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Relation between circulating miR-125a, miR-126 and miR-146a and nightly sleep duration.

Table.

Selected subject characteristics

Values expressed as Mean±SD. BMI: body mass index. HDL-C: high-density lipoprotein. LDL-C: low-density lipoprotein. HOMA-IR: homeostasis model of insulin resistance.

* P<0.05