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PERSON-TO-PERSON BACTERIAL TRANSMISSION CAN CHANGE THE SLEEP PATTERN IN NEWLY MARRIED COUPLES

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Abstract – *Objective:* The composition of the gut microbiota varies significantly among healthy individuals, as well as insomniacs, hypersomniacs, and healthy people. On the other hand, a substantial bacterial strain is shared across these populations with distinct intra-population, mother-to-infant, and intra-household transmission patterns. Based on these premises, we propose a hypothesis stating that person-to-person bacterial transmission can change the sleep pattern in couples.
Patients and Methods: In this pilot study, 157 couples who had been married and living together for an average of 5.91 months were enrolled. A wide range of questionnaires were administered to participants to measure sleep patterns. Gut microbiota composition was analyzed at two-time points: baseline and 3 months later.
Results: Three months after the marriage, spouses with healthy sleep patterns were significantly more likely to resemble their insomniac or hypersomniac couples. Gut microbiota composition in participants with normal sleep patterns was significantly changed and became similar to that of the participant's spouse, i.e., if the spouse was insomniac or hypersomniac, then gut composition became similar to his/her insomniac or hypersomniac spouse, respectively. The results of mediation analysis confirmed the association between the changes in the sleep pattern and changes in the gut microbiota. We provide for the first time evidence of gut microbial community structure alterations in newly married couples, which parallels reduced sleep quantity and quality.
Conclusions: The research will have important implications in terms of diagnosis and treatment of sleep disturbances through microbiota modulation, particularly from the perspective of diagnostic, predictive, preventive, and personalized medicine.

Keywords: Gut microbiota, Bacterial transmission, Person-to-person contact, Sleep disturbance, Newly married couples.

INTRODUCTION

The metabolic activity, diversity, and composition of the gut microbiota vary significantly between healthy individuals and insomniacs[1] and also between hypersomniacs and healthy people[2]. While Clostridiales and Bacteroides are regarded to be the two most important biomarkers for differentiating between healthy people and insomniacs[3], a recent study[4] demonstrated that an enhanced relative abundance of five genera, including *Lachnospiraceae UCG010*, Hungatella, *Collinsella*, *Gordonibacter* and *Blautia* may be correlated with a diminished risk of some types of hypersomnia (narcolepsy type one). Contrarily, an enhanced relative abundance of class *Betaproteobacteria*, genus *Ruminiclostridium*, and genus *Alloprevotella* may potentially increase the risk of narcolepsy type one[4].

It is worth noting a study conducted by Valles-Colomer et al[5], who detected substantial bacterial strain sharing across people with distinct intra-population, mother-to-infant, and intra-household transmission patterns. There was considerable strain sharing among cohabiting people, with 32% and 12% median strain-sharing rates for the time since cohabitation and gut and oral microbiomes affected strain sharing more than genetics or age did. Building on these premises, we propose the following hypothesis: bacterial transmission between individuals can influence sleep patterns in couples.

PATIENTS AND METHODS

Participants

Data were drawn from a private sleep clinic in Tehran, Iran. Respondents who had been officially married during the past six months and were in a cohabiting relationship were invited to participate in this study together with their official spouses. One hundred and eighty-four heterosexual couples participated in the gut microbiota composition and sleep study. Six couples were excluded because the women were taking medicines known to affect gut/oral microbiota composition or were pregnant. One hundred and seventy-eight participants provided stool samples, of which twenty-one were excluded due to either low readings [(n = 10) or missing data (n = 11)]. The remaining 157 couples were all living with their spouses in the same house. At baseline interviews, respondents and their spouses were telephoned on two consecutive days and interviewed separately about their daily experiences, including time use, physical symptoms, mood, and stressful events.

Sample Collection

Fecal samples were voluntarily collected from participants using the DNA/RNA Shield Fecal Collection Tubes (Zymo Research, Freiburg, Germany). Samples were then transferred to the laboratory and frozen within 15-30 min after collection. All samples were stored at -80°C until further processing. On day 1 and day 2, all couples participated in a gut microbiota composition study. Three months later, gut microbiota composition was analyzed again using the same protocol. All the respondents participated in the study except one couple who were divorced from each other and had spent significant time living apart. Thirty-two couples were excluded due to their baseline microbiota resemblance (insomniac or hypersomniac phenotype) to avoid overlap bias. Data drawn from 152 couples were analyzed.

Sleep Study

The participants voluntarily completed the validated Persian versions of the Pittsburgh Sleep Quality Inventory (PSQI)[6]. Insomnia was defined as the coexistence of both daytime dysfunction and difficulty resuming sleep[7]. Hypersomnia was defined by a bed-rest total sleep time ≥19 hours during the 32-hour recording[8]. SPSS ver.16 (SPSS Inc., Chicago, IL, USA) was used to analyze the data.

RESULTS

Men had an average age of 37.20 years, with a standard deviation (SD) of 8.01, and 84.3% had attained a college degree. Women had an average age of 31.02 years (SD = 9.30), and 87.2% had attained a college degree. All participants were Iranian (ethnicities including 83 Persian, 64 Azeri, and 5 Arab). The couples had been married and living together for an average of 5.91 months (SD = 2.03).

Briefly, gut microbiota composition in participants with normal sleep patterns was significantly changed and became similar to that of the participant's spouse, i.e., if the spouse was insomniac or hypersomniac, then gut composition became similar to his/her insomniac or hypersomniac spouse, respectively (all *p*-values <0.0001). Interestingly, in support of our hypothesis, similar and parallel changes were observed in the sleep pattern of subjects with normal sleep patterns. Women/men with a normal sleep pattern who had married a hypersomniac or insomniac spouse reported a disturbance in their normal sleep pattern.

Table 1 demonstrates results of the Chi-square test. Statistical analyses with an array of sleep questionnaires, including the PSQI, ESS, ISI, and GSAQ confirmed the report (data are only provided for PSQI). Results remained significant after controlling for confounders. The formal mediation analysis confirmed the results. As portrayed in Table 2, three months after the marriage, spouses with healthy sleep patterns were significantly more likely to resemble their insomniac or hypersomniac couples (Figure 1).

DISCUSSION

We found that sleep disturbances in couples can be partially explained by changes in gut microbiota. Many types of physiologic synchrony have been reported between couples before, for instance, synchrony of diurnal cortisol pattern[9], cardiac synchrony[10], and also, sleep concordance[11]. To the best of the author's knowledge, this is the first study showing that sleep disturbances can be mediated *via* a spouse's gut microbiota transamination, particularly in such a short term, i.e., almost 6 months after marriage. Previous studies have highlighted the substantial role of affective experience in the regulation of sleep through behaviors, such as touching and "sleep-touch" among couples[12]. Most definitely, socioeconomic status[13], couples' sleep, and psychological distress[14] can also significantly change the sleep pattern in couples. It is also known that anxiety can partially predict dyadic sleep characteristics in couples experiencing insomnia but not in couples without sleep disorders[15]. Many other confounding factors are at play in the pathophysiology of sleep disturbances.

TABLE 1. SLEEP QUALITY MEASURES AT BASELINE IN THREE GROUPS OF PARTICIPANTS.

	Healthy spouses married with an insomniac person (n=49)		Healthy spouses married with a hypersomniac person (n=46)		Insomniacs (n=49)		Hypersomniacs (n=46)	
	Day 1	Day 90	Day 1	Day 90	Day 1	Day 90	Day 1	Day 90
Sleep quality	0.5±0.6	1.0±0.8	0.5±0.7	1.2±1.0	2.0±0.7	2.1±0.8	1.0±0.6	1.1±0.9
Sleep latency	0.8±0.9	1.4±0.9	0.9±1.0	1.2±1.1	2.3±0.9	2.2±1.1	1.0±0.9	0.9±1.1
Sleep duration	0.4±0.8	2.6±1.4	0.5±0.9	2.2±1.7	2.2±0.9	2.1±0.8	0.4±0.7	0.3±0.8
Sleep efficiency	0.3±0.6	2.2±1.7	0.3±0.8	1.1±1.2	1.8±1.1	1.8±1.1	0.5±0.8	0.5±0.9
Sleep disturbance	0.6±0.6	1.1±0.9	0.5±0.7	0.7±0.9	1.8±0.5	1.9±0.6	1.1±04	1.3±0.6
Sleep medication	0.03±0.2	2.4±1.7	0.01±0.3	0.2±1.1	1.6±1.4	1.7±1.3	0.2±0.7	0.2±0.9
Daytime dysfunction	0.7±0.9	3.1±1.7	0.7±1.0	1.1±0.9	1.7±0.9	1.8±1.1	1.1±0.7	1.2±0.9
Total PSQI** score	3.5±3.0	9.5±4.2	3.3±2.6	7.2±4.9	13.5±3.8	14.5±3.9	5.6±2.8	6.4±3.1

**Pittsburgh Sleep Quality Index: In scoring the PSQI, seven component scores are derived, each scored from zero (no difficulty) to three (severe difficulty). The component scores are summed to yield a global score (range 0-21). Higher scores demonstrate worse sleep quality. Data were analyzed by the Kruskal-Wallis test. All Tukey-HSD post-hoc tests between groups were significant (*p*-values<0.001), with the exception of "Healthy spouses married with an insomniac person" *vs.* "Healthy spouses married with a hypersomniac (Day 1)".

TABLE 2. DISTRIBUTION OF STUDY PARTICIPANTS ACCORDING TO GENDER, GUT MICROBIOTA COMPOSITION AND SLEEP PATTERN.

	Sleep pattern		
Gender	**Healthy sleep pattern**	**Insomniac pattern**	**Hypersomniac pattern**
		Baseline[€]*:*	
Men	28 (28.28) [0.00] *GMT**: Normal	26 (24.07) [0.16] *GMT:* Insomniacs had significantly decreased family *Ruminococcaceae*, family *Bacteroidaceae*, and genus *Bacteroides*, along with significantly increased family *Prevotellaceae* and genus *Prevotella*, compared with healthy participants Genus *Fusicatenibacter* and genus *Gemmiger* were dominant in insomniacs, while genus *Clostridium* XI, genus *Oscillibacter*, genus *Coprococcus*, and family *Peptostreptococcaceae* were dominant in healthy participants.	20 (21.66) [0.13] *GMT:* Hypersomnics had significantly in creased relative abundance of class *Betaproteobacteria*, genus *Ruminiclostridium*[6] and genus *Alloprevotella*.
		Three months later[£]*:*	
	7 (13.38) [3.04] *GMT:* Normal	83 (71.56) [1.83] *GMT:* As above	15 (20.06) [1.28] *GMT:* As above
		Baseline:	
Women	19 (18.72) [0.00] *GMT:* Normal	14 (15.93) [0.23] *GMT:* As above	16 (14.34) [0.19] *GMT:* As above
		Three months later[£]*:*	
	13 (6.62) [6.14] *GMT:* Normal	24 (35.44) [3.69] *GMT:* As above	15 (9.94) [2.58] *GMT:* As above

**GMT*: Gut microbiota composition. [€] At baseline, there were no significant differences among three groups for gut microbiota composition, sex and sleep pattern. [£] Three months after the marriage, there were significant differences in terms of gut microbiota composition and sleep pattern. Individuals who were married with a hypersomniac or an insomniac spouse were more likely to become hypersomniac or insomniac after 3 months ($p<0.0001$). These changes were parallel to the gut microbiota composition ($p<0.0001$).

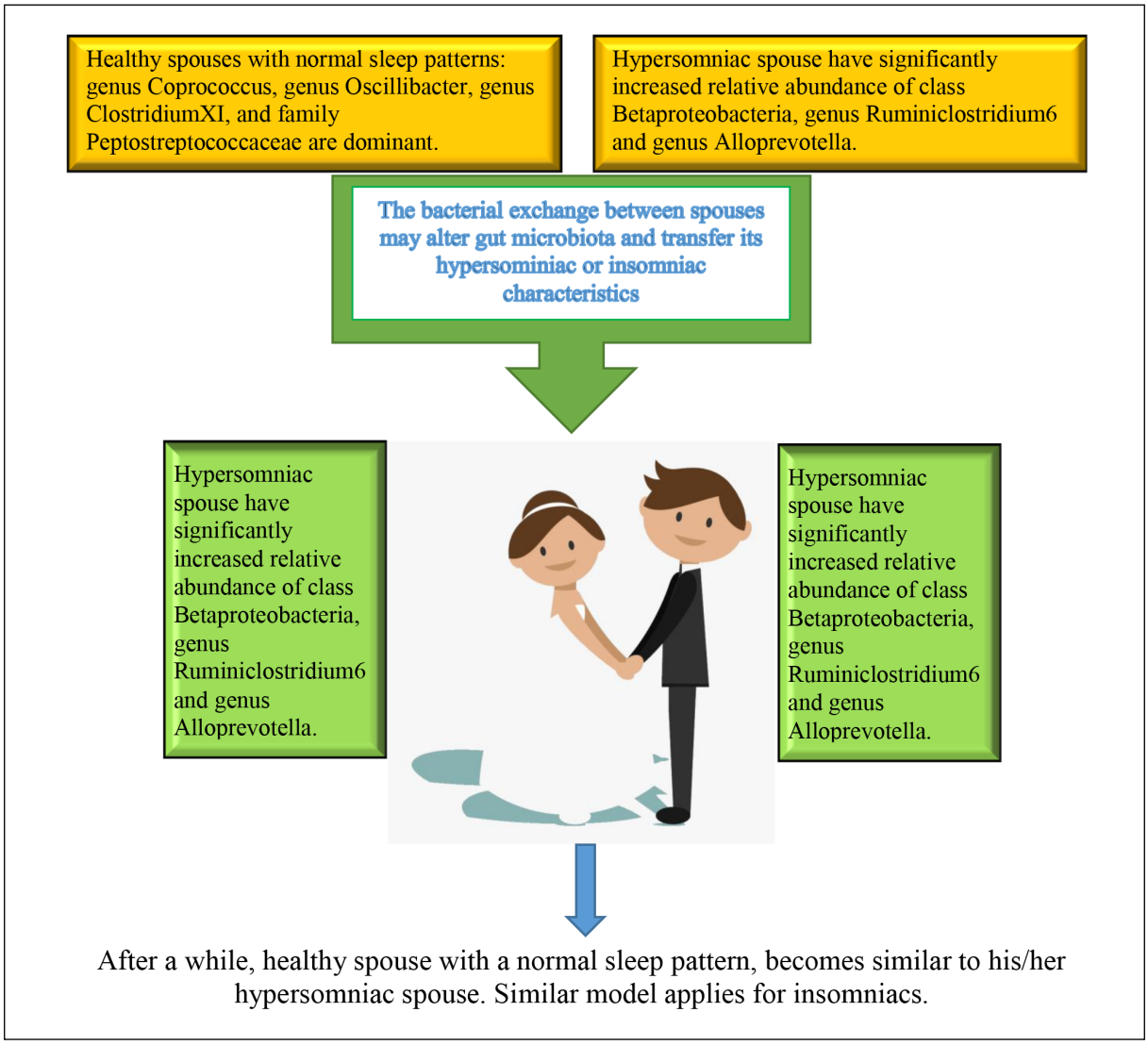

Figure 1. A simplified model showing how bacterial transmission between couples may change the sleep pattern.

CONCLUSIONS

We provide for the first time evidence of gut microbial community structure alterations in newly married couples, which parallels reduced sleep quantity and quality. However, further larger and longitudinal multiomics studies are required to replicate and elucidate the relationship between gut microbiota and sleep disturbances in newly married couples. The research will have important implications, particularly from the perspective of personalized medicine.

Conflict of Interest

The authors declare no conflict of interest.

Informed Consent and Ethics Approval

All the participants were assured of confidentiality of their personal details and that the information obtained would be only used for research purposes. Their profiles would be kept confidential during the research and thereafter. The authors conducted this study in a private sleep clinic, and all the participants expressed their informed consent to par-

ticipate in the research voluntarily. Written informed consent was obtained from all study participants. Ethical approval was obtained from the Human Research Ethics Committee (IT. 24001670). We adhered to the tenets of the Declaration of Helsinki and its latest amendments.

Authors' Contributions

RR and FM wrote the manuscript. RR critically reviewed the manuscript. All authors approved the final version of the manuscript.

Data Availability

The datasets used and analyzed during the current study are available from the corresponding author on reasonable request

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