Supplemental Material

Time-on-Task Effect during Sleep Deprivation in Healthy Young Adults Is Modulated by Dopamine Transporter Genotype

Brieann C. Satterfield, PhD[a,b], Jonathan P. Wisor, PhD[a], Michelle A. Schmidt, MS[a], Hans P.A. Van Dongen, PhD[a]

[a] Sleep and Performance Research Center and Elson S. Floyd College of Medicine, Washington State University, Spokane, WA, USA

[b] Currently at the Department of Psychiatry, College of Medicine, University of Arizona, Tucson, AZ, USA

Table S1. Subject demographics and genotypes for the three studies used for analysis. Subjects in a well-rested control group (used only in the supplemental material, Fig. S1) are indicated in parentheses. The TNFα308 assay failed for 1 control subject, leaving 57 subjects for analysis. Note that DAT1 8/8 and 10/11 genotypes are included here for representation of our sample; these genotypes were excluded from analysis. SD: standard deviation.

	Study 1 *n*=34 (*n*=15)	**Study 2** *n*=36 (*n*=30)	**Study 3** *n*=12 (*n*=13)	**Total** *N*=82 (*N*=58)
Sex				
Female	14 (9)	22 (12)	7 (3)	43 (24)
Male	20 (6)	14 (18)	5 (10)	39 (34)
Age (mean ± SD)	27.7 ± 5.0 (26.3 ± 4.3)	26.6 ± 4.8 (26.4 ± 4.9)	26.6 ± 4.4 (25.2 ± 3.8)	27.0 ± 4.8 (26.1 ± 4.5)
Race/Ethnicity				
Caucasian	30 (14)	33 (30)	7 (10)	70 (53)
Hispanic	0 (0)	1 (0)	1 (0)	2 (0)
African-American	1 (0)	0 (0)	0 (0)	1 (0)
Asian	0 (0)	0 (0)	1 (0)	1 (0)
American Indian	0 (0)	0 (0)	0 (1)	0 (1)
Pacific Islander	0 (0)	0 (0)	0 (1)	0 (1)
Mixed	1 (1)	2 (0)	3 (1)	6 (2)
Undisclosed	2 (0)	0 (0)	0 (0)	2 (0)
DAT1				
8/8	1 (1)	0 (0)	0 (0)	1 (1)
9/9	4 (0)	2 (3)	1 (1)	7 (4)
9/10	10 (4)	14 (12)	3 (2)	27 (18)
10/10	19 (10)	18 (15)	8 (10)	45 (35)
10/11	0 (0)	2 (0)	0 (0)	2 (0)
COMT				
Met/Met	9 (3)	7 (11)	1 (2)	17 (16)
Val/Met	19 (9)	21 (12)	6 (8)	46 (29)
Val/Val	6 (3)	8 (7)	5 (3)	19 (13)
TNFα				
A/A	0 (0)	0 (0)	0 (0)	0 (0)
A/G	8 (5)	14 (7)	2 (3)	24 (15)
G/G	26 (10)	22 (22)	10 (10)	58 (42)

Table S2. Descriptive statistics for number of responses in each 1 min bin of the 10 min PVT. SD: standard deviation.

Bin	Minimum	Median	Maximum	Mean	SD
1	6	9	13	9.08	1.19
2	7	9	14	9.43	1.19
3	6	9	13	9.32	1.14
4	6	9	14	9.42	1.26
5	6	9	13	9.31	1.20
6	5	9	14	9.33	1.19
7	6	9	13	9.29	1.22
8	6	9	14	9.31	1.21
9	4	9	14	9.24	1.17
10	6	9	13	9.28	1.14

Table S3. Summary of statistical results for the TSD group discussed in the main text. Bold indicates statistical significance (*P*<0.05). df: degrees of freedom; RT: response time; TOT: time on task; TSD: total sleep deprivation.

	DAT1			**COMT**			**TNFα**		
Genotype Analyses	χ^2 / *F*	*df*	*P*	χ^2 / *F*	*df*	*P*	χ^2 / *F*	*df*	*P*
Gender	<0.01	1	0.97	1.15	2	0.56	0.59	1	0.44
Race/Ethnicity	2.01	1	0.16	1.59	2	0.45	2.22	1	0.14
Age (*F* test)	<0.01	1, 77	0.95	1.43	2, 79	0.25	0.81	1, 80	0.37
Sleep Duration (*F* test)	0.10	1, 77	0.75	0.29	2, 79	0.75	0.14	1, 80	0.71
Time-on-Task Analyses	*F*	*df*	*P*	*F*	*df*	*P*	*F*	*df*	*P*
Time Awake (bout)	321.66	11, 86772	**<0.001**	223.02	11, 90055	**<0.001**	296.57	11, 90174	**<0.001**
TOT (bin)	81.01	9, 86772	**<0.001**	54.59	9, 90055	**<0.001**	75.33	9, 90174	**<0.001**
Genotype	3.18	1, 86772	0.075	1.04	2, 90055	0.352	1.52	1, 90174	0.217
Time Awake x TOT	7.56	99, 86772	**<0.001**	4.9	99, 90055	**<0.001**	7.01	99, 90174	**<0.001**
Time Awake x Genotype	21.9	11,86772	**<0.001**	9.2	22, 90055	**<0.001**	9.20	11, 90174	**<0.001**
TOT x Genotype	3.07	9, 86772	**0.001**	2.93	18, 90055	**<0.001**	2.16	9, 90174	**0.022**
Time Awake x TOT x Genotype	1.35	99, 86772	**0.011**	1.13	198, 90055	0.103	1.21	99, 90174	0.08
Study	2.86	2, 86772	0.057	2.09	2, 90055	0.124	2.55	2, 90174	0.078
RT Distribution Analyses	*F*	*df*	*P*	*F*	*df*	*P*	*F*	*df*	*P*
Baseline									
RT bin	4353.28	27, 4235	**<0.001**	3664.33	27, 4345	**<0.001**	3869.53	27, 4400	**<0.001**
RT bin x 5 min block	2.95	28, 4235	**<0.001**	2.02	28, 4235	**0.001**	3.02	28, 4400	**<0.001**
RT bin x Genotype	0.54	28, 4235	0.976	2.24	56, 4235	**<0.001**	15.76	28, 4400	**<0.001**
RT bin x 5 min block x Genotype	0.05	28, 4235	>0.999	0.17	56, 4345	>0.999	0.09	28, 4400	>0.999
Study	0.68	2, 4235	0.508	1.36	2, 4345	0.258	0.42	2, 4400	0.655
Daytime TSD									
RT bin	4804.49	27, 4235	**<0.001**	4134	27, 4345	**<0.001**	4213.75	27, 4400	**<0.001**
RT bin x 5 min block	17.99	28, 4235	**<0.001**	16.17	28, 4345	**<0.001**	17.72	28, 4400	**<0.001**
RT bin x Genotype	1.6	28, 4235	**0.022**	1.73	56, 4345	**0.001**	3.37	28, 4400	**<0.001**
RT bin x 5 min block x Genotype	0.15	28, 4235	>0.999	0.11	56, 4345	>0.999	0.34	28, 4400	>0.999
Study	1.58	2, 4235	0.206	1.07	2, 4345	0.344	1.51	2, 4400	0.222

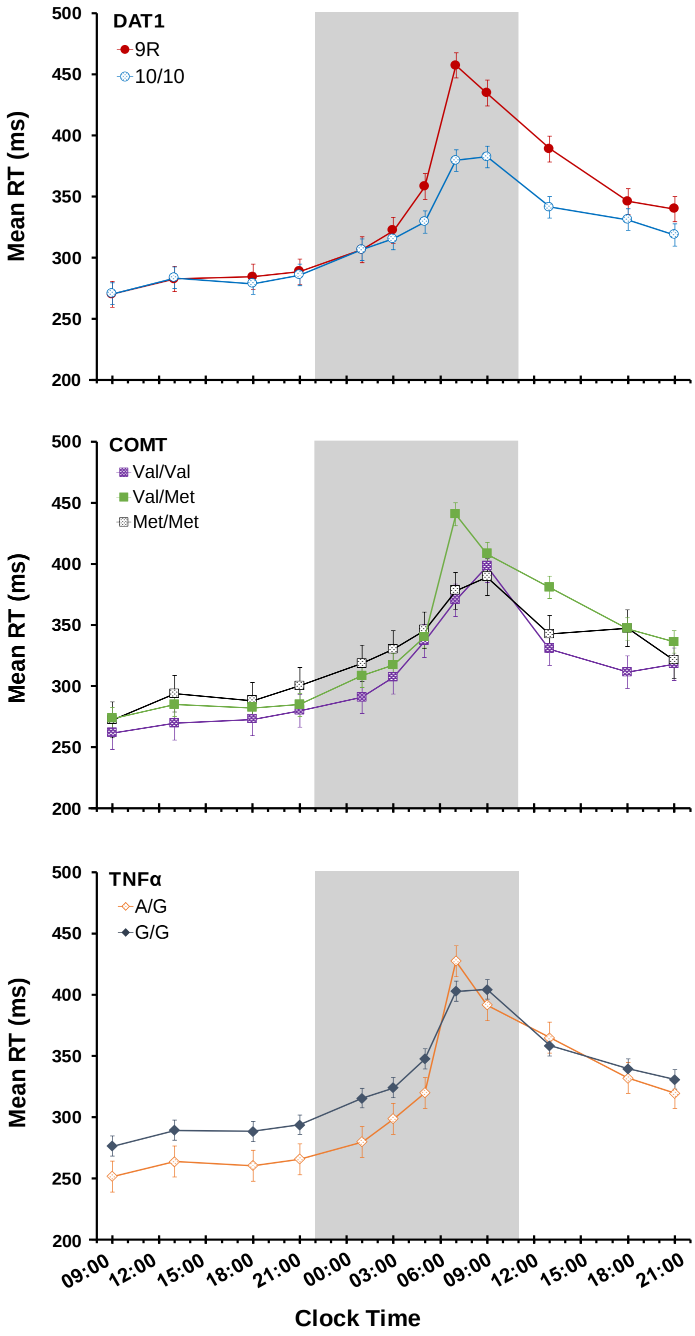

Figure S1. Mean RT (± standard error) on the 10 min PVT across test bouts during 38 h of TSD, for each of the three genes, collapsed across TOT. Shaded area: nighttime test bouts during TSD. PVT: psychomotor vigilance test; RT: response time; TOT: time-one-task; TSD: total sleep deprivation.

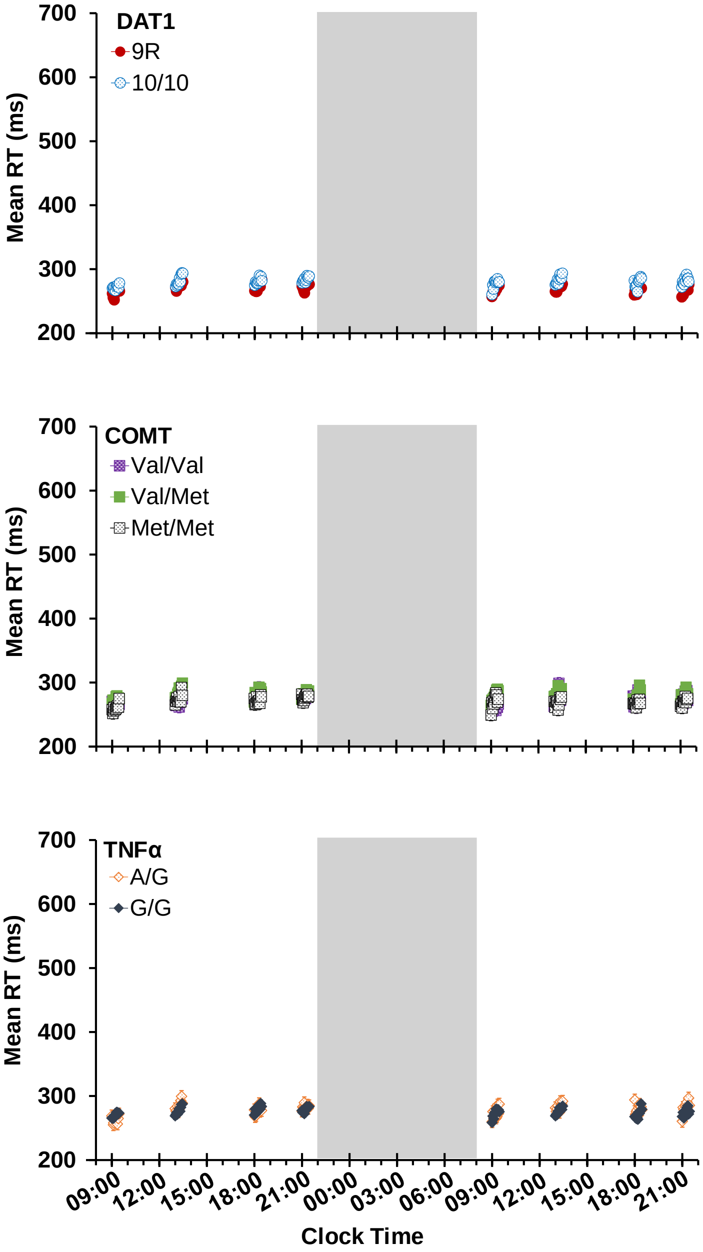

Figure S2. Mean RT (± standard error) in 1 min bins on the 10 min PVT across test bouts in the well-rested control group, for each of the three genes. Data are plotted against the start times of the PVT bouts; placement of the 1 min bins in each test bout is not to scale on the clock time axis. The shaded area represents a nighttime sleep opportunity (22:00–08:00).

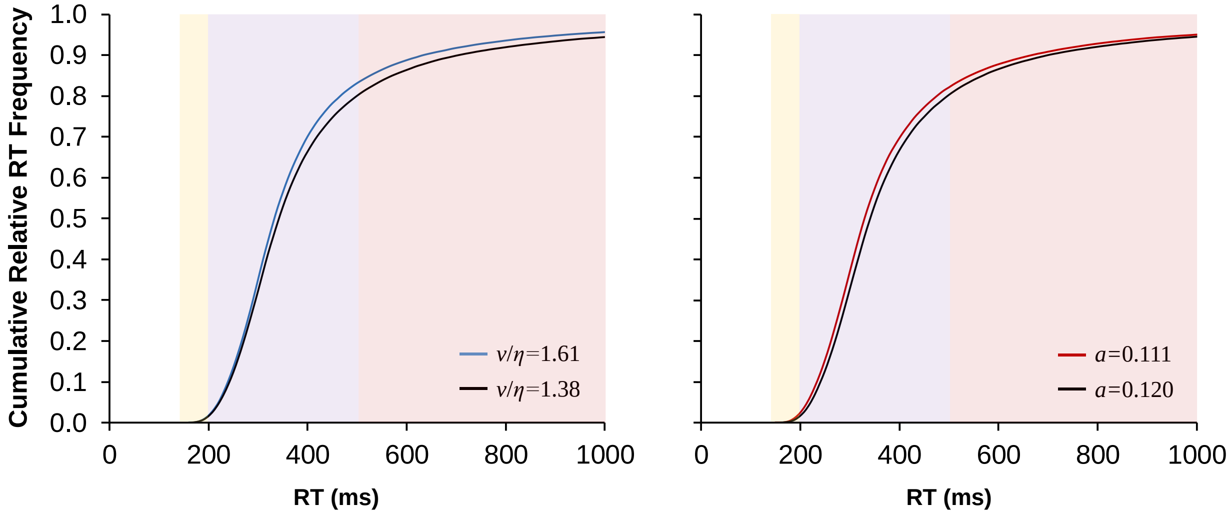

Figure S3. Computer simulations of cumulative relative RT frequency distributions using the diffusion model for the PVT.[37] These simulations are based on model parameters fixed at values previously observed for TSD (Table S1 in the PVT diffusion model publication[37]) but with varying drift ratio v/η (left panel) or boundary separation a (right panel). In the left panel, resilience to performance impairment is simulated by changing drift ratio from v/η=1.38 (previously observed TSD value) to v/η=1.61 (20% toward previously observed baseline value). This manipulation affects RTs in the lapse domain of the distribution (red-shaded area). In the right panel, resilience to performance impairment is simulated by changing boundary separation from a=0.120 (previously observed TSD value) to a=0.111 (previously observed baseline value). This manipulation primarily affects RTs in the heart of the distribution (purple-shaded area). The yellow-shaded area contains the fastest RTs; the purple-shaded area shows the heart of the cumulative relative frequency distributions; and the red-shaded area shows the slower RTs or lapse domain (cf. Fig. 1, right).