

Identifying new susceptibility genes on dopaminergic and serotonergic pathways for the framing effect in decision-making

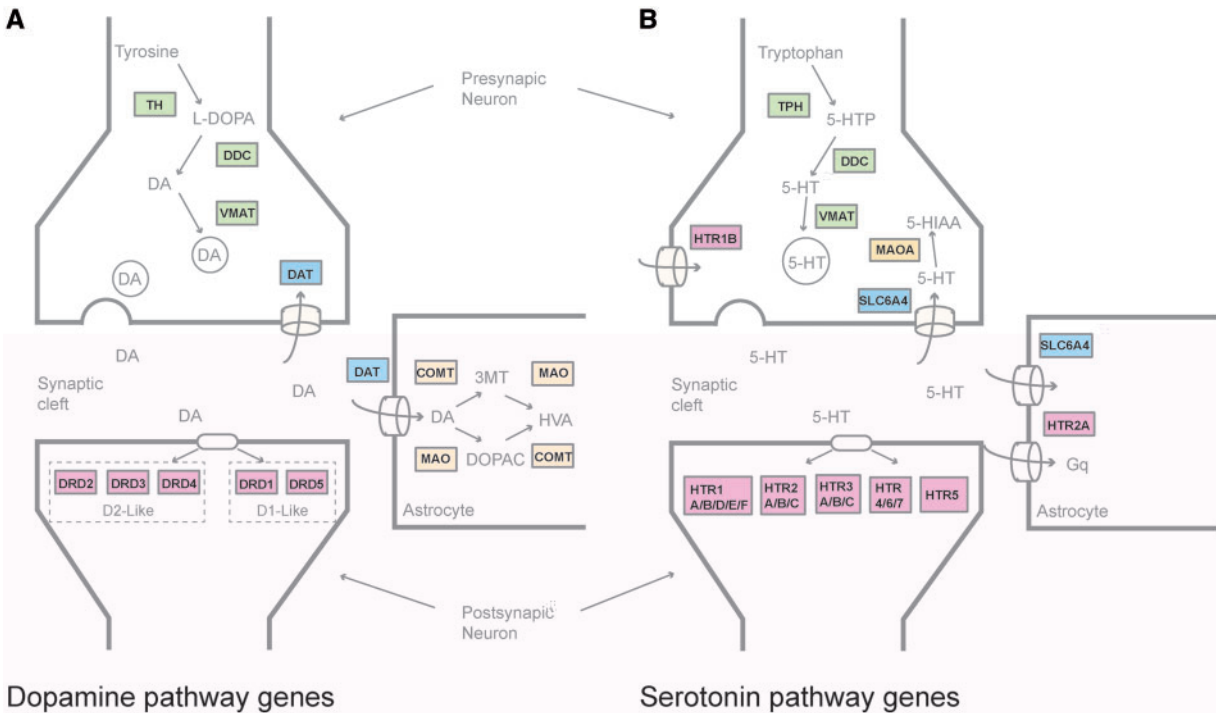
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Abstract

Decision-making is a complex process involving multiple brain regions and neurotransmitters. The framing effect is a cognitive bias where the way information is presented influences decision-making. Dopaminergic and serotonergic pathways are key players in this process. This study identifies new susceptibility genes on these pathways. Key genes include SLC6A4, COMT, and DDC. The study also examines the role of these genes in decision-making and the framing effect.

Key words: decision-making; framing effect; DDC; COMT; SLC6A4; GABA

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Dopamine pathway genes

Serotonin pathway genes

Fig. 1. D (A) (B) (C) (D) (E) (F) (G) (H) (I) (J) (K) (L) (M) (N) (O) (P) (Q) (R) (S) (T) (U) (V) (W) (X) (Y) (Z) (AA) (AB) (AC) (AD) (AE) (AF) (AG) (AH) (AI) (AJ) (AK) (AL) (AM) (AN) (AO) (AP) (AQ) (AR) (AS) (AT) (AU) (AV) (AW) (AX) (AY) (AZ) (BA) (BB) (BC) (BD) (BE) (BF) (BG) (BH) (BI) (BJ) (BK) (BL) (BM) (BN) (BO) (BP) (BQ) (BR) (BS) (BT) (BU) (BV) (BW) (BX) (BY) (BZ) (CA) (CB) (CC) (CD) (CE) (CF) (CG) (CH) (CI) (CJ) (CK) (CL) (CM) (CN) (CO) (CP) (CQ) (CR) (CS) (CT) (CU) (CV) (CW) (CX) (CY) (CZ) (DA) (DB) (DC) (DD) (DE) (DF) (DG) (DH) (DI) (DJ) (DK) (DL) (DM) (DN) (DO) (DP) (DQ) (DR) (DS) (DT) (DU) (DV) (DW) (DX) (DY) (DZ) (EA) (EB) (EC) (ED) (EE) (EF) (EG) (EH) (EI) (EJ) (EK) (EL) (EM) (EN) (EO) (EP) (EQ) (ER) (ES) (ET) (EU) (EV) (EW) (EX) (EY) (EZ) (FA) (FB) (FC) (FD) (FE) (FF) (FG) (FH) (FI) (FJ) (FK) (FL) (FM) (FN) (FO) (FP) (FQ) (FR) (FS) (FT) (FU) (FV) (FW) (FX) (FY) (FZ) (GA) (GB) (GC) (GD) (GE) (GF) (GG) (GH) (GI) (GJ) (GK) (GL) (GM) (GN) (GO) (GP) (GQ) (GR) (GS) (GT) (GU) (GV) (GW) (GX) (GY) (GZ) (HA) (HB) (HC) (HD) (HE) (HF) (HG) (HH) (HI) (HJ) (HK) (HL) (HM) (HN) (HO) (HP) (HQ) (HR) (HS) (HT) (HU) (HV) (HW) (HX) (HY) (HZ) (IA) (IB) (IC) (ID) (IE) (IF) (IG) (IH) (II) (IJ) (IK) (IL) (IM) (IN) (IO) (IP) (IQ) (IR) (IS) (IT) (IU) (IV) (IW) (IX) (IY) (IZ) (JA) (JB) (JC) (JD) (JE) (JF) (JG) (JH) (JI) (JJ) (JK) (JL) (JM) (JN) (JO) (JP) (JQ) (JR) (JS) (JT) (JU) (JV) (JW) (JX) (JY) (JZ) (KA) (KB) (KC) (KD) (KE) (KF) (KG) (KH) (KI) (KJ) (KL) (KM) (KN) (KO) (KP) (KQ) (KR) (KS) (KT) (KU) (KV) (KW) (KX) (KY) (KZ) (LA) (LB) (LC) (LD) (LE) (LF) (LG) (LH) (LI) (LJ) (LK) (LL) (LM) (LN) (LO) (LP) (LQ) (LR) (LS) (LT) (LU) (LV) (LW) (LX) (LY) (LZ) (MA) (MB) (MC) (MD) (ME) (MF) (MG) (MH) (MI) (MJ) (MK) (ML) (MM) (MN) (MO) (MP) (MQ) (MR) (MS) (MT) (MU) (MV) (MW) (MX) (MY) (MZ) (NA) (NB) (NC) (ND) (NE) (NF) (NG) (NH) (NI) (NJ) (NK) (NL) (NM) (NN) (NO) (NP) (NQ) (NR) (NS) (NT) (NU) (NV) (NW) (NX) (NY) (NZ) (OA) (OB) (OC) (OD) (OE) (OF) (OG) (OH) (OI) (OJ) (OK) (OL) (OM) (ON) (OO) (OP) (OQ) (OR) (OS) (OT) (OU) (OV) (OW) (OX) (OY) (OZ) (PA) (PB) (PC) (PD) (PE) (PF) (PG) (PH) (PI) (PJ) (PK) (PL) (PM) (PN) (PO) (PP) (PQ) (PR) (PS) (PT) (PU) (PV) (PW) (PX) (PY) (PZ) (QA) (QB) (QC) (QD) (QE) (QF) (QG) (QH) (QI) (QJ) (QK) (QL) (QM) (QN) (QO) (QP) (QQ) (QR) (QS) (QT) (QU) (QV) (QW) (QX) (QY) (QZ) (RA) (RB) (RC) (RD) (RE) (RF) (RG) (RH) (RI) (RJ) (RK) (RL) (RM) (RN) (RO) (RP) (RQ) (RR) (RS) (RT) (RU) (RV) (RW) (RX) (RY) (RZ) (SA) (SB) (SC) (SD) (SE) (SF) (SG) (SH) (SI) (SJ) (SK) (SL) (SM) (SN) (SO) (SP) (SQ) (SR) (SS) (ST) (SU) (SV) (SW) (SX) (SY) (SZ) (TA) (TB) (TC) (TD) (TE) (TF) (TG) (TH) (TI) (TJ) (TK) (TL) (TM) (TN) (TO) (TP) (TQ) (TR) (TS) (TT) (TU) (TV) (TW) (TX) (TY) (TZ) (UA) (UB) (UC) (UD) (UE) (UF) (UG) (UH) (UI) (UJ) (UK) (UL) (UM) (UN) (UO) (UP) (UQ) (UR) (US) (UT) (UU) (UV) (UW) (UX) (UY) (UZ) (VA) (VB) (VC) (VD) (VE) (VF) (VG) (VH) (VI) (VJ) (VK) (VL) (VM) (VN) (VO) (VP) (VQ) (VR) (VS) (VT) (VU) (VV) (VW) (VX) (VY) (VZ) (WA) (WB) (WC) (WD) (WE) (WF) (WG) (WH) (WI) (WJ) (WK) (WL) (WM) (WN) (WO) (WP) (WQ) (WR) (WS) (WT) (WU) (WV) (WW) (WX) (WY) (WZ) (XA) (XB) (XC) (XD) (XE) (XF) (XG) (XH) (XI) (XJ) (XK) (XL) (XM) (XN) (XO) (XP) (XQ) (XR) (XS) (XT) (XU) (XV) (XW) (XX) (XY) (XZ) (YA) (YB) (YC) (YD) (YE) (YF) (YG) (YH) (YI) (YJ) (YK) (YL) (YM) (YN) (YO) (YP) (YQ) (YR) (YS) (YT) (YU) (YV) (YW) (YX) (YZ) (ZA) (ZB) (ZC) (ZD) (ZE) (ZF) (ZG) (ZH) (ZI) (ZJ) (ZK) (ZL) (ZM) (ZN) (ZO) (ZP) (ZQ) (ZR) (ZS) (ZT) (ZU) (ZV) (ZW) (ZX) (ZY) (ZZ)

SLC6A3), (COMT), (MAOA) (MAOB) (TPH 1 (TPH2), (HTR1A/B/D/E/F, HTR2A/B/C, HTR3A/B/C/D/E, HTR4, HTR5A/B, HTR6-7, HTRA1-4), (SLC6A4) (HTR3E) (DRD2, DRD3, DRD4, DRD1, DRD5, HTR1A/B/D/F, HTR5B, HTRA2) (G A (LI K (et al., 2007; et al., 2014): (H E (AF) 0.1 () 0.05 () 0.05 () (D) (et al., 2006; et al., 2007) (et al., 2006). F

Principle component analysis

A (C) (LD (A, 2008). (C) (A, 2008; et al., 2014). (LD (et al., 2001; et al., 2001; G et al., 2002), (1). F DDC 47 G A

Gene-behavior association analysis

(A, 2008; H et al., 2011,) -F

Table 1.

D	m	F _v	G	C	% _v	R ²	A	R ²	Partial-F	P _{unc}	P _{perm}	P _{emp}													
													TH	DDC	VMAT2	DAT1	COMT	MAOA	MAOB	DRD1	DRD2	DRD3	TPH1	TPH2	SLC6A4
			TH	2	2	100	0.001	<0.001	0.712	0.491	0.484	0.485													
			DDC	47	6	90	0.010	0.006	2.329	0.031*	0.031*	0.038*													
			VMAT2	17	9	90	0.003	<0.001	0.501	0.875	0.878	0.862													
		/	DAT1	16	6	91	0.005	<0.001	1.027	0.406	0.408	0.466													
		C	COMT	18	6	91	0.012	0.009	2.648	0.015*	0.014*	0.027*													
			MAOA	6	3	90	0.003	<0.001	1.143	0.331	0.325	0.346													
			MAOB	37	5	92	0.005	0.002	1.367	0.234	0.232	0.293													
			DRD1	1	1	100	0.000	<0.001	0.097	0.756	0.756	0.780													
			DRD2	16	8	90	0.004	<0.001	0.721	0.673	0.680	0.770													
			DRD3	41	12	92	0.014	0.006	1.617	0.081	0.081	0.099													
			TPH1	2	2	100	0.001	<0.001	0.719	0.487	0.476	0.477													
			TPH2	6	4	93	0.002	<0.001	0.519	0.721	0.718	0.753													
			SLC6A4	8	3	90	0.006	0.004	2.795	0.039*	0.038*	0.037*													
			HTR1E	16	6	91	0.007	0.003	1.545	0.160	0.158	0.199													
			HTR2A	44	12	90	0.013	0.005	1.492	0.120	0.121	0.123													
			HTR2B	3	2	100	0.001	<0.001	0.596	0.551	0.551	0.519													
			HTR2C	22	8	90	0.006	<0.001	0.920	0.499	0.499	0.517													
			HTR3A	4	4	100	0.001	<0.001	0.364	0.834	0.831	0.833													
			HTR3B	22	6	90	0.001	<0.001	0.228	0.968	0.967	0.970													
			HTR3C	2	1	99	0.000	<0.001	0.124	0.725	0.724	0.677													
			HTR4	46	14	91	0.015	0.005	1.422	0.135	0.136	0.075													
			HTR5A	7	4	92	0.006	0.003	1.866	0.114	0.114	0.118													
			HTR6	2	1	100	0.000	<0.001	0.000	0.990	0.992	0.982													
			HTR7	22	6	93	0.006	0.002	1.316	0.247	0.242	0.301													
			HTRA1	34	9	91	0.007	<0.001	0.974	0.460	0.456	0.441													
			HTRA3	19	5	92	0.004	0.001	1.133	0.341	0.356	0.370													

C, m, %_v, R², A, R², Partial-F, P_{unc}, P_{perm}, P_{emp}; * P < 0.05.

Principle component analysis (PCA) was used to identify the genetic architecture of the data. The first principal component (PC1) explained 6.2% of the variance (F = 1.0, P = 0.001). The second principal component (PC2) explained 0.62% of the variance (F = 1.0, P = 0.001). The third principal component (PC3) explained 0.08% of the variance (F = 1.0, P = 0.001).

$$F_k, df(full) = \frac{RSS(reduced) - RSS(full)}{df(reduced) - df(full)} / \frac{RSS(full)}{df(full)} \quad (1)$$

Gene-behavior association results (COMT, SLC6A, DDC, MAOB; COMT: P = 0.028, SLC6A4: P = 0.029, MAOB: P = 0.070). Permutation tests (H et al., 2011; et al., 2014). Empirical tests (C, 2003), m = 0.62% ± 0.08% (E) (1). A

Gene-behavior association results (COMT, SLC6A, DDC, MAOB; COMT: P = 0.028, SLC6A4: P = 0.029, MAOB: P = 0.070).

Permutation tests

(H et al., 2011; et al., 2014). (B m, 2001; 2004; C m et al., 2008; G m et al., 2014), P). (C, 2003).

Empirical tests

m

MAOB $R^2 = 0.028$,
 $-F = 2.499$, $P = 0.031$.
 $(P = 0.038)$ $(P = 0.043)$.
 MAOA
 CA
 SLC6A4
 COMT
 MAOB
 I G
 (COMT, SLC6A4, DDC MAOB)
 G CA (F 1).
 (H, 1975),
 (F 2
 COMT 4680
 LD
 CHB): 15.1863 0 D 5

m 能 v 能
DDC 能
FC- m 能 v v .

MAOB 能 m m v v
m 能 m

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