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Citation

Achterberg, M., Duijvenvoorde, A. C. K. van, Meulen, M. van der, Bakermans, M. J., & Crone, E. A. M. (2018). Heritability of aggression following social evaluation in middle childhood: An fMRI study. *Human Brain Mapping*, 39(7), 2828-2841.
doi:10.1002/hbm.24043

Version: Not Applicable (or Unknown)

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Downloaded from: <https://hdl.handle.net/1887/67642>

Note: To cite this publication please use the final published version (if applicable).

Heritability of aggression following social evaluation in middle childhood: an fMRI study

Short title: Heritability of aggression and social evaluation

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Supplementary Materials

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Genetic modeling - comparison of parsimonious models

Similarities among twin pairs are divided into similarities due to shared genetic factors (A) and shared environmental factors (C), while dissimilarities are ascribed to unique environmental influences and measurement error (E). Behavioral genetic modeling with the OpenMX package (Neale, et al., 2016) in R (R Core Team, 2015) provides estimates of these A, C, and E components. To investigate whether the more parsimonious AE model (with C fixed to zero), CE model (with A fixed to zero) or E model (with both A and C fixed to zero) showed a better fit to the data, we subtracted the log-likelihood of the AE and CE models from the log-likelihood of the ACE model and the fit of the E model from the fit of the AE or CE models to get an estimate of the Log-likelihood Ratio Test (LRT). In most circumstances LRT follows the X^2 distribution, with 3.84 as a critical value at $p=.05$, thus a $LRT > 3.84$ indicates a significantly worse fit of the data. In addition, we used the Akaike Information Criterion (AIC; Akaike (1974)) a standardized model-fit metric, to compare the different models. Lower AIC values indicate a better model fit. When ACE models show the best fit, both heritability, shared and unique environment are important contributors to explain the variance in the outcome variable. AE models indicate that genetic and unique environmental factors play a role; whilst CE models indicate influences of the shared environment and unique environment. If the E model has no worse fit than AE or CE models, variance in the outcome variable is accounted for by unique environmental factors and measurement error.

Table S1. Twin analyses on noise blast difference scores. ACE models compared to parsimonious AE, CE and E models.

Noise blast difference	model	A ²	C ²	E ²	LTR	AIC
Negative - Positive	* ACE	0.20	0.06	0.74		7542.16
	AE	0.24	-	0.76	4.17	7544.33
	CE	-	0.14	0.86	38.67	7578.84
	E	-	-	1.00	>22.18	7599.02
Negative - Neutral	ACE	0.10	0.08	0.82		7173.47
	AE	0.09	-	0.91	-0.33	7171.13
	* CE	-	0.20	0.80	-.5.58	7165.88
	E	-	-	1.00	>23.81	7192.95
Neutral - Positive	ACE	0.10	0.00	0.90		6888.43
	AE	0.10	-	0.90	<.001	6886.43
	CE	-	0.07	0.93	0.19	6886.63
	* E	-	-	1.00	<1.39	6885.83

¹ LTR < 3.85 equals a significant better fit of the model ($p < .05$)

² Lower AIC values indicate a better model fit

* asterics indicate the best model fit

Table S2. Twin analyses on brain activation in the regions of interest (ACC: Anterior Cingulate Cortex; PFC: prefrontal cortex; IFG: inferior frontal gyrus; SMA: supplementary motor area; DLPFC: dorsolateral prefrontal cortex). ACE models compared to parsimonious AE, CE and E models for

ROI	model	A ²	C ²	E ²	LTR ¹	AIC ²
<i>Conjunction Negative>Neutral and Positive>Neutral</i>						
ACC gyrus	ACE	0.00	0.04	0.96		944.02
	AE	0.02	-	0.98	0.38	942.41
	CE	-	0.04	0.96	<0.001	942.02
	* E	-	-	1.00	<0.50	940.53
Left Insula	ACE	0.00	0.00	1.00		1130.48
	AE	0.00	-	1.00	<0.001	1128.48
	CE	-	0.00	1.00	<0.001	1128.48
	* E	-	-	1.00	<0.001	1126.48
Right Insula	ACE	0.01	0.00	0.99		1072.13
	AE	0.01	-	0.99	<0.001	1070.13
	CE	-	0.00	1.00	<0.001	1070.13
	* E	-	-	1.00	<0.001	1068.13
<i>Negative > Positive</i>						
Medial PFC	ACE	0.01	0.00	0.99		950.65
	AE	0.01	-	0.99	<0.001	948.65
	CE	-	0.00	1.00	0.01	948.66
	* E	-	-	1.00	<0.01	946.66
Left IFG	ACE	0.00	0.00	1.00		1141.15
	AE	0.00	-	1.00	<0.001	1139.15
	CE	-	0.00	1.00	<0.001	1139.15
	* E	-	-	1.00	<0.001	1137.15
Right IFG	ACE	0.00	0.04	0.96		1160.12
	AE	0.04	-	0.96	0.07	1158.19
	CE	-	0.04	0.96	<0.001	1158.12
	* E	-	-	1.00	<0.021	1156.32

¹ LTR < 3.85 equals a significant better fit of the model ($p < .05$)

² Lower AIC values indicate a better model fit

* asterics indicate the best model fit

Table S2. (continued)

ROI	model	A ²	C ²	E ²	LTR ¹	AIC ²
Positive > Negative						
SMA	ACE	0.10	0.00	0.90		1003.64
	AE	0.10	-	0.90	<0.001	1001.64
	CE	-	0.00	1.00	0.87	1002.52
	* E	-	-	1.00	<0,87	1000.52
Right caudate	ACE	0.10	0.00	0.90		1308.21
	AE	0.10	-	0.90	<0.001	1306.21
	CE	-	0.08	0.92	0.24	1306.45
	* E	-	-	1.00	<1.48	1305.36
Left DLPFC	ACE	0.13	0.00	0.87		1064.97
	AE	0.13	-	0.87	<0.001	1062.97
	CE	-	0.07	0.93	0.96	1063.93
	* E	-	-	1.00	<1,64	1062.61
Right DLPFC	ACE	0.14	0.00	0.86		1108.45
	AE	0.14	-	0.86	<0.001	1106.45
	CE	-	0.03	0.97	1.83	1108.29
	* E	-	-	1.00	<1.97	1106.42

¹ LTR < 3.85 equals a significant better fit of the model ($p < .05$)

² Lower AIC values indicate a better model fit

* asterics indicate the best model fit

Table S3. MNI coordinates for local maxima activated for the whole brain contrasts without participants with pathology (N=377).

Anatomical Region	Voxels	pFWE	T	x	y	z
<i>Conjunction Negative>Neutral and Positive>Neutral</i>						
Lateral Occipital Cortex	3379	<.001	13,74	-45	-82	1
			13,57	-48	-76	-5
			12,52	48	-70	-5
Lateral Occipital Cortex	113	<.001	6,81	-24	-64	61
Right insula	80	<.001	6,31	39	23	-11
			6,07	33	17	-14
Left insula	28	.001	5,15	-33	26	-5
			4,95	-30	20	-11
Medial PFC	5	.013	5,03	-6	53	-2
Right IFG	7	.009	4,93	51	23	13
Rostral ACC	31	<.001	4,91	12	47	13
			4,85	3	56	19
			4,81	0	47	10
Left insula (posterior)	2	.024	4,67	-45	14	-5
Supplementary Motor Cortex	1	.032	4,61	6	5	67
Supplementary Motor Cortex	1	.032	4,57	6	11	64
ACC	1	.032	4,52	0	47	1
<i>Negative > Positive</i>						
Occipital pole	132	<.001	16,55	-9	-97	13
Occipital pole	118	<.001	8,39	27	-91	13
			8,19	18	-94	13
Medial PFC	138	<.001	6,95	-9	56	25
			5,46	9	62	25
Left IFG	57	<.001	6,35	-54	29	4
			5,24	-45	26	-8
Right IFG	16	.003	5,15	51	32	-2
			4,86	57	32	7
Right Occipital Fusiform Gyrus	3	.021	4,83	18	-85	-5
Left Lateral Occipital Cortex	9	.008	4,72	-48	-82	1
Left Central Opercular Cortex	1	.033	4,63	-36	-16	25
<i>Positive > Negative</i>						
Lingual gyrus	844	<.001	14,75	6	-76	-2
			13,96	-18	-85	-8
			10,93	18	-73	-11
Right superior frontal gyrus	353	<.001	7,27	24	5	55
			7,07	-6	14	49
			6,41	9	11	52
Right Lateral Occipital Cortex	133	<.001	6,90	30	-82	31
			5,74	42	-76	46
			5,62	39	-73	55

Table S3. (continued)

Anatomical Region	Voxels	pFWE	T	x	y	z
Positive > Negative						
Precuneous	151	<.001	6,14	0	-70	49
			5,20	9	-73	64
Left Superior Frontal Gyrus	98	<.001	6,05	-24	2	58
Right OFC	32	.001	6,03	42	59	-8
			5,62	48	53	-2
			4,89	36	56	-14
Left Lateral Occipital Cortex	58	<.001	5,69	-36	-85	40
			5,36	-39	-70	58
			5,23	-51	-67	49
Left OFC	15	.004	5,68	-45	56	4
Right dorsolateral PFC	47	<.001	5,51	39	32	37
			4,89	39	32	46
Left dorsolateral PFC	41	<.001	5,43	-45	41	34
			5,06	-48	32	37
			4,82	-36	47	40
Right Caudate	6	.012	4,95	9	20	4
Left middle OFC	2	.026	4,88	-18	56	-17
Right Supermarginal gyrus	13	.005	4,82	60	-43	49
			4,62	57	-40	58
Left Supermarginal gyrus	2	.026	4,73	-48	-58	58
Dorsal ACC	3	.021	4,73	6	35	31
Left OFC	2	.026	4,69	-48	50	-5
Left Supermarginal gyrus	1	.033	4,54	-57	-46	55

ACC: Anterior Cingulate Cortex; IFG: Inferior Frontal Gyrus; OFC: Orbitofrontal Cortex; PFC: Prefrontal Cortex

Table S4. Brain-behavior associations without participants with pathology (N=377). Least square regressions with heteroskedasticity corrected standard error estimations with brain activation in the regions of interest predicting behavioral aggression.

		Conjunction			Negative>Positive			Positive>Neutral			
Noise blast difference		ACC gyrus	left insula	right insula	medial PFC	left IFG	right IFG	SMA	right caudate	left DLPFC	right DLPFC
Negative - Positive	<i>r</i>	.08	.08	.07	.01	.03	.05	.11	.04	.09	.13
	<i>p</i>	.146	.125	.186	.832	.548	.407	.032	.433	.083	.019
Negative - Neutral	<i>r</i>	.06	.09	.03	.01	.00	.05	.09	.00	.13	.13
	<i>p</i>	.263	.096	.504	.817	.896	.346	.089	.914	.011	.014

ACC: Anterior Cingulate Cortex; DLPFC: dorsolateral Prefrontal Cortex IFG: Inferior Frontal Gyrus; OFC: Orbitofrontal Cortex; PFC: Prefrontal Cortex; SMA: Supplementary Motor Cortex