

# **Brain serotonin deficiency affects female aggression**

*Niklas Kästner<sup>\*1,2</sup>, S. Helene Richter<sup>1,2</sup>, Sarah Urbanik<sup>3</sup>, Joachim Kunert<sup>3</sup>, Jonas Waider<sup>4</sup>, Klaus-Peter Lesch<sup>4,5,6</sup>, Sylvia Kaiser<sup>1,2</sup>, Norbert Sachser<sup>1,2</sup>*

## Affiliations

<sup>1</sup> Department of Behavioural Biology, University of Münster, Germany

<sup>2</sup> Münster Graduate School of Evolution, University of Münster, Germany

<sup>3</sup> Department of Mathematical Statistics and Applications in Science, Technical University of Dortmund, Germany

<sup>4</sup> Division of Molecular Psychiatry, Center of Mental Health, University of Würzburg, Würzburg, Germany

<sup>5</sup> Laboratory of Psychiatric Neurobiology, Institute of Molecular Medicine, I.M. Sechenov First Moscow State Medical University, Moscow, Russia

<sup>6</sup> Department of Neuroscience, School for Mental Health and Neuroscience (MHeNS), Maastricht University, Maastricht, The Netherlands

## Supplementary Methods M1

### Detailed statistical analyses

Global Test: We tested the hypothesis

$H_0$ : There is no effect of the focal animal's genotype to the focal animal's behaviours *approaching, facial/body sniffing, ano-genital sniffing, following, chasing, attacking, escalated fighting, avoiding, fleeing and mounting.*

against the alternative

$H_1$ : There is an effect of the focal animal's genotype to at least one of the focal animal's behaviours *approaching, facial/body sniffing, ano-genital sniffing, following, chasing, attacking, escalated fighting, avoiding, fleeing or mounting.*

A standard method to compare two vectors of means is Hotelling's  $T^2$ - test with test statistic

$$T^2 = \frac{n_1 * n_2}{n_1 + n_2} (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2)^T \mathbf{S}^{-1} (\bar{\mathbf{x}}_1 - \bar{\mathbf{x}}_2) \frac{n_1 + n_2 - p - 1}{p * (n_1 + n_2 - 1)}$$

where  $n_1 = 20$  is the number of animals with genotype WT,  $n_2 = 20$  is the number of animals with genotype KO,  $p = 10$  is the number of variables (behaviours),  $\bar{\mathbf{x}}$  describes the sample mean and  $\mathbf{S}$  describes the sample covariance. Under  $H_0$ , the test statistic  $T^2$  approximately follows an  $F$  distribution with  $p = 10$  and  $n_1 + n_2 - p - 1 = 29$  degrees of freedom<sup>1</sup>. The behavioural data clearly were not normally distributed. This suggests that the assumption of an  $F$  distribution may not be appropriate. We therefore applied a permutation test at significance level 5% with 10,000 permutations using the test statistic  $T^2$ .

Further Analysis (descriptive): We further analysed the behavioural data for an effect of the focal animal's genotype, the partner animal's genotype and for an effect of interactions between these factors on each single focal animal's behaviour. For each effect and each behaviour, we applied a permutation test at level 5%. Note that (to avoid the so-called inflation of the alpha-level) an interpretation of the results is valid only in a descriptive sense. For a

fixed behaviour, let  $x_{klj}^{(d)}$  describe the behaviour of focal animal  $j \in \{1, \dots, 10\}$  in group  $(k, l)$ ,  $k, l \in \{1 = WT, 2 = KO\}$ , at day  $d \in \{1, 5\}$ . We assume that the variables satisfy the following identities

$$E(x_{WT,WT,j}^d) = \mu + \alpha + \beta + \gamma \quad E(x_{WT,KO,j}^d) = \mu + \alpha - \beta - \gamma$$

$$E(x_{KO,WT,j}^d) = \mu - \alpha + \beta - \gamma \quad E(x_{KO,KO,j}^d) = \mu - \alpha - \beta + \gamma$$

where  $\alpha$  describes the effect of the focal animal's genotype,  $\beta$  describes the effect of the partner animal's genotype and  $\gamma$  describes the effect of interactions between focal and partner animal's genotype. Then each group's sample mean yields an estimator for

$$\mu + (-1)^{k+1}\alpha + (-1)^{l+1}\beta + (-1)^{k+l}\gamma$$

For that reason, the application of a permutation test requires an appropriate adjustment of the observations such that a certain mean coincides with a certain effect. Therefore, for each permutation, we first adjusted the observations and then calculated the test statistic.

In the case of the focal animal's genotype, we tested the hypothesis  $H_0: \alpha = 0$  against the alternative  $H_1: \alpha \neq 0$ , in the case of the partner animal's genotype, we tested the hypothesis  $H_0: \beta = 0$  against  $H_1: \beta \neq 0$ , and in the case of interactions we tested the hypothesis  $H_0: \gamma = 0$  against  $H_1: \gamma \neq 0$ . In each case, we use an adjusted  $t$ -test statistic.

Reference:

1. Srivastava & Carter (1983). An introduction to applied multivariate statistics. North Holland, New York.

## Supplementary Dataset S1