

Overview of study protocol timing for **A systematic review of *Drosophila* short-term-memory genetics: meta-analysis reveals robust reproducibility**

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Protocol component	Timing
The main hypothesis: “ <i>Drosophila</i> memory genetics has limited reproducibility”	Proposed prior to data extraction.
The search phrase	Formulated prior to data extraction.
Eligibility criteria	Initially homozygous, heterozygous, and RNA-interference alleles were included. After data extraction, heterozygous mutants were excluded after the decision was made that these represented insufficiently severe alleles.
Databases	EMBASE database was decided upon during the study, after reviewers for another study (Mohammad et al., 2016) recommended that at least two databases be used for a meta-analysis.
Summary measures	Decided prior to data extraction (Yildizoglu et al., 2015).
Outlier effect size exclusion	This was formulated after data extraction and initial rounds of analysis, when it became apparent that single outliers were contributing to elevated heterogeneity. Outlier trimming is an established method in biostatistics (Pagano et al., 2000). For transparency, the outliers are plotted in the forest plots in gray.

Replication categories	Established prior to data extraction.
Reproducibility measures	Heterogeneity inspection was planned <i>a priori</i> ; the MAD metric was devised during the study.

References

Mohammad, F., Ho, J., Woo, J.H., Lim, C.L., Poon, D.J.J., Lamba, B., and Claridge-Chang, A. (2016). Concordance and incongruence in preclinical anxiety models: Systematic review and meta-analyses. *Neurosci. Biobehav. Rev.*

Pagano, M., Gauvreau, K., and Pagano, M. (2000). *Principles of biostatistics* (Duxbury Pacific Grove, CA).

Yildizoglu, T., Weislogel, J.-M., Mohammad, F., Chan, E.S.-Y., Assam, P.N., and Claridge-Chang, A. (2015). Estimating Information Processing in a Memory System: The Utility of Meta-analytic Methods for Genetics. *PLoS Genet.* *11*, e1005718.