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NEWS

Announcement of the Fulker Award for a Paper Published in Behavior Genetics, Volume 48, 2018

The Fulker Award was established by the Behavior Genetics Association in memory of David Fulker, a past President of the Association and Executive Editor of the journal, who died in 1998 (Hewitt 1998). The award is for 'a particularly meritorious paper' published in the journal during the preceding year. The annual prize is $1000 'and a nice bottle of wine' (given only when the recipient is present at the Association's annual meeting).

Volume 48 included 38 rigorously peer reviewed papers on human and animal behavior genetics, including both methodological and empirical studies. To select the paper for the Fulker award, I solicit nominations from the journal's Associate Editors and follow their advice closely.

Six different papers were nominated by the Associate Editors; this year there was an emphasis on outstanding human empirical and methodological papers, and several that combined both topics. Among the papers nominated were Dorret Boomsma et al. (2018) report of an extended twin-pedigree study of neuroticism in the Netherlands Twin Register, Moscati et al.'s (2018) Cross-lagged analysis of interplay between differential traits in sibling pairs, Laurin et al.'s (2018) paper on Partitioning phenotypic variance due to parent-of-origin effects using genomic relatedness matrices, Park et al.'s (2018) Adaptive SNP-set association testing in generalized linear mixed models with application to family studies, and Ip et al.'s (2018) very nice paper exploring the role of tissue specificity in the relation between expression QTLs and complex traits. These are five incredibly high quality papers that I hope we will all take the time to read, use, and cite in our own research.

However, this year's winner is a methodological paper that opens up the possibility of utilizing the wealth of twin study data that many of us have collected, and are collecting, in the context of tests of causation employing Mendelian randomization. Specifically, the paper sets out a model that elegantly and powerfully extends traditional twin study based causality tests by incorporating genetic instruments like polygenic risk scores. There are a number of challenges in doing this, and assumptions that have to be identified and tested. There are many ways to get this wrong, but this rigorous paper provides an approach that demonstrates the complementarity and synergy of genome wide molecular data combined with traditional twin and family studies—something that is important to many of us. So congratulations to Camelia Minica, Connor Dolan, Dorret Boomsma, Eco deGeus, and Mike Neale (2018) for this year's Fulker Award winning paper: Extending causality tests with genetic instruments: an integration of Mendelian randomization with the classical twin design.

John K. Hewitt
Editor-in-Chief

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