# **Development of reporting guidelines for pharmacogenetic studies to facilitate evidence synthesis**

Outcomes in pharmacogenetic studies are often explained by several genetic variants each having a small effect on outcome. Consequently, large sample sizes are typically required to detect statistically significant associations between a pharmacogenetic marker and treatment response. Meta-analysis allows aggregation of data from several studies to increase sample size, and consequently power to detect significant genetic effects. However, differences often exist between pharmacogenetic studies in terms of the genetic variants investigated, how genetic subgroups are defined, outcome definitions, and the underlying assumptions made, for example about mode of inheritance, within the analyses. Since combining studies within a meta-analysis relies on them investigating the same underlying effect, these differences can significantly reduce the number of contributing studies. This problem is compounded by poor reporting of key data in study reports. The aim of our project is to develop reporting guidelines for authors of pharmacogenetic studies in order to facilitate the conduct of high-quality systematic reviews and meta-analyses. To produce this set of guidelines, we established a preliminary checklist of reporting items by i) including items from existing relevant guidelines, and ii) supplementing this list with any additional items thought to be important, identified through discussion and personal experience in conducting meta-analyses of pharmacogenetic studies. We have identified additional criteria specific to pharmacogenetic studies that are not specified in existing guidelines, and that are often not adhered to in pharmacogenetic study reports. We are currently planning a Delphi survey to gain consensus opinion on reporting items for our final reporting guideline.