Metformin Genetics (MetGen) Consortium

Rules of Engagement

1. This consortium consists of partners who share a common interest in investigating the phenotypic and genetic determinants of metformin response.

2. The aim of the consortium is to collaborate to replicate phenotypic and genetic findings relating to metformin response.

3. The consortium will be administered by Ewan Pearson, who will collate requests and lists of members.

4. Membership of the consortium is open to anyone with metformin response cohorts of >100 patients. All participants should 'sign up' to these rules of engagement by return of email stating that they agree with the rules.

5. Members who wish for a genetic variant or phenotypic model to be replicated within the consortium should produce a short rationale detailing the background and initial findings and pass this to Ewan, who will check against previous or ongoing work and assuming no duplication of request, will circulate to the consortium. All consortium members will consider any data circulated confidential.

6. The consortium is unfunded so genotyping will usually be done at each group's cost; unless one partner has funding and is able to fund the replication analysis in all groups. No partner is obliged to undertake the replication.

7. If a genetic variant is proposed for analysis or a phenotypic model is proposed for replication and this overlaps (same gene/SNP/model) with work ongoing within a group such that there is a clear conflict then the group should declare this conflict as soon as possible (within 1 week of notification of the analysis proposal). A likely outcome would be that both groups would work together on this data.

8. 'No surprises'. Any information material to the objectives of the MetGen consortium should be declared openly to others. (This might include participation in parallel efforts, existing work on a gene of interest etc)

9. Publication. Any consortium publication will consist of up to three (exceptionally four) authors from each consortium where contribution of each author to the work can be justified. However, the group who has made the original observation that is seeking replication can decide on how many 'discovery' authors are included. Changes to this arrangement can be made by agreement of consortium members on a paper-by-paper basis. The allocation of first and last author will usually be clear and will be according to who has had the original discovery and/or whose data contributes most critically to the results. Where possible: "for the MetGen Consortium" will

be included in the author list. Consortium members who are not active in that paper and therefore not co-authors will be listed as collaborators in the online Appendix.