



I am writing to respond to the questions regarding MRC funding for research in genomic medicine in your e-mail of 9th May, and also to follow up with some more detail on points made in the oral evidence session on 30th April.

Within the total figure of £50 million spend in the financial year 2006/7, the major scientific categories are, Genetics of specific disease, Genetic epidemiology, Genome instability (all > £9m p.a.), followed by Global Health and Gene therapy (£3m - £4m p.a.). Spend on genetic biomarkers and pharmacogenomics, is as yet very low (<£2m p.a.).

The spend was split across various forms of support as follows:

| Type of funding | Amount spent in 2006/07 |
|-------------------------|-------------------------|
| Fellowship (extramural) | £2 million |
| Grant (extramural) | £15 million |
| Unit (intramural) | £33 million |
| Grand Total | £50 million |

Our records show, in addition to the UK Biobank project to which MRC has committed a total of £26.5 million to date:

The three major MRC Institutes (NIMR, LMB, CSC), and the MRC Human Genetics Unit, Functional Genomics Unit; Epidemiology Unit; and Mammalian Genetics Unit all represent investments of over £5m every quinquennium.

There are 4 individual grant programmes of more than £5 million each – though in some cases the investment covers 5-10 years, as the grant has been renewed:

| Type | Principal Investigator | Organisation | Title | Amount Awarded* |
|------------|--|--|---|-----------------|
| Grant | Professor J Connell / Professor M Caulfield | University of Glasgow / Queen Mary, University of London | The MRC British Genetics of Hypertension Study | £5.1 million |
| Grant | Professor T Moffitt | Institute of Psychiatry | Gene - environment interplay in early-onset psychopathology | £5.4 million |
| Grant | Professor J Golding | University of Bristol | ALSPAC: A reference population for genetic & environmental epidemiology | £8.3 million |
| Unit/Grant | Professor T Rabbitts** | MRC Laboratory of Molecular Biology / Leeds | Modelling the role of chromosomal abnormalities in cancer | £5.4 million |

*For the grants, the Amount Awarded is the amount awarded over the whole life of the grant. For the unit project, it is the amount spent over the period 2003/04 to 2006/07 (comparable Amount Awarded not available).

**Professor Rabbitts has since moved to the University of Leeds where he has a somewhat smaller MRC funded programme.

Complete figures for spend on Genomic Medicine are only available from 2003/04 onwards. They are as follows:

| Spend | Total |
|---------|-------------|
| 2003/04 | £49 million |
| 2004/05 | £36 million |
| 2005/06 | £52 million |
| 2006/07 | £50 million |

MRC spend on genomic research and genomic medicine over the next 3-5 years is difficult to estimate, but it is likely to remain at approximately the same level.

Professor Van Heyningen has provided some additional information to follow up the points made in the oral session. She confirms that availability of sufficient computer processing power is currently a problem in carrying out discovery phase studies to identify genetic risk. The initial genome-wide association studies with individual markers are feasible, but it is not possible to do genome-wide haplotype analysis or imputation for lack of computing power, even when using the Edinburgh Parallel Computing Centre. Marker interactions are also not feasible to assess genome-wide.

Population stratification will be and is already beginning to be feasible for determining on the basis of allelic markers who should be screened for several cancer phenotypes, for example colorectal and breast cancer.

In many later onset diseases there is a very significant genetic component as yet unaccounted for by genetic association studies. Re-sequencing and identification of rare larger effect variants is going to be important for many diseases where we know there is quite a lot of familial recurrence but where common variants do not account for a large proportion of this genetic component. The recent Science paper (Walsh et al Science. 2008 Apr 25; 320(5875):539-43) associating copy number variants (CNVs) with schizophrenia is a potential landmark. Much of the familial risk will come from rare large effect variants coming from a moderately large pool of genes. It will be difficult to identify which are causative pathological mutations but this area will probably be more important clinically because the effects are much stronger and risk predictions correspondingly improved. There is a need for increased re-sequencing capacity and also more research on how best to identify causative variation.

I hope this additional information is helpful to the committee.