Report of the Australian Genetic Testing Survey 2006

Contact for this document:

Dr G Suthers
PhD FRACP FRCPA
Familial Cancer Unit
Department of Genetic Medicine
Children's Youth & Women's Health Service
North Adelaide SA 5006

Tel 08-8161 6995
Email graeme.suthers@health.sa.gov.au

This document has been prepared for the Royal College of Pathologists of Australasia in consultation with the Human Genetics Society of Australasia. The views expressed in this document do not necessarily represent the views of either organisation.

File name: **Australian Gene Survey 2006**
Version date: **31 July 2009**

Table of Contents

Summary

1. **Advances in genetic knowledge have led to the introduction of genetic tests for clinical purposes. Information regarding the current level of testing in Australia would assist in the development of policy and resourcing for such testing.**
2. **In 2007-08, the Royal College of Pathologists of Australasia undertook a survey to document the genetic testing provided in Australia during 2006, with projections for 2007. The survey was funded by the Australian Department of Health & Ageing through the Quality Use of Pathology Program, and involved close collaboration with the Human Genetics Society of Australasia.**
3. **The goal of the survey was to place data about current genetic testing activity in the public domain. This Report summarises the data but does not make recommendations arising from the Survey.**
4. **56 laboratories were identified as providing molecular genetic testing for clinical purposes during 2006 that was not Medicare-rebated (MBS). Data about MBS tests were obtained from Medicare; laboratories were not queried about this activity. 93% of the 56 laboratories provided data for the Survey.**
5. **During 2006, there were five types of MBS molecular genetic tests. A further 437 types of test were offered by Australian laboratories. 55% of these additional types of test were offered by only one laboratory. A further 21% were offered by only two laboratories.**
6. **There were 41,497 assays for MBS molecular genetic tests i.e. 0.07% of all MBS assays. A further 119,354 assays for non-MBS tests were provided. For 75% of the types of test involved, there were less than 100 assays during the year.**
7. **40% of the assays were for medical screening purposes e.g. pre-transfusion testing or neonatal screening. 28% of the assays were for diagnostic purposes. 8% were assays for non-heritable variants in cancer. 5% of assays were to define the genetic status of unaffected relatives in families with a documented mutation. The reason for testing could not be identified in 18% of assays.**
8. **Half of the types of test were provided by laboratories offering less than 10 types of test; 10% of the laboratories offered 40 or more types of test.**
9. **17% of the laboratories reported doing less than 100 assays during 2006; 27% reported doing more than 1,000 assays during this period.**
10. **The majority of types of test were provided by laboratories in only one State or Territory. Only 56 types of test (13%) were provided by laboratories in four or more regions. Some laboratories provided services for patients in other regions, but the rate of testing was higher for samples from within the region than elsewhere.**
11. **28 laboratories (54%) reported that all the types of test they provided were within the scope of their NATA accreditation. Six (11%) reported that none of the types of test they provided were accredited. 18 (35%) reported that they provided a mixture of accredited and non-accredited types of test.**
12. **83% of all types of test were offered only as accredited tests. 4% were offered only as non-accredited types of test. 8% were offered as both accredited and non-accredited types of test by different laboratories.**
13. **The rate of testing for MBS genetic tests varied from 4-fold to over 10-fold across States and Territories. If the non-MBS test data were pooled for each State and Territory, the greatest difference in testing rates between regions was 21-fold. The unequal rates of testing were confirmed on a test-by-test basis.**
14. **The diversity of types of test offered in 2007 increased by approximately 8%. The number of assays rose by 67%, reflecting an increased volume of MBS testing rather than an increase in non-MBS testing.**

1 Introduction

With the continuing "explosion" of genetic knowledge in medicine, there is an increasing gap between the genetic testing that could be provided and the resources that are available. The provision of such resources will probably require support by State and Federal governments, as well as the private sector, and there are a number of models of service provision that could be developed.

There has been a lack of data regarding the current level of demand and supply of genetic testing in Australia. To address this deficiency, the Royal College of Pathologists of Australasia (RCPA), in consultation with the Human Genetics Society of Australia (HGSA), undertook a survey of the genetic testing provided Australia-wide in 2006. The project was funded by the *Quality Use of Pathology Program* of the Australian Department of Health & Ageing, but the Department was not involved in the data collection, analysis, or the production of this report. Dr Graeme Suthers was appointed Survey Coordinator for the project.

Laboratories in the public, academic, and private sectors in Australia were asked to provide details of the type and volume of molecular genetic testing that they provided for medical purposes in Australia during 2006. Medicare-rebated testing was excluded from the request as this information was already in the public domain, and Medicare data are included in the analysis provided below. Testing for research or non-clinical (e.g. paternity testing) purposes was excluded, as was microbial testing for medical purposes. The letter requesting this information, a copy of the questionnaire, and the guideline for completing the Survey are provided in the Appendix to this Report.

The laboratories were not asked to provide any information that might potentially identify a patient or family. Hence there are no privacy concerns in reporting these data. However, the data could be perceived as being commercially sensitive, and the raw data from each laboratory was deemed to be “privileged” and subject to a confidentiality agreement (see Appendix). The tables in the Report provide pooled information, with no details regarding which laboratory in which sector provided the testing.

It is difficult to predict the future demand for testing. While it is obvious that the demand will increase, the demand is closely linked to the level of awareness of testing by both clinicians and patients, the resources available for testing, and the commitment of funders to promote cost-effective testing. Laboratories were asked to provide activity data (actual or predicted) for 2007 to provide a comparison with the "benchmark" year 2006. It was recognized that this represents a short timeline on which to base projections, but the field is changing and growing rapidly, and projections over a longer timeline would not necessarily have been more accurate.

The principle aim of the Survey has been to provide data to inform research and policy discussion rather than to interpret and present recommendations. Hence this Report does not make recommendations about future policy in relation to genetic testing. This Report will be placed in the public domain.

2 The Survey

2.1 Terminology

The Survey sought data both about the types of investigations performed, and the volume of investigations performed. In this Report, the term "tests" refers to types of molecular genetic investigations, and the term "assays" refers to volume of molecular genetic investigations.

The definition of the term "gene" is by no means simple. For the purpose of this survey, a "gene" was defined as a discrete position or locus in the human genome. The great majority of tests

involved interrogation of a genetic sequence which encodes a protein. However, some tests involved interrogation of discrete regions of non-coding DNA.

A test may involve the simultaneous interrogation of multiple genes. Some methodologies currently allow interrogation of 40 or more genes in a single assay e.g. MLPA for micro-deletions which cause intellectual disability. Although highly parallel (or multiplexed) testing represents an efficient approach to molecular genetic testing, the purpose of this survey was to document the diversity of tests provided rather than the efficiencies with which testing was achieved. If the result of a multiplexed assay was a discrete outcome for each gene interrogated, and if the laboratory identified these genes, this was counted as multiple simultaneous tests i.e. one test per gene.

Tests which provided a result for a whole chromosome e.g. assay for trisomy 21, were not included in the Survey. This excluded most cytogenetic investigations with the exception of fluorescent *in situ* hybridisation (FISH) studies directed at a specific gene.

In presenting the results of the Survey, the term "region" refers to an Australian State or Territory.

2.2 Scope of survey

Laboratories were asked to provide information about tests which fulfilled all of the following criteria:

- DNA- or RNA-based testing of human genes for medical purposes.
- Testing for heritable or non-heritable (somatic) genetic variants.
- The samples being tested were collected within Australia.
- The samples were tested during the 2006 calendar year.
- The testing was either performed in an Australian laboratory, or sent from an Australian laboratory to an overseas laboratory (including New Zealand).
- Testing was performed using non-Medicare funds.

The Survey excluded tests which fulfilled any of the following criteria:

- Testing done using Medicare funds.
- Medical testing of non-human genes (e.g. microbial genetic testing).
- Non-medical testing of human genes (e.g. paternity testing).
- Testing done principally for research purposes in relation to a specific project.
- Testing performed on samples received from overseas (including New Zealand).

Laboratories were asked if they wished to offer testing of this gene through an RCPA/HGSA website. This information will be used in the development of an online resource that will assist healthcare professionals and individuals identify laboratories which provide genetic testing, but this information is not provided in this Report.

2.3 Invitations to laboratories, and the responses

There is no single list of laboratories which provide molecular genetic testing in Australia. For the purpose of this survey, a list of laboratories providing molecular genetic testing was developed from the HGSA website[1] (45 laboratories) and the NATA list of laboratories which have been accredited as providers of medical genetic testing[2] (27 laboratories). The directors of research at all Australian universities were asked to provide contact details for any academic laboratories which might have provided testing during 2006, and a further eight laboratories were identified. The Australian Society of Cytogenetics identified seven laboratories. A total of 11 Red Cross offices and laboratories were contacted. A further three laboratories were identified through personal contacts.

In total, 101 letters of invitation to provide data for the Survey were sent. As might be expected, there was some overlap in the mailout, with 22 contacts being identified as redundant. A further 23 laboratories reported that they did not provide testing within the scope of the Survey during 2006.

[1] www.hgsa.com.au
[2] www.nata.asn.au

Responses from the remaining 56 laboratories provide the basis for this Report. It is recognised that there are probably other laboratories providing molecular genetic testing for clinical purposes in Australia. However, the current Survey appears to cover the great majority of the larger laboratories. One challenge for the future is to develop a better method for identifying laboratories which provide such testing.

Some organisations hosted a number of laboratories, raising the question of how a laboratory should be defined for the Survey. Each response detailing tests and assay volume was counted as "one laboratory", and so some organisations were recorded as having a number of laboratories. A total of 39 postcodes were recorded for the 56 respondents to the Survey.

Invitations were initially posted to laboratories in November 2007. Of the 56 laboratories, 52 (93%) provided data. Three laboratories agreed to provide data but did not do so by the deadline (14 April 2008); one laboratory did not respond to repeated invitations.

The distinction between public sector, private sector, and academic laboratories is not always clear. As an approximation, 60% of the 57 laboratories were categorised as being in the public sector, with 20% being in the private sector and 20% being principally academic laboratories.

2.4 Names of test types

Laboratories used a wide variety of names for tests. For reasons of consistency, protein-encoding genes were named using the standard international nomenclature provided by the Human Genome Nomenclature Committee[3]. Fusion genes i.e. abnormal genes resulting from one gene fragment being linked to another, are not listed by the HGNC but were named following the HGNC conventions (as implemented by Gulley et al [2007]). Other tests were provided with non-standard names which are indicated with the suffix "#" in this Report.

2.5 Tests rebated by Medicare

The Survey did not seek any information about the sources of funding utilised in the provision of genetic testing. The majority of types of test presented in this Report were provided with State funds, research funds, or patient charges. However, a few tests were available on the Medicare Benefits Schedule.

Medicare data were sourced from the Medicare website[4]. This source does not indicate the name or location of the laboratory which provided the test. In addition, the data are tabulated in relation to the patient's place of residence, not the laboratory's location. Hence the Medicare data provides no information about laboratory practice. For this reason, these data are excluded from some of the analyses presented below; such instances are indicated.

The Medicare-funded tests that were available by the end of 2007 are listed below. This list constitutes the complete list of genetic tests (Group P7) in the pathology section of the Schedule. The assay volumes are catalogued in this Report by type of test i.e. HGNC gene name, not by item number. For example, item #73309 is an administrative item that involves testing of the same gene and patient group as described in #73308; the assay volumes for these two items were combined in this analysis. In tabulated data presented in this Report, the suffix "[MBS]" has been added to the test name to distinguish tests funded by Medicare from identical tests funded from other sources.

Item #	Description	Test name
73308	Characterisation of the genotype of a patient for Factor V Leiden gene mutation, or detection of other relevant mutations in the investigation of proven venous thrombosis or pulmonary embolism - 1 or more tests. [Previously #65168]	**F5 [MBS]**

[3] www.genenames.org/

[4] Data from http://www.medicareaustralia.gov.au/statistics/dyn_mbs/forms/mbsgtab4.shtml in April 2008. Non-test items such as the patient episode initiation item were not considered in the Report.

73309	A test described in item 73308, if rendered by a receiving APP – 1 or more tests.	**F5 [MBS]**
73311	Characterisation of the genotype of a person who is a first degree relative of a person who has been proven to have 1 or more abnormal genotypes under item 73308- 1 or more tests. [Previously #65174]	**F5 [MBS]**
73317	Detection of the C282Y genetic mutation of the HFE gene and, if performed, detection of other mutations for haemochromatosis where: (a) the patient has an elevated transferrin saturation or elevated serum ferritin on testing of repeated specimens; or (b) the patient has a first degree relative with haemochromatosis; or (c) the patient has a first degree relative with homozygosity for the C282Y genetic mutation, or with compound. heterozygosity for recognised genetic mutations for haemochromatosis. [Previously #66794]	**HFE [MBS]**
73318	A test described in item 73317, if rendered by a receiving APP - 1 or more tests.	**HFE [MBS]**
73320	Detection of HLA-B27 by nucleic acid amplification. Includes a service described in 71147 unless the service in item 73320 is rendered as a pathologist determinable service.	**HLA-B [MBS]**
73321	A test described in item 73321, if rendered by a receiving APP - 1 or more tests.	**HLA-B [MBS]**
73323	Determination of HLAB5701 status by molecular techniques or cytotoxicity assay prior to the initiation of Abacavir therapy including item 71203 if performed	**HLA-B [MBS]**
73300	Detection of genetic mutation of the FMR1 gene by nucleic acid amplification (NAA) where: (a) the patient exhibits one or more of the clinical features of fragile X (A) syndrome, including intellectual disabilities; or (b) the patient has a relative with a fragile X (A) mutation. 1 or more tests	**FMR1 [MBS]**
73305	Detection of genetic mutation of the FMR1 gene by Southern Blot where the results in item 73300 are inconclusive	**FMR1 [MBS]**
73314	Characterisation of gene rearrangement by nucleic acid amplification in the diagnosis and monitoring of patients with laboratory evidence of: (a) acute myeloid leukaemia; or (b) acute promyelocytic leukaemia; or (c) acute lymphoid leukaemia; or (d) chronic myeloid leukaemia; each test to a maximum of 4 tests in a 12 month. [Previously #65280]	**BCR/ABL1 [MBS]**
73315	A test described in item 73314, if rendered by a receiving APP - 1 or more tests.	**BCR/ABL1 [MBS]**
73289	*Chromosome studies, including preparation, count, karyotyping and identification by banding techniques of blood – 1 or more tests*	
73287	*Chromosome studies, including preparation, count, karyotyping and identification by banding techniques of 1 or more of any tissue of fluid except blood – 1 or more tests*	

The last two items in this table refer to cytogenetic tests that lay outside the scope of the Survey; they are included in the list for completeness, and some comparative data of cytogenetic versus molecular genetics assay volumes are presented below.

Items #73308, #73309, and #73311 refer to analysis for a specific variant in the F5 gene or to “other relevant mutations”. In practice, many laboratories also test for specific variants in F2 and MTHFR in addition to the variant in F5. However, this is not necessarily the case and these MBS items were counted only as tests of F5.

2.6 Accredited testing

Laboratories were asked to note whether the test (as performed in the specified patient group [see below]) was included within the laboratory's scope of practice in 2006. NATA evaluates laboratories which provide medical testing against NPAAC standards. If a laboratory meets those standards within a particular field or scope of laboratory practice e.g. genetics, the laboratory is accredited and is given a specified “scope of accreditation”. The laboratory is obliged to validate (on an ongoing basis) each test performed within that scope of accreditation.

A “non-accredited” test could refer to a test provided by an non-accredited laboratory (i.e. no successful NATA assessment), or to a test provided by a laboratory that has a different scope of accreditation (i.e. successful NATA assessment in another field of pathology e.g. haematology), or a non-validated test provided by an accredited laboratory (i.e. successful NATA assessment in genetics, but validation of the specific test is incomplete). The Survey did not differentiate between these three possibilities.

2.7 Patient groups tested

For each test, laboratories indicated the type of patients being tested. The distinction in patient group was restricted to diagnostic testing, family testing, screening, testing for somatic variants, and unknown.

- “Diagnostic” refers to testing of an affected patient (of any age, including prenatal) to determine the genetic basis of the disease.
- “Family” refers to testing of an unaffected person (of any age, including prenatal) who is at increased risk of carrying the mutation on the basis of family history[5]. This will usually refer to testing for a mutation already identified in the family, and includes predictive/presymptomatic testing, and carrier testing.
- “Pharmacogenetic" refers to testing of an affected person for heritable genetic variants to guide choice and dose of drug treatment.
- “Screening” refers to testing an unaffected person who is not recognised as being at increase risk of carrying a mutation. This includes neonatal screening for cystic fibrosis, or screening a patient for pharmacogenetic variants prior to commencing drug therapy.
- “Somatic” refers to testing for non-heritable variants, typically in cancer tissue.

Two additional categories were defined for coding purposes:

- "Supplementary" refers to additional testing (in any patient group) to clarify an initial result
- “Unknown” refers to testing for unknown purposes.

For MBS-rebated tests, the description in the MBS schedule was used to categorise the test. However, the descriptions for HFE and FMR1 testing encompass both diagnostic and family testing, and for these tests the patient group was categorised as "unknown”.

2.8 Methods of testing

Laboratories were asked to indicate the method used for each test. There is enormous variety in both the types of method and the implementation of each method in different laboratories. For this reason, the categorisation of methodologies used in the Survey was simple and intended to be indicative rather than exhaustive:

- “Mutation screen” referred to screening for unspecified variants by a method such as DHPLC, SSCP, DGGE, PTT etc that is recognised as potentially missing sequence variants.
- “Sequencing” refers to sequencing of the coding regions of the gene (and adjacent intronic regions) to identify unspecified variants.
- “Sequencing plus MLPA” referred to sequencing of the gene plus assays for duplication/deletion of exons (or larger re-arrangements) to detect unspecified variants using dosage assays such as MLPA, QPCR, and FISH.
- “Southern” referred to a Southern or Northern blot study.
- “Specific assay/s” referred to any assay for a specific variant . This included testing for one or more specific sequence variants, sizing a specific allele, testing for an abnormality of gene methylation, and screening for deletions. The key feature of this method is that the test focussed on a specific mutation or class of mutations in a gene, and did not search for other mutations in the gene.
- Fluorescent *in situ* hybridisation (“FISH”) is a specific assay but it was listed separately as it

[5] The term “predictive” was used in the Survey, but this carries a specific and more limited meaning in clinical genetic practice and so the term "family" has been used in this Report.

was performed as a cytogenetic investigation (involving chromosome preparations and light microscopy) rather than the usual molecular genetic methods.
- "Segregation study" referred to a study based on the inheritance of genotypes or haplotypes within a pedigree.
- "Sent overseas" referred to samples sent overseas (including New Zealand) by the laboratory.

If the laboratory used multiple methods to test a gene, the test was categorised on the basis of the least sensitive method used.

2.9 Number of assays

Laboratories listed the number of assays performed for each type of test in the different patient groups in their state during 2006 and 2007.

Laboratories also listed the number of assays performed each year in different patient groups where the patient resided in another Australian State or Territory. Testing for overseas patients (including New Zealand) was excluded. The source of interstate samples was not documented.

2.10 Test sensitivity

Laboratories were asked to estimate the sensitivity of the test in the specific patient group i.e. the proportion of all clinically relevant mutations in this gene that would be detected. For recessive disorders, the sensitivity was defined as the proportion of people with the disease in whom both mutations could be identified. For family testing i.e. testing a relative for a mutation already identified in the family, the sensitivity is, by definition, 100%.

2.11 Detection rate

Laboratories were asked to indicate the proportion of patients tested who had an abnormal result. For recessive disorders, this referred to the proportion of people in whom two mutations (homozygous or compound heterozygote) were identified.

3 Release of survey data

The raw data provided by the laboratories was regarded as confidential. These data were not available to the oversight committee for this project, the RCPA, the HGSA, or any State or Federal Government Department. The raw data were handled only by the Survey Coordinator who signed a confidentiality agreement (see Appendix) with most laboratories; some laboratories provided data without requiring a confidentiality agreement. The raw data were destroyed when this Report was completed.

In this Report, the data are summarised and presented on a regional i.e. State and Territory, basis. The data are not presented in such a way that within-region or between-laboratory comparisons can be made. It is recognised that this approach may effectively identify the only laboratory in a particular region which provides a particular service, but this is unavoidable. State funding is a major consideration in the provision of genetic testing, and regional comparisons were an essential component of the Survey.

Some laboratory-based measures are also included in this Report. They represent pooled data in which there is no identifying information (including any indication of region).

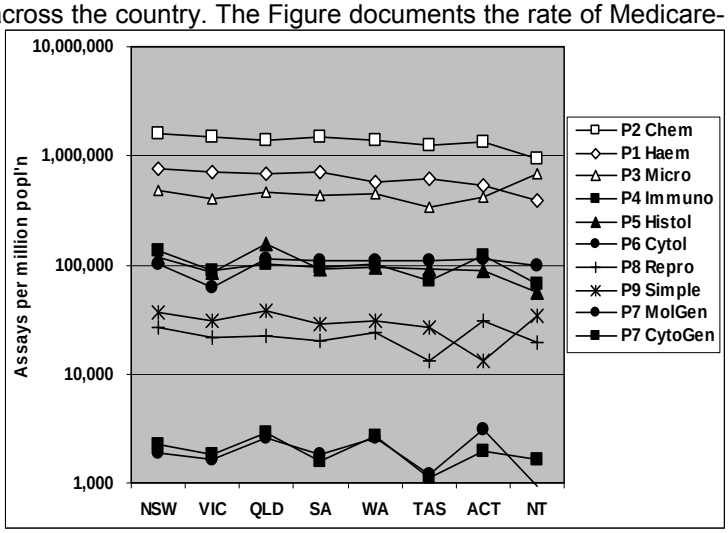
The collated regional and pooled data, including the data underlying figures and graphs in this Report, are tabulated at the end of the Report[6]. These files do not include any identification of the laboratories which provided data.

[6] Electronic copies of this Report (as a WORD file) are available at www.rcpa.edu.au.

4 Medical testing in 2006

During the calendar year 2006, there were 59.5 million pathology assays rebated by Medicare (data in Section **Error! Reference source not found.**). Molecular and cytogenetic assays (Group P7 in the Schedule) accounted for 0.15% of this volume. Cytogenetic assays (items #73287 and #73289) accounted for 52% of the P7 assays i.e. molecular genetic tests that fall within the scope of this Report accounted for just 0.07% of the assays rebated by Medicare during that year.

The rate of testing varied markedly across the country. The Figure documents the rate of Medicare-rebated testing in each of the disciplines of medical testing during 2006. The rates are expressed as tests per million population in each region (population data in Section **Error! Reference source not found.**). Molecular genetic tests and cytogenetic tests have been presented separately. Note that the rate is presented on a logarithmic scale. This highlights that the differences in testing rates across the disciplines varied by three orders of magnitude. Cytogenetic and molecular genetic testing exhibited the lowest rate of utilisation.



However, the logarithmic scale also has the effect of masking differences between regions. Within each discipline, the rate of testing varied by up to 1.7- to 3.3-fold between different regions.

5 Types of test in 2006

Data for this Section are tabulated in Section **Error! Reference source not found.**.

5.1 Types of test

During 2006, 437 different types of test were nominally provided by Australian molecular genetic laboratories. This figure is the number of different types of test for which data were provided for 2006 and 2007.

This figure overestimates the real level of test diversity available during the year. Some types of test were only introduced at the end of the year and should more properly be regarded as being “new tests” that were introduced in 2007. Other types of test were well-established investigations for rare disorders but there were no requests during 2006. In other words, the assay volume for a particular type of test was not necessarily a good guide as to whether the test was an established or new test. Nor did the laboratories always make this distinction clear.

There were 85 types of test (19% of 437) for which there were no assays reported in 2006. Of these, 20 also had no assays reported in 2007. Of the remaining 65 types of test, 61 had 1-10 assays reported in 2007, and the remaining four (<1% of 437) had 11-61 assays. It was likely that these four types of test were new tests in 2007.

In 2007, there were 38 types of test (9% of 437) for which no assays were reported. This included the 20 tests mentioned above for which no assays were reported in either year. Of the remaining 18 types of test, 11 had had small assays volumes (<10 assays per year each) in 2006, and the low level of activity may have simply represented a fluctuation in demand for rare tests. But the

remaining seven (1.6% of 437) had had relatively high assay volumes in the preceding year (12-317 assays per year each) and presumably represented the laboratory ceasing to offer the specific type of test.

These differences in assay volume will be considered in more detail below (Section 11), but there has been no attempt to further dissect when tests were introduced during the period 2006-2007 as only modest assay volumes were reported for 1-2% of tests that appeared to have been introduced or withdrawn during the Survey period. Subsequent discussion in this document refers to the 437 tests irrespective of the possibility that some were introduced or ceased during the Survey period.

5.2 Test nomenclature

Almost all (97%) of these tests were investigations of protein-encoding genes or fusion genes. These tests have been catalogued for this Report using the HGNC approved gene name or the derived name (for fusion genes). It is important to note that the HGNC name is not necessarily the most familiar name for a test. However, in the interests of consistency and reproducibility, the HGNC name has been used in this Report. The Table lists some tests as examples of genes for which the HGNC name may not be readily recognized.

Common name	*HGNC name*
AAT	**SERPINA1**
aml-eto	**RUNX1/RUNX1T1**
bcr-abl	**BRC/ABL1**
CHOP	**DDIT3**
CX26	**GJB2**
CX30	**GJB6**
DM	**DMPK**
DRPLA	**ATN1**
E-cadherin	**CDH1**
FRAXA	**FMR1**
GSD1a	**G6PC**
HD	**HTT**
Lamin A/C	**LMNA**
LIS1	**PAFAH1B1**
MCAD	**ACADM**
MEN2	**RET**
MYH	**MUTY**
p53	**TP53**
Rb	**RB1**
SCA1	**ATXN1**
SCA2	**ATXN2**
SCA3	**ATXN3**
SCA6	**CACNA1A**
SCA7	**ATXN7**
tel-aml	**ETV6/RUNX1**
TWIST	**TWIST1**

Tests described as “Prader-Willi/Angelman” (or similar) were coded as being tests of both UBE3A and SNRPN. It is recognized that there are a number of potential targets that could be interrogated on this region of chromosome 15, but specific details were not provided by some laboratories. Similarly, “ANCR” was coded as UBE3A.

Some immunogenetic tests are conventionally described according to the specific DNA variant being sought e.g. HLA-B5701, or HLA-B27. For the purpose of this Report these tests were simply designated as HLA-B tests involving a specific assay rather than being catalogued according to each variant being sought.

Overall, 33% of the tests of protein-coding genes were described with non-standard nomenclature. Attempts were made to ensure that tests with non-standard names were catalogued correctly, but it is possible that errors in assignment were made.

The remaining 13 tests (3%) had non-standard names, and are identified in this Report with “#” as a suffix:

- AZF# assessment of multiple discrete regions on the Y chromosome (no consensus among laboratories re nomenclature);
- Chimerism# assessment of multiple discrete regions (differing between laboratories) to identify mixtures of cells from different people e.g. fetal and maternal cells, or host and donor cells;
- D13S319# assessment of a discrete non-coding DNA region for a deletion indicating cancer prognosis (no HGNC name);
- D19S545# assessment of a discrete non-coding DNA region for a deletion indicating cancer prognosis (no HGNC name);
- D19S851# assessment of a discrete non-coding DNA region for a deletion indicating cancer prognosis (no HGNC name);
- D4Z4# assessment of discrete DNA region associated with a form of muscular dystrophy (no HGNC name);
- D5S721# assessment of a discrete non-coding DNA region for a deletion

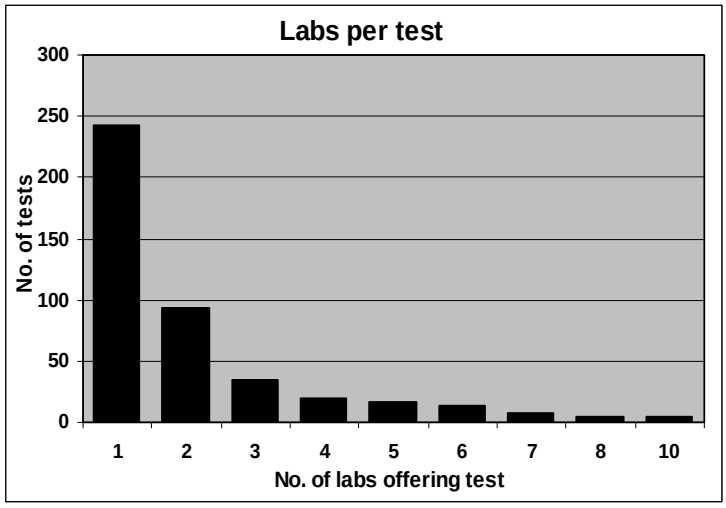
indicating cancer prognosis (no HGNC name);

- D7S613# assessment of a discrete non-coding DNA region for a deletion indicating cancer prognosis (no HGNC name);
- MSI# assessment of multiple discrete regions (differing between laboratories) to identify a global characteristic of a type of familial colorectal cancer;
- MT-deletion# assessment for unspecified discrete deletions in mitochondrial DNA;
- Somatic hypermutation# assessment of multiple discrete regions to identify a global characteristic of a type of cancer'
- STR# assessment of multiple discrete regions (differing between laboratories) to identify unspecified deletions or abnormalities of chromosome segregation that carry consequences re a single locus;
- Subtel deletion# assessment of multiple discrete regions (differing between laboratories) to identify unspecified deletions;

Samples that were sent overseas for testing were listed as a single entry rather than being listed for each test requested. The tests done overseas are detailed below (see Section 7.4).

5.3 Laboratories providing type of test

The Figure documents the distribution of the number of Australian laboratories providing a specific test in 2006 (data in Sections **Error! Reference source not found.** and **Error! Reference source not found.**). Of the 437 tests offered, 243 (55%) were offered by only one laboratory in Australia. A further 94 (21%) tests were offered by only two laboratories nationwide.



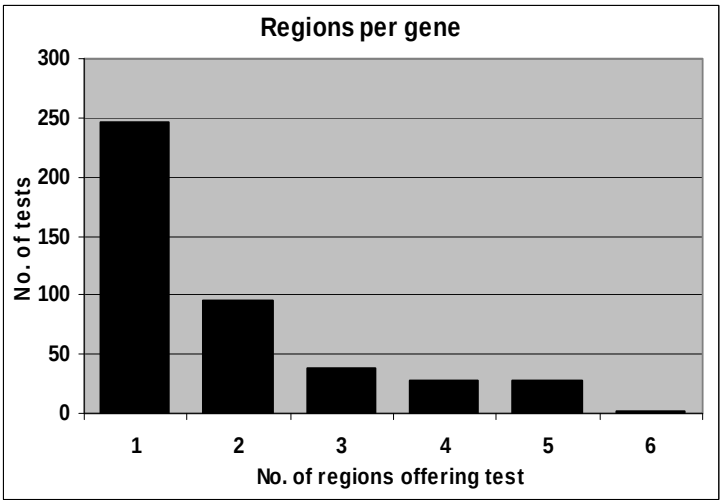
Only 5% of genetic tests were provided by more than five laboratories. Note that Medicare-funded testing is excluded from this Figure as Medicare does not provide laboratory-based data.

5.4 Types of test per region

The number of types of test offered in each region varied. This does not necessarily imply that access to tests was restricted to that region as many laboratories have the potential to act as *de facto* national laboratories for rare tests. But this issue is considered in more detail in Section 10.

Region	*No. of types of test*
ACT	**4**
QLD	**88**
NSW	**135**
VIC	**171**
SA	**191**
WA	**216**

The Figure summarises the number of regions in which tests were done (data in Sections **Error! Reference source not found.** and **Error! Reference source not found.**). The majority of tests were provided by one or more laboratories in a single region. Only 56 tests (13% of the total offered) were done in four or more regions. No tests were done in all States and Territories.



Two regions did not report doing any tests (Tasmania and the Northern Territory). Both regions have clinical and laboratory genetic services provided on a contractual basis by other States.

6 Number of assays in 2006

The principle source of data for this section is in Section **Error! Reference source not found.**.

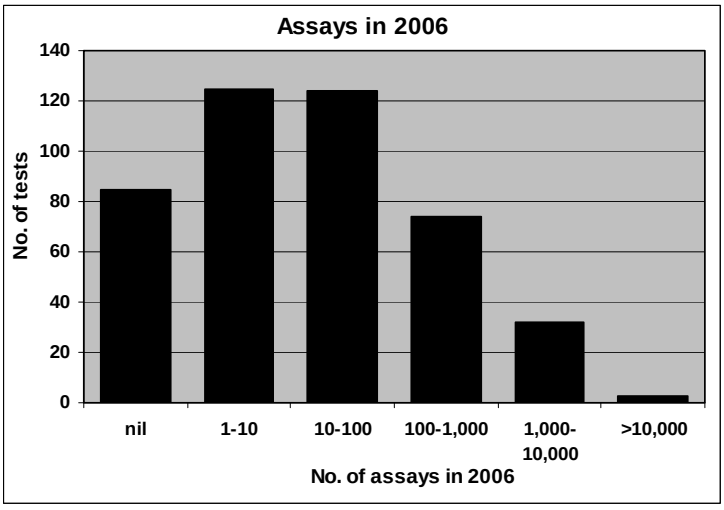
6.1 Assay volume

During 2006, a total of 41,497 assays for molecular genetic tests were rebated by Medicare in Australia. As noted above, this accounted for 0.07% of all pathology tests rebated by Medicare in 2006.

In addition to the Medicare tests, a further 119,354 molecular genetic tests were provided by laboratories using non-Medicare funding. The molecular genetic tests provided with non-Medicare funding accounted for 74% of the molecular genetic tests provided overall. The total number of molecular genetic assays (160,851) was equivalent to 0.2% of all pathology investigations rebated by Medicare during the year.

6.2 Assays per type of test

This Figure documents the distribution of the number of assays provided in 2006 per type of test (data in Section **Error! Reference source not found.**). Medicare-funded and non-Medicare-funded testing of the same gene have been counted separately e.g. “F5 [MBS]” and “F5” are counted a separate tests.



There were no assays reported for 85 tests. As noted above (Section 5.1), this could reflect fluctuations in demand for low volume tests, or the introduction of new tests during 2006. The great majority of types of test involved less than 100 assays per year.

6.3 Assays in different patient groups

The Table documents the number of assays performed in different patient groups during the year.

Patient Group	*Assays (n)*	*Assays (%)*
Screening	**64,547**	**40%**
Diagnostic	**45,437**	**28%**
Somatic	**13,092**	**8%**
Family	**7,614**	**5%**
Pharmacogenetic	**470**	**<1%**
Supplementary	**281**	**<1%**
Unknown	**29,411**	**18%**
Total	**160,851**	**100%**

The bulk of the screening assays related to tests for cystic fibrosis (CFTR), immuno-typing (CD109, GP1BA, HLA-A, HLA-B, HLA-B, HLA-C, HLA-DPB1, HLA-DQA1, HLA-DQB1, HLA-DRB1, HLA-DRB3, HLA-DRB4, HLA-DRB5, ITGA2, ITGA2B, ITGB3), and common Jewish mutations (HEXA) (>1,000 assays each).

The most common diagnostic tests were Factor V Leiden (F5), cystic fibrosis (CFTR), thalassaemias (HBA1, HBA2, HBB), haemochromatosis (HFE), α-1-antitrypsin deficiency (SERPIN1A), and sub-telomere deletions causing intellectual disability (subtel deletion#) (>1,000 assays each).

The most common somatic tests were for haematological malignancies: BCL2, BCR/ABL1, IGH@, TRB@, and TRG@ (>1,000 assays each).

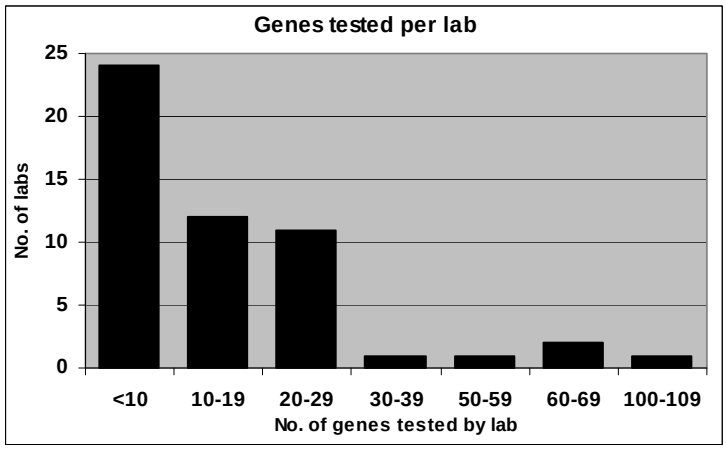
Two of the assays for family members were done more than 1,000 times: cystic fibrosis (CFTR) and Factor V Leiden (F5).

The descriptors for the Medicare items for HFE and FMR1 do not differentiate between diagnostic and family testing. These two tests accounted for the bulk of assays provided to the "unknown" group.

7 Provision of tests

7.1 Types of test per laboratory

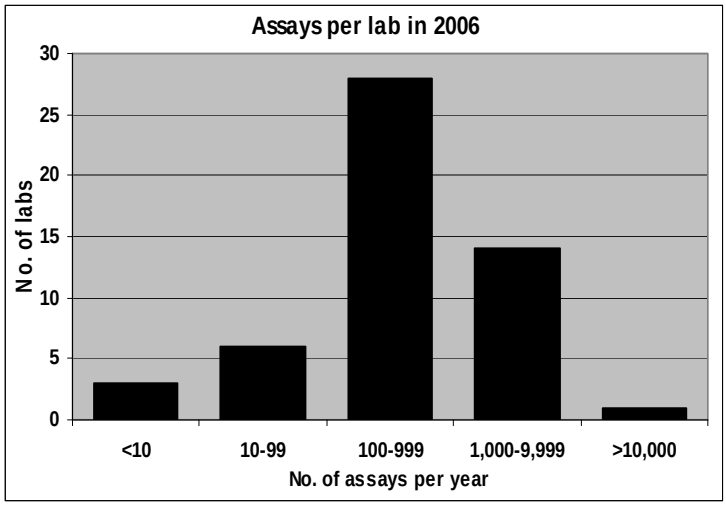
The Figure presents the distribution of the number of laboratories providing a specified number of types of test (data in Section **Error! Reference source not found.**).



The median number of types of test offered by a laboratory was 10, but the range was one to 103. Almost half of the laboratories offered less than 10 types of test. Only 10% of laboratories offered 40 or more types of test. Note that a panel of investigations on a single sample was counted as one assay for each gene included in the panel (see Section 2.1).

7.2 Assays per laboratory

The Figure documents the distribution of the number of laboratories providing a specified number of assays for all tests offered during the year (data in Section **Error! Reference source not found.**). Medicare-rebated tests are not included because those data were not laboratory-based.

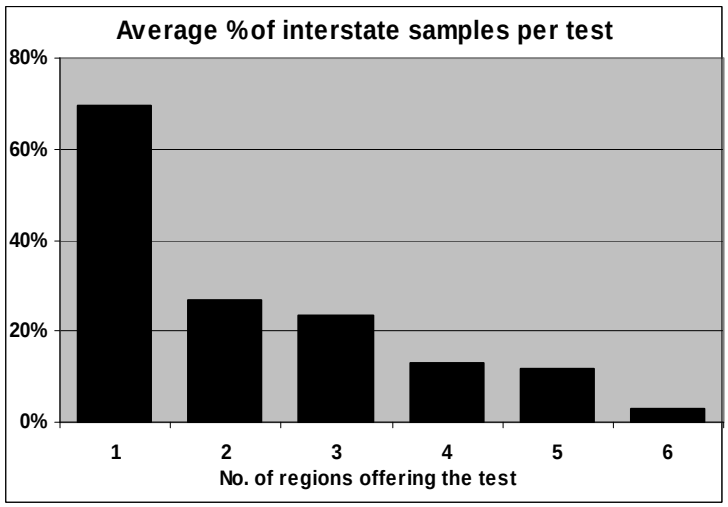


The median number of assays done by a laboratory was 424 per year, but the range was two to 44,150. Three laboratories reported doing a total of less than 10 assays during 2006; in each case, there was at least one other laboratory providing the same type of test in Australia in 2006. Most laboratories did more than 100 assays per year.

7.3 Assays for interstate patients

Testing involved samples from other regions ("interstate samples") for 195 tests (45% of the total of 437 tests). A total of 6,941 interstate samples were tested: this is equivalent to 9% of the intra-region assays for those tests, and an average of 35.6 samples per test for which interstate testing was done (data in Section **Error! Reference source not found.**).

As might be expected, the interstate assay volume was greater for the types of test that were offered by a limited number of regions. If a test is already available in the patient's region, it is less likely that the sample would be sent interstate for testing. The Figure documents the distribution of the average proportion per type of test of assays done on interstate samples versus the number of regions in which the type of test was offered (data in Section **Error! Reference source not found.**).



However, this analysis is limited to those tests for which assays on interstate samples were reported. There were a further 242 tests for which no assays on interstate samples were reported. If the interstate samples reported are apportioned across all tests offered, the proportion of interstate samples per test is much lower. For example, 247 tests were available in only one region (see Section 5.4). A total of 13,881 assays for these tests were performed on intrastate samples during 2006. Only 747 additional assays (an additional 5%) were reported for these tests on interstate samples. This is far lower than might be expected for tests that are only available in one region of Australia. For example, the most populous State (NSW) had 33% of Australia's population in 2006. If there was equivalent access to testing for rare disorders in all regions of Australia, then at least

67% of the assays provided by a sole laboratory in NSW offering a test should be for interstate patients. The proportion should be even higher for sole laboratories operating in the regions which have a smaller proportion of the Australian population. The fact that the average proportion of assays performed on interstate samples for single region tests was only 5% highlights that patients residing outside the region in which the test is done had limited access to that test.

7.4 Overseas testing

The 426 samples sent for testing overseas accounted for only 0.3% of assays done during 2006. However, many laboratories were unable to provide accurate data on the number of samples sent or the types of test that had been requested in that year. It is likely that the number of samples sent overseas for testing was higher than reported.

A total of 58 types of tests were specified as being requested from an overseas laboratory. At least one Australian laboratory was offering sequencing of the gene in 2006 for 25 (43%) of these types of test. However, the Survey did not collect sufficient data to determine whether the requirements of the requesting laboratory could have been addressed by the Australian laboratory offering sequencing of the gene.

Sequencing was not offered in Australia for 33 of these types of test (57%). The tests involved were ABCA12, ABCA4, ABCB11, ATP7B, BEST1, CDKN2A, COL3A1, COL4A5, DKC1, EDAR, ENG, EYA1, FH, FRG1, IKBKG, MAA, MYH3, NPHS2, PAX3, PAX6, PHEX, PHOX2B, PKD1, PRSS1, REN, RPS19, SALL4, SOX10, SPINK1, TBX5, TEK, TFAP2B, and ZEB2.

8 Characteristics of tests

8.1 Test accreditation

Of the 52 laboratories which provided data for the Survey,

- 28 (54%) only offered accredited tests,
- 6 (11%) only offered non-accredited tests, and
- 18 (35%) provided a mix of both accredited and non-accredited tests.

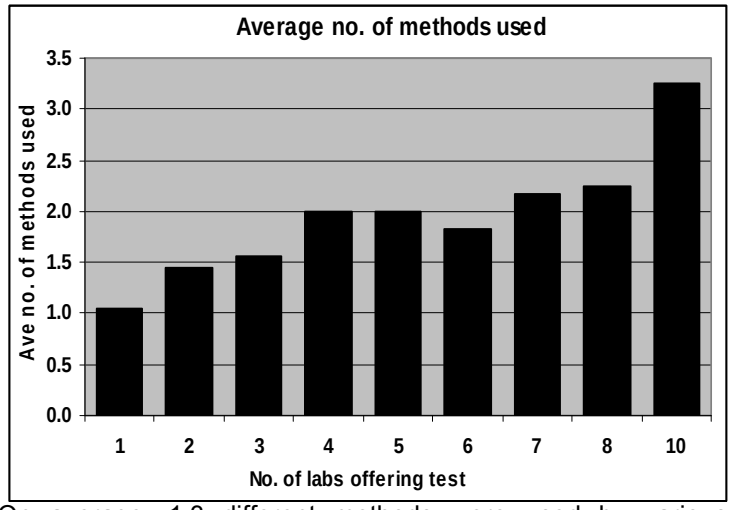
Of the 437 types of test offered,

- 365 tests (83%) were only offered as accredited tests. This included 208 tests that were only available through one laboratory nationally. The number of laboratories offering these accredited types of test ranged from 1 to 10 per test.
- 16 tests (4%) were only offered as non-accredited tests. 12 of these tests were only available through one laboratory nationally, and the remaining four were available through two laboratories.
- 33 tests (8%) were offered as both accredited and non-accredited tests. All of these tests were offered by two or more laboratories nationally.
- Accreditation was not specified for 23 types of test (5%) from two laboratories. Each test was available through only one laboratory nationally.

The data regarding the number of laboratories in a region offering accredited or non-accredited testing of a gene are tabulated in Section **Error! Reference source not found.**.

8.2 Test methods

Laboratories were asked to provide a simple categorisation of the method used for each type of test in each patient group (see Section 2.8). Analysis for common mutations, or for mutations already identified in the family ie "family" testing, is technically much simpler than diagnostic testing which may involve exhaustive examination of an entire gene sequence.



Methodological data were provided for diagnostic testing of 365 different genes (data in Sections **Error! Reference source not found.** and **Error! Reference source not found.**). On average, 1.3 different methods were used by various laboratories for each type of test. The maximum number of methods used for a test was four. The Figure demonstrates a direct relationship between the number of laboratories offering a type of test and the average number of methods used for the test (data in Section **Error! Reference source not found.**).

8.3 Test sensitivity

The Survey did not seek to document the analytical performance of each test. However, the Survey did note, in general terms, the method used for testing in different clinical settings and the sensitivity of testing expected by the laboratory. This estimate of sensitivity was the laboratory's expectation of the sensitivity based on experience and publications; it was not the result of a quality assessment.

For family testing, the mutation present in the family has already been defined. The sensitivity of a test for that mutation is, by definition, 100% and so analytical performance for family testing is not addressed.

8.3.1 SCREENING

Screening typically involves testing for a limited number of common mutations using a specific assay. The were 59 reports from laboratories regarding 45 different types of screening test using specific assays. There were a further eight reports of screening tests using more complex methods such as sequencing (with and without MLPA) and mutation screening; these reports may represent a misunderstanding in the definition of the method categories and they are not considered further in this report.

The Table lists the method, the number of types of test based on that method, the number of reports, the range of expected sensitivities, and number of discordant sensitivities i.e. expected sensitivity for the same method and type of test varying by >20% in different laboratories.

Method	*No. of tests*	*No. of reports*	*Sens. range*	*No. of discordant reports*
Specific assays	45	59	<20% to >94%	3

8.3.2 DIAGNOSTIC TESTING

Diagnostic testing involves searching for a mutation, and laboratories typically use different methods that have different sensitivities. Test sensitivity data in a diagnostic setting were reported for 295 tests.

The Table lists the method, the number of types of test based on that method, the number of reports, the range of expected sensitivities, and number of discordant sensitivities i.e. expected sensitivity for the same method and type of test varying by >20% in different laboratories.

Method	*No. of tests*	*No. of reports*	*Sens. range*	*No. of discordant reports*
Mutation screening	48	48	60% to >94%	nil
Sequencing	146	174	20% to >94%	4
Sequencing plus MLPA	51	101	60% to >94%	2
Specific assays	108	177	<20% to >94%	2
FISH	25	47	60% to >94%	1

8.3.3 SOMATIC TESTING

Analysis for somatic mutations can utilise a number of different methodologies. Sensitivity data were reported for 66 tests.

The Table lists the method, the number of types of test based on that method, the number of reports, the range of expected sensitivities, and number of discordant sensitivities i.e. expected sensitivity for the same method and type of test varying by >20% in different laboratories.

Method	*No. of tests*	*No. of reports*	*Sens range*	*No. of discordant reports*
Mutation screening	2	2	80% to >94%	nil
Sequencing	3	3	80% to >94%	nil
Specific assays	29	66	40% to >94%	8
FISH	32	51	>94%	nil

9 Frequency of abnormal test results

The frequency with which a test is abnormal will reflect both the sensitivity of the method used and the selection of patients for the test. A high frequency of abnormal results might suggest that the laboratory's method is highly sensitive, or that clinical indications for testing are too stringent with patients having less characteristic features of the disorder being denied appropriate testing. Conversely, a low-frequency of abnormal results might suggest that the test methodology has a low sensitivity or that the clinical indications for testing are too loose. In other words, the frequency with which a test is abnormal reflects characteristics of both the clinicians requesting the test and the laboratory providing the test.

Laboratories reported the frequency of abnormal results for 220 diagnostic tests. These frequencies were converted into five categories ("ABN categories" in the Table) of 20% increments i.e. 0-19%, 20-39%, 40-59%, 60-79% and 80-100%. The concordance of the 142 reports describing tests offered by two or more laboratories is summarised below. (The 78 reports describing tests offered by a single laboratory were, by definition, concordant in the reported frequency of abnormal results and are not included).

		No. of ABN categories reported by labs			
No. of labs doing test	*No. of tests*	*1*	*2*	*3*	*4*
2	63	55	8		
3	26	22	4		
4	14	7	6	1	
5	15	7	6	2	
6	11	3	7	1	
7	5	2	2	1	

8	4	2	1		1
10	4	2	1	1	

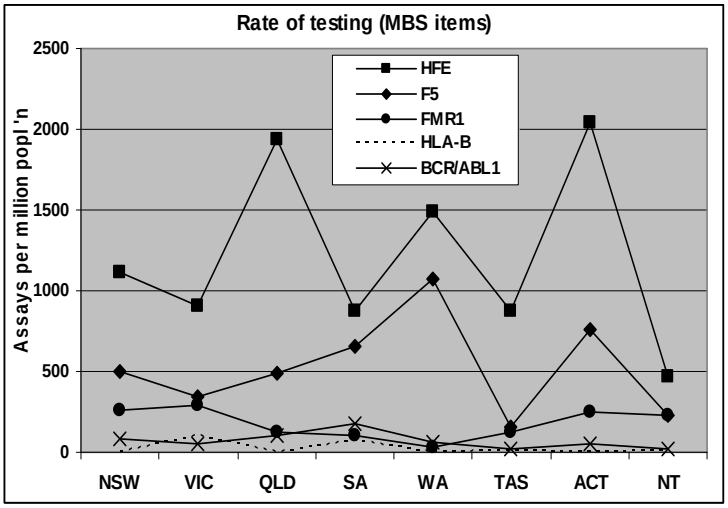
For the majority of tests, the reported frequencies of abnormal results were usually concordant irrespective of the number of laboratories providing the test. For example, of the 26 types of test provided by three laboratories, the three laboratories reported the same frequency of abnormal results for 22 tests. But for four of these tests, the reported frequencies of abnormal results were distributed over two categories. As the number of laboratories doing a type of test increased, the reported frequencies of abnormal results were scattered over an increasing number of categories.

The comparatively wide ranges of test sensitivities (Section 8.2) and frequencies of abnormal results raises the possibility that, for many tests, there is a lack of consistency in patient and method selection.

10 Rates of testing by regions

10.1 Rate of testing for Medicare-rebated tests

The five tests funded by Medicare (BCR/ABL1, F5, FMR1, HFE, and HLA-B) accounted for 25% of the molecular genetic assays performed in Australia in 2006. These tests were available at no financial disadvantage to people in all regions. Nonetheless, there was marked variation in the rate at which these tests were done during 2006.



The Figure documents the number of assays per million population for each of these five types of test (data in Section **Error! Reference source not found.**). The rate of testing varied from 4-fold to more than 10-fold across regions for the different tests. These variations were not consistent by region i.e. there was no single region which had the highest or lowest rates for all tests, and the pooled rate of tests by region was less marked and varied 3.3-fold (Section 4)

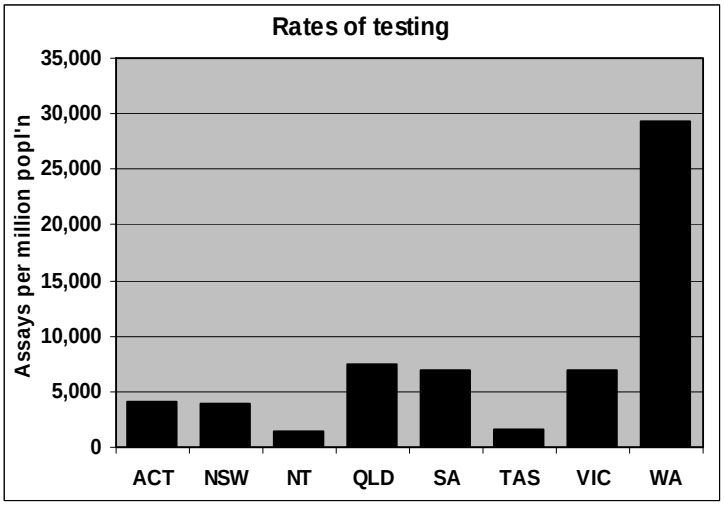
10.2 Pooled rate of testing for non-Medicare tests

The Medicare data are provided on the basis of the patient's region of residence, thus simplifying comparisons of the rate of testing between regions. The bulk of the non-Medicare tests done during 2006 were for intrastate samples, but a proportion of the assays related to interstate samples. Hence some adjustment must be made for these interstate samples in calculating the rate of testing for non-Medicare tests. The laboratories indicated the number of assays for each test that related to interstate samples, but did not specify the regions from which the samples had been received. For the purpose of calculating rates of testing by region, these interstate samples were allocated to other regions on the basis of the relative populations in those regions. It is recognized that this is unlikely to represent accurately the source of interstate samples referred to a laboratory, but there were no other data to direct how these interstate samples should be apportioned.

The rate of testing in each region for each gene is tabulated in Section **Error! Reference source not found.**. The rate of testing varied widely, with the greatest difference between regions being, on average, 257-fold. The median for the greatest difference between regions was 11-fold. These

figures exclude tests for which the rate of testing in any region was zero (and hence the largest ratio of differences between regions was infinite).

The Figure summarises the pooled data for all tests for each region (data in Section **Error! Reference source not found.**). The rate of molecular genetic testing varied by over more than an order of magnitude between regions, with the lowest rate being 21 times less than the highest rate. This difference is 2- to 4-fold greater than regional differences in testing rates noted for Medicare-rebated types of genetic test (Section 10.1).



The high level of testing in WA reflects tissue typing of multiple genes by genetic rather than immunological means; there was only a low volume of such testing by genetic means in other regions. If WA is excluded from the analysis, the greatest difference in pooled testing rates in the remaining regions was 5-fold.

This analysis underestimates the actual difference as it was assumed that the number of interstate assays is distributed uniformly across all regions (other than the one in which the testing laboratory is located). This assumption is essentially the same as the question being asked: is the rate of testing the same in different regions? It would be more accurate to assess the rate of intrastate versus interstate testing for each gene (see Section 10.3). Nonetheless, despite this assumption reducing the variation in estimated testing rates in different regions, substantial differences in rates of testing were identified.

10.3 Rate of testing for each non-Medicare test

The rate of testing for an individual genetic test is very low compared with the population size, and can be modelled using the Poisson distribution. For each test, the rate of testing for intrastate samples was taken as the mean rate; if testing was provided in multiple regions, the mean rate was calculated from the pooled assay volumes and the pooled populations. The rate of testing for interstate samples was estimated on the basis of the number of interstate assays (Section **Error! Reference source not found.**) and the population in regions that did not have a laboratory providing that test (Section **Error! Reference source not found.**). This assessment could not be completed on 108 tests because they had no intrastate assays reported, precluding calculation of the mean rate of testing. Medicare-rebated and overseas tests were excluded.

The rate of intrastate versus interstate testing was compared for each of the remaining 328 tests using the Poisson distribution. 74% of these had a p-value of 0.0001 or lower[7], indicating a significant reduction in the rate of testing provided to patients living outside the region in which the testing was done (data in Section **Error! Reference source not found.**). This confirms that the marked variation in testing rates identified in the pooled data reflects marked variations in the rates of testing for most genes.

[7] A p-value of 0.0001 represents a conservative threshold for determining statistical significance in this setting. There were 328 comparisons, and so the usual threshold of p = 0.05 should be reduced by a factor of 328 i.e. p = 0.00015, to make allowance for these comparisons.

11 Molecular genetic testing in 2007

The data for this Section is in Section **Error! Reference source not found.**.

11.1 Types of test

During 2007, the same number of types of test were nominally provided as in 2006. But, as discussed in Section 5.1, this overestimates the real level of test diversity available during year. The challenge lies in determining whether a lack of testing in one year represented low demand for a rare test, or lack of provision of the test.

There were four types of test for which no assays were performed during 2006 and more than 10 assays were performed in 2007; this could represent an increase in test availability of 0.9%. Conversely, there were seven types of test for which more than 10 assays were performed in 2006 and no assays were performed in 2007; this could represent a decline in test availability of 1.6%. The net change would be a **loss** of three types of test (0.7%). But the threshold of 10 assays is a stringent one for drawing this conclusion. During 2006, 28% of all types of test had assay volumes of between one and 10. If a threshold of 2 assays is used, there were 44 new types of test introduced in 2007 and 11 ceased, a net **increase** of 7.6%.

11.2 Assay volumes

During 2007, the volume of all Medicare-rebated testing increased by 7% compared with 2006. As shown in the Table, the assay volume increased by 3-9% for most Groups. The exception was Medicare-rebated molecular genetic testing which increased by 90%. In 2007, this accounted for 0.12% of all Medicare-rebated tests, up by 0.05% since 2006.

Group	*YR2006*	*YR2007*	*% increase In 2007*
P1Haem	13,842,185	14,393,977	4%
P2 Chem	29,385,064	32,134,761	9%
P3 Micro	8,844,425	9,356,662	6%
P4 Immun	2,153,199	2,330,808	8%
P5 Histol	2,218,777	2,300,512	4%
P6 CYTOL	1,905,817	1,953,894	3%
P7 MolGen	**41,497**	**78,806**	**90%**
P7 CytoGen	45,646	47,556	4%
P8 REPRO	463,066	482,441	4%
P9 SIMPLE	665,979	643,791	-3%
Total	**59,565,655**	**63,723,208**	**7%**

The assay volumes for the five tests rebated by Medicare are shown below. The most dramatic proportional increases related to tests that were only introduced in 2006, reflecting the uptake of a new test rather than an expansion of an existing pattern of testing.

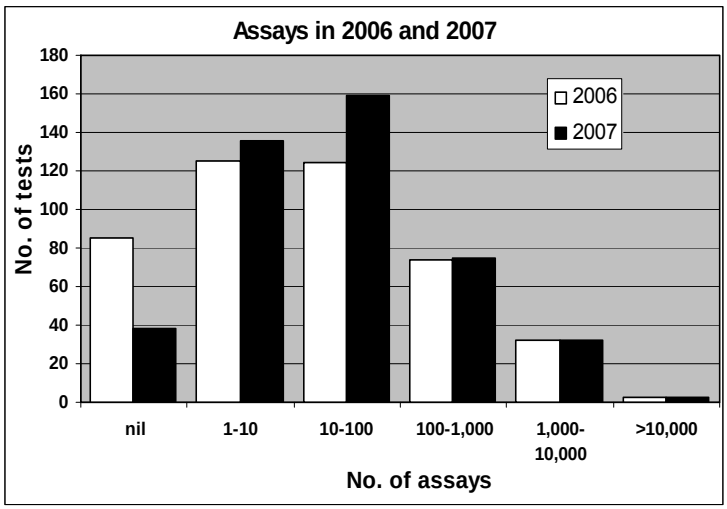
Test	*YR2006*	*YR2007*	*% increase*	*YR introduced*
BCR/ABL1 [MBS]	1,631	3,833	235%	2006
F5 [MBS]	10,338	19,548	189%	2006
FMR1 [MBS]	4,083	4,506	110%	2003
HFE [MBS]	24,767	49,020	198%	2006
HLA-B [MBS]	678	1,899	280%	2006 & 2007

In addition to the Medicare tests, a further 117,342 molecular genetic tests were provided by laboratories using non-Medicare funding. This was a reduction in assay volume of 2,012 (1.7%)

compared with 2006. In 2007, the molecular genetic tests rebated by Medicare accounted for 40% of the molecular genetic tests provided overall, an increase of 14% since 2006. The total number of molecular genetic assays (196,148) is equivalent to 0.3% of all pathology investigations rebated by Medicare during the year; this was an increase of 0.1% since 2006.

11.3 Assays per type of test

This Figure documents the shift in the assay volume per type of test from 2006 to 2007 for each test (data in Section **Error! Reference source not found.**). Medicare-funded testing has been included and counted separately e.g. "F5 [MBS]" and "F5" are counted as separate tests.



11.4 Assays in different patient groups

The Table documents the number of assays performed in different patient groups during 2007. As noted previously, the descriptors for the Medicare items for HFE and FMR1 do not differentiate between diagnostic and family testing. The assay volume for Medicare-rebated HFE almost doubled in 2007, and this accounts for the increased proportion of tests provided to the "unknown" group.

	Assays (n) 2006	*Assays (n) 2007*	*Change from 2006*
Screening	**64,547**	**60,960**	**-6%**
Diagnostic	**45,437**	**55,902**	**+23%**
Somatic	**13,092**	**16,094**	**+23%**
Family	**7,614**	**7,775**	**+2%**
Pharmacogenetic	**470**	**944**	**+101%**
Supplementary	**281**	**362**	**+29%**
Unknown	**29,411**	**54,110**	**+84%**
Total	**160,851**	**196,147**	**+22%**

12 Acknowledgements

This Survey would not have been possible without the financial support of the *Quality Use of Pathology Program* of the Australian Department of Health & Ageing. The encouragement, advice, and support of colleagues in the RCPA and HGSA is gratefully acknowledged. Special thanks to Leslie Burnett, Jacqueline Armstrong, and Mike Ralston.

The greatest "thank you" must go to the many laboratory colleagues who provided the data that underpins this Survey. As per the principle of confidentiality regarding which laboratories provided data, they must remain nameless. But there were many hours - many "after hours" – spent in gathering the data. Thank you.

13 Reference

Gulley ML, Braziel RM, Halling KC, Hsi ED, Kant JA, Nikiforova MN et al (2007). Clinical laboratory reports in molecular pathology. Arch Pathol Lab Med 131:852-863