OPEN LETTER

Genomic variant sharing: a position statement [version 1; referees: awaiting peer review]

Caroline F. Wright 1, James S. Ware 2, Anneke M. Lucassen 3, Alison Hall 4, Anna Middleton 5,6, Nazneen Rahman 7, Sian Ellard 1, Helen V. Firth 8,9

1Institute of Biomedical and Clinical Science, University of Exeter, Exeter, UK
2National Heart and Lung Institute, Imperial Centre for Translational and Experimental Medicine, London, UK
3Department of Clinical Ethics and Law, Faculty of Medicine, University of Southampton, Southampton, UK
4PHG Foundation, Cambridge, UK
5Faculty of Education, University of Cambridge, Cambridge, UK
6Connecting Science, Wellcome Genome Campus, Cambridge, UK
7Division of Genetics and Epidemiology, Institute of Cancer Research, UK, London, UK
8Department of Clinical Genetics, University of Cambridge Addenbrooke's Hospital Cambridge, Cambridge, UK
9Wellcome Trust Sanger Institute, Cambridge, UK

Abstract
Sharing de-identified genetic variant data is essential for the practice of genomic medicine and is demonstrably beneficial to patients. Robust genetic diagnoses that inform medical management cannot be made accurately without reference to genetic test results from other patients, as well as population controls. Errors in this process can result in delayed, missed or erroneous diagnoses, leading to inappropriate or missed medical interventions for the patient and their family. The benefits of sharing individual genetic variants, and the harms of not sharing them, are numerous and well-established. Databases and mechanisms already exist to facilitate deposition and sharing of pseudonomised genetic variants, but clarity and transparency around best practice is needed to encourage widespread use, prevent inconsistencies between different communities, maximise individual privacy and ensure public trust. We therefore recommend that widespread sharing of a small number of individual genetic variants associated with limited clinical information should become standard practice in genomic medicine. Information robustly linking genetic variants with specific conditions is fundamental biological knowledge, not personal information, and therefore should not require consent to share. For additional case-level detail about individual patients or more extensive genomic information, which is often essential for clinical interpretation, it may be more appropriate to use a controlled-access model for data sharing, with the ultimate aim of making as much information as open and de-identified as possible with appropriate consent.

Keywords
medical genomics, variant, data sharing, data ethics
This article is included in the *Transforming Genetic Medicine Initiative (TGMI)* gateway.

**Corresponding authors:** Caroline F. Wright (caroline.wright@exeter.ac.uk), Sian Ellard (Sian.ellard@nhs.net), Helen V. Firth (hvf21@cam.ac.uk)

**Author roles:** Wright CF: Conceptualization, Writing – Original Draft Preparation, Writing – Review & Editing; Ware JS: Writing – Original Draft Preparation, Writing – Review & Editing; Lucassen AM: Writing – Original Draft Preparation, Writing – Review & Editing; Hall A: Writing – Review & Editing; Middleton A: Writing – Review & Editing; Rahman N: Conceptualization, Writing – Original Draft Preparation, Writing – Review & Editing; Ellard S: Conceptualization, Writing – Original Draft Preparation, Writing – Review & Editing; Firth HV: Conceptualization, Writing – Original Draft Preparation, Writing – Review & Editing

**Competing interests:** No competing interests were disclosed.

**Grant information:** This work was supported by the Wellcome Transforming Genomic Medicine Initiative [200990].

**Copyright:** © 2019 Wright CF et al. This is an open access article distributed under the terms of the Creative Commons Attribution Licence, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

**How to cite this article:** Wright CF, Ware JS, Lucassen AM et al. Genomic variant sharing: a position statement [version 1; referees: awaiting peer review] Wellcome Open Research 2019, 4:22 (https://doi.org/10.12688/wellcomeopenres.15090.1)

**First published:** 05 Feb 2019, 4:22 (https://doi.org/10.12688/wellcomeopenres.15090.1)
Recommendations

1. Open and widespread sharing of plausibly causal genetic variants with high-level phenotypes should be routine clinical practice and should not be dependent upon consent from individual patients.

2. A single genetic variant is not personally identifiable information; however, it is good practice to maintain a cryptic link to the laboratory or clinical service that shared the genetic data so that clinical follow-up remains possible should knowledge of the implications of a variant change.

3. Disclosing detailed case-level clinical detail, larger variant sets or genome-wide data outside of the patient’s clinical team may be crucial for variant interpretation or clinical management, but requires explicit consent to share openly.

Introduction

Making an accurate diagnosis is the cornerstone of good medical practice, essential for determining prognosis, guiding treatment and informing patient management. Across all medical specialties, the interpretation of diagnostic test results relies upon knowledge of what is ‘normal’ in the population versus what ‘disease’ looks like. This knowledge relies upon sharing test results from previous patients and population controls. Without such data, the sensitivity and specificity of the test is unknown, its clinical utility is questionable, and its continued use may be harmful.

Genomic medicine is no exception to this rule, but determining what constitutes ‘normal’ and ‘disease’ can be extremely complicated and arguably the need for ongoing data sharing is even greater than in other branches of medicine. Increasingly, clinical testing will rely on genome-wide sequencing, rather than targeted single-gene testing, and the enormous amount of normal variation in every genome means that interpreting the results from one person’s genome requires knowledge of thousands of other genomes across different populations. Despite ongoing efforts to sequence large cohorts, every genome examined contains novel changes not previously seen. For diseases with a substantial genetic component, caused by a specific rare variant in an individual’s genome, determining which variants are responsible for disease—and which are simply incidental—is an enormous challenge. The only way to meet that challenge is by sharing data on individual variants with associated high-level phenotype terms.

Advantages of sharing genetic variant data

The main purpose of sharing individual genetic variants is to improve the diagnostic accuracy of genetic testing; the main data processors are clinicians and clinical scientists, and the main beneficiaries are patients. Within this context, there are many benefits of sharing individual genetic variants associated with specific conditions:

1. **Making accurate and safe diagnoses.** Genetic testing often benefits the individual patient undergoing testing, whose diagnosis can be accurately determined and prognosis further refined. All such genetic testing is dependent on being able to compare the variant of interest to variants from thousands of other people (via a database that is accessed by the scientist or clinician doing the analysis); at a minimum, this variant comparison is necessary to characterise and usually exclude variants that are relatively common in the general population. Numerous examples exist where making a successful genetic diagnosis has only been possible as a result of being able to access variant and phenotype data from other individuals undergoing testing, and many new genetic causes of disease have been uncovered this way. While most of the published cases are clinician-led, there are an increasing number of patient-led examples of variant sharing that have also catalysed the formation of disease-specific patient support groups and created new avenues of research.

2. **More effective disease management and precision medicine.** In some cases, an accurate genetic diagnosis leads to specific targeted therapies that can more effectively treat disease, or, in rare cases, may even reverse or prevent disease. As a result of variant sharing, individuals may also be recruited to clinical trials that are tailored to their specific genotype, offering the potential for therapy where none currently exists. In addition, new fundamental biological insights from genetic studies may identify novel targets for future therapies.

3. **Accurate advice for family members.** Due to the shared familial nature of most genetic changes, the benefits of making a robust genetic diagnosis may be cascaded out to biological relatives and have a profound impact on both existing and future generations. Given the value of making a genetic diagnosis across a plethora of different (mostly individually rare) diseases, a strong argument can be made that individuals have a moral duty to help family members and other similar patients by allowing information derived from them to be shared if it is easy to do so.

4. **Improved understanding of genetic disease.** There are also wider benefits to the community, including patients, clinicians and researchers across the globe, who are trying to understand and treat the causes of disease. Reports of new gene-disease associations, and sharing of variant-level information to discern which specific variants within each gene are pathogenic or benign, or carry some degree of risk, are critical to advance our understanding of genetic disease. Moreover, sharing variants together with phenotype and age will allow an evolving understanding of penetrance, improving interpretation of both diagnostic and predictive testing.

Disadvantages of not sharing genetic variant data

There is a substantial opportunity cost to not sharing clinically-oriented data that could otherwise be used to accelerate medical
progress. The harms of not sharing individual genetic variants are well established and include delayed, missed and erroneous diagnoses, leading to inappropriate care\textsuperscript{14–27} and sometimes litigation\textsuperscript{26,29}. (See Box 1 and Box 2 for examples where variant sharing had a direct impact on clinical care.) Due to the familial nature of genetics, any diagnostic mistakes can easily be compounded by cascading erroneous information out to family members, thus multiplying the harms. Furthermore, without data sharing, research progress would be impeded, and the growing genomics knowledgebase—upon which the promise of personalised medicine is based—will stagnate. Historical mistakes that exist in public variant databases\textsuperscript{30} can never be fixed without an influx of new data to allow reclassification of variants\textsuperscript{31}, without which misdiagnoses and errors in predictive algorithms will continue. Individual organisations that actively maintain private genetic variant databases, such as commercial companies that do not share variant information for proprietary reasons, are thus inhibiting diagnoses for other patients and undermining public health efforts in this area.

**Perceived harms of sharing genetic variant data**

We have not been able to find any evidence that sharing data relating to individual genetic variants in the context of clinical applications causes harm. Nonetheless, perceived harms include re-identification of individuals across different datasets, loss of security of associated medical information (about the individual or their relatives), and the maleficient misuse of data\textsuperscript{25,34}. Early fears relating to genetic discrimination and the impact of genetic data on insurance premiums have proven to be largely unfounded in the UK and many other countries, thanks in part to genetic non-discrimination legislation and the ongoing Concordat and Moratorium on Genetics and Insurance\textsuperscript{34,35}. Identification of an individual through knowledge of their genetic variant(s) is now perhaps the main concern. Although it is never possible to guarantee anonymity, individual genetic variants—even very rare ones—are not uniquely identifying, and re-identification would require an intimate knowledge of the individual’s genotype or phenotype together with some information to trace that genotype/phenotype to a specific person. In practice, only an individual patient or their clinician would easily be able to re-identify themselves from a specific variant, neither of which would constitute a breach of confidentiality\textsuperscript{36}. A related concern is the perception that all genetic data are personal and therefore inherently sensitive, which stems from conflating genome-wide data with individual genetic variants. All possible genetic variants (of which there are many billions) can easily be computed and their predicted consequences stored; if one particular variant is then found in a patient, it makes no sense for any of the existing information about that variant to then become personal or unique. The only new information is simply that the variant has now been seen in a particular disease case and not in controls.

**Finding a balance**

In our view, the definite and provable harms of not sharing genetic data outweigh the potential and largely hypothetical harms of sharing, a view that is corroborated by several recent litigation cases\textsuperscript{26,29} and supported by several large opinion surveys\textsuperscript{37,38}. Some empirical research has shown that patients and research participants support widespread data sharing\textsuperscript{39} and believe that the positive consequences outweigh the potential negatives\textsuperscript{37}. Recognising these benefits, 13 European countries have recently signed a declaration for delivering cross-border access to their genomic information. Nonetheless, in our

---

**Box 1. Example 1: The hazard of variant over-interpretation.**

In the early 2000’s, a routine scan from a woman in her second trimester of pregnancy showed increased signal in the fetal bowel. This can be a sign of a chromosomal anomaly, viral infection or cystic fibrosis (CF) so an amniocentesis was offered. DNA analysis showed the fetus carried two CFTR variants that were said to be pathogenic. The parents were counselled that their baby would be affected by CF. They elected to continue the pregnancy.

After birth, the child was started on prophylactic antibiotics, twice daily physiotherapy, regular nebulisers and pancreatic supplements. Years later, the child was referred to the genetics clinic for review because the disease seemed unusually mild. The clinical geneticist told the family that the status of one mutation had changed in the CFTR2 database and this combination was no longer thought to cause cystic fibrosis.

As a direct consequence of this change in variant interpretation, the child’s prognosis changed from a life-limiting disorder to one of near-normal life expectancy and the day-to-day life of the child was transformed. The intensive regime of care was substantially reduced.

---

**Box 2. Example 2: The need for population-specific variation data.**

A middle-aged Turkish man was referred to clinical genetics because he had colorectal cancer and numerous polyps were discovered at surgery. A homzygous variant in MUTYH was identified and reported to be of “unknown significance” in the diagnostic laboratory report. Biallelic MUTYH mutations cause MUTYH-associated polyposis (MAP), a recessive syndrome consistent with the diagnosis. Specific mutations are found at different frequencies in different populations.

Evaluation of available databases revealed that the variant had been identified once before in a patient with colon cancer and polyposis. Notably this second patient was also Turkish. No functional data were available and in silico analyses were inconclusive. The variant is extremely rare; present in only 7 individuals, all of South or East Asian origin, in the Exome Aggregation Data set of 61,486 individuals. However, no Turkish samples are listed as contributing to any of these datasets and no MUTYH or exome data from the general Turkish population is available.

Thus it is unclear whether this MUTYH variant is a pathogenic Turkish founder mutation or a non-pathogenic variant that is particularly prevalent in the Turkish population, but rare/absent in other populations. This lack of clarity presents significant clinical challenges in managing the patient and his relatives. Sharing data generated in laboratories worldwide and across more ethnic groups would provide information to differentiate between these options and would allow clear classification of this and many other variants and reduce the potential for health disparities.
increasingly data-aware society, there is a perception that data sharing is inherently risky\textsuperscript{39}. A balance must therefore be struck between sharing sufficient data to reap the benefits, but only as much data as is needed to avoid the potential (perceived and actual) harms.

We have previously proposed a principle of proportionality in genetic data sharing, that balances the depth of data shared with the breadth of sharing\textsuperscript{40}. With any dataset, decisions must be made about what specifically to share and how widely to share it. Many of the clinical benefits of data sharing in genetics can be realised by sharing a tiny subset of de-identified genetic variants, together with limited medical data, rather than necessarily whole genomes. This principle is in accordance with data privacy laws such as the new European General Data Protection Regulation (GDPR), which mandates that stored data are “adequate, relevant and limited to what is necessary in relation to the purposes for which they are processed”\textsuperscript{41}.

The specifics of implementation are critical, and agreeing standards for sharing variants and associated clinical data is essential. Specific data elements for sharing individual genetic variants have been outlined previously\textsuperscript{42} and include (see Table 1):

1. a standardised genetic description of the variant(s), including Human Genome Variation Society (HGVS) nomenclature and genomic coordinates of the variant;

2. a standardised clinical description of the clinical features in the patient using appropriately controlled vocabulary/ontology;

3. the inheritance pattern of the disease (e.g. dominant/recessive);

4. the clinical significance and summary of evidence upon which that assertion was based; and

5. a cryptic link to the laboratory or clinical service that submitted the data (to enable further information to be requested and avoid data duplication).

We recommend that openly sharing genetic variant data at this level should be routine practice. No personal identifiers should be openly shared (e.g. name, hospital IDs, geographical location, etc), and only the minimal genetic and clinical information required (as outlined in the five points above) to assist with interpreting a similar variant should be included. We recommend a cryptic link to the individual case-level data is maintained in a de-identified fashion via the laboratory or clinical service that submitted the data, that may obscure its geographical location by deposition via another platform, to enable clinical follow-up if needed. Linking basic clinical information with information about genetic variation is crucial for supporting variant interpretation and aiding diagnoses. However, as with more extensive genome-wide data, or genomic risk scores, different levels of clinical detail will require different modes of sharing, i.e. open versus controlled access. Additional phenotype detail enables a clinical genomics team to assess the strength of the diagnostic claim and evaluate the evidence for a purported diagnosis. Including this detailed clinical information with a genetic test result avoids potential attrition, where individual clinicians need to go back to the original data generator to obtain sufficient information with which to make a diagnosis in their patient.

A flexible platform with broad international sharing of variant data together with national/local sharing of more granular phenotypic data would enable both needs to be addressed. Numerous

\begin{table}[h]
\centering
\caption{Example of genomic variant sharing.}
\begin{tabular}{|c|p{8cm}|p{8cm}|}
\hline
\textbf{Variant 1} & \textbf{Variant 2} \\
\hline
\textbf{Variant} & Standardised description of variant, including genomic coordinates & Standardised description of variant, including genomic coordinates \\
\hline
\textbf{Gene} & \textit{e.g. MYH7} & \textit{e.g. MYH7} \\
\hline
\textbf{Genotype} & Heterozygous & Heterozygous \\
\hline
\textbf{Phenotype} & Hypertrophic cardiomyopathy & Hypertrophic cardiomyopathy \\
\hline
\textbf{ACMG/AMP variant-level evidence\textsuperscript{43}} & PS1 – a different variant at the same position has previously been established to be pathogenic; PM1 – occurs in the head of the protein (a functional domain with high probability pathogenicity); PM2 – absent from the general population; PP3 – computational evidence suggests deleterious effect on gene product & PM1 – occurs in the head of the protein (a functional domain with high probability pathogenicity); PM2 – absent from the general population; PP3 – computational evidence suggests deleterious effect on gene product \\
\hline
\textbf{Interpretation (based on public data)} & Likely pathogenic & Variant of uncertain significance \\
\hline
\textbf{Aggregated case-level evidence} & Observed in 1/10,000 individuals referred with diagnosis of HCM & Lab A – variant observed in 2/3,000 total patients sequenced; Lab B – 2/4,000; Lab C – 1/3,000; Lab D – 1/1,000 patients \\
\hline
\textbf{Interpretation (with variant sharing)} & Likely pathogenic & Likely pathogenic \\
\hline
\end{tabular}
\end{table}
databases already exist for collating and sharing genetic information, which may have differing requirements for data deposition and thus offer different advantages and disadvantages. For example, US-based ClinVar\textsuperscript{44,45} is perhaps the leading genetic variant deposition database, with >600,000 open access variants assayed primarily through clinical genetic testing services, but most variants have only very limited or no clinical information and no supporting evidence associated with them. UK-based DECIPHER\textsuperscript{5,46,47} contains detailed case-level clinical data associated with >65,000 variants, but uses a tiered access model whereby around half the cases are completely open access and half are only accessible to members of closed groups. DECIPHER and many other databases are part of Matchmaker Exchange\textsuperscript{7}, which enables data sharing and case-matching across separate and otherwise potentially siloed genetic datasets.

Establishing good practice

Uncertainty about what are permissible types of genetic variant sharing and when explicit consent is required means that current data sharing practices across regional genetics centres are highly variable\textsuperscript{8}. The inclusion of genetic data within Article 9 of the European GDPR, “Processing of special categories of personal data”, has created further confusion about the legality of sharing individual variants. There is therefore a need to establish and agree best practice\textsuperscript{8} for data sharing within genomic medicine, to avoid inconsistent practices across different regions, communities and jurisdictions, and ensure transparency and consistency when speaking to patients. Genetic variant data of the sort described above does not meet a recently proposed Data Sharing Privacy Test\textsuperscript{9}, as the data is neither inherently sensitive nor uniquely identifying. Within the UK, the National Data Guardian has stated that “the duty to share information can be as important as the duty to protect patient confidentiality”\textsuperscript{10}, a principle that applies to all data generated across the National Health Service. The American College of Medical Genetics and Genomics recently published a position statement in 2017 that “laboratory and clinical genomic data sharing is crucial to improving genetic health care”\textsuperscript{11}. However, genomic medicine is inherently a global enterprise, so more countries need to follow suit\textsuperscript{12}. The approach to data sharing espoused by the Global Alliance for Genomics and Health\textsuperscript{13,34} is rooted in international human rights legislation, focusing on our ‘solidarity rights’ to genomic information\textsuperscript{13,36} and emphasising the social good that can derive from appropriate data sharing. The handful of patients with the same rare diagnosis may be scattered across different countries, and are therefore best served when data are shared as openly and as widely as possible. Patients across the globe currently benefit from shared data and derived knowledge in databases such as ClinVar and DECIPHER, and services that are not currently sharing their clinical data owe a substantial data debt and risk perpetuating current data biases.

Separate consent should not be required for individual variant sharing

Clinical experience suggests that most patients are keen for their variant data and associated phenotypes to be shared when the risks and benefits are explained to them. Indeed, discussion of the need for data sharing should be so integral in the discussion about genomic diagnosis that separate consent should not be required. Variants of uncertain significance are regularly generated from genome-wide testing and can most easily be resolved through being able to access and explore the context in which such variants have been observed elsewhere (which depends on data sharing, see Figure 1\textsuperscript{8}). In addition to variants from current and future patients, enormous swathes of legacy data exist from

---

**Figure 1.** Global open variant sharing enables robust diagnoses to be made as quickly as possible; facilitating sharing of detailed case-level information also informs clinical management and aids diagnosis in complex cases.
decades of patients who have undergone genetic testing, some of whom are no longer alive, and most of whom are no longer in touch with their clinicians. Sharing variants from these tests could potentially benefit many thousands of patients, and poses little or no harm to the data subjects.

Rather than considering ownership of data as the route to determine what can be done with it, examining who controls access to the data is perhaps a more plausible solution than entering into ownership debates\(^9\). Individuals have a right to control access to data relating to them, but we argue that when it also pertains to others—as is the case for genetic variants—individual rights of veto should be limited to the most unusual situations. A link between a particular genetic variant and clinical features of a disease is not personal information any more than the link between high blood cholesterol and heart disease, for example. We therefore propose that patient consent should not be required to share data on individual genetic variants, with minimal clinical information sufficient to provide other clinical professionals with a reasonable overview of the case(s) to provide appropriate medical care\(^7\). Agreeing this principle of “clinical de-identified variant-level sharing”\(^8\) would remove the onus from data generators to ensure that they have the appropriate written consents and permissions in place, which can be extremely daunting when data may ultimately end up in multiple different databases, and replace it with an unambiguous policy that is clear and transparent for both data generators and data subjects. In addition, for many rare disorders, we suggest that more detailed case-specific information generated within a particular healthcare system should initially remain within that healthcare system, sensitive to the quirks of each individual regulatory regime, but with the aim of eventual open data sharing following discussion with the patient and subject to their explicit consent.

Conclusions

All genetic interpretation is fundamentally dependent upon data sharing, since it is impossible to demonstrate an association between a particular rare genetic change and a disease with an “N-of-one”. Therefore, sharing genetic variant data—albeit aggregated at some level and de-identified as far as possible—is inseparable from the practice of genomic medicine. Clinicians cannot treat patients appropriately if they cannot compare their patient’s data with data from healthy populations and other patients and establish a safe genetic diagnosis. It is therefore beholden upon those who generate and interpret genetic test results to allow access to relevant data as widely and as openly as possible, by depositing the data into appropriate databases and making it available to others to access. Numerous databases exist with aggregated genetic information, and although they differ in their deposition requirements and governance structures, ensuring interoperability between them will prevent information silos and ensure longer-term sustainability.

Despite the overwhelming benefits of genetic variant sharing, and paucity of proven harms, there remain ambiguities over the level of consent required for deposition of individual genetic variants to open access databases. We propose that consent should not be required for widespread, open sharing of individual pseudonymised genetic variants linked with high-level phenotypes, and that sharing such data should become standard practice in genomic medicine. We also recommend that richer case-level phenotypic detail is shared within healthcare systems to facilitate robust diagnosis and that consent is routinely sought at the time of diagnosis to share such data openly. Ultimately, both the promise and the safety of genomic medicine depends on our ability to share.

Data availability

No data are associated with this article.

Grant information

This work was supported by the Wellcome Transforming Genomic Medicine Initiative [200990].

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgments

The authors wish to thank Fiona Cunningham, Ewan Birney, Matthew Hurles, David FitzPatrick, Graeme Black and Patrick Chinnery for helpful comments and input on this manuscript.

References

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Reference Source

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Reference Source

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text

Pubmed Abstract | Pubmed Full Text | Free Full Text


Publisher Full Text


