Update to rare disease database

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The tool is used worldwide, including by every NHS genetics centre in the UK, and has enabled diagnoses for thousands of families affected by rare diseases, and enhanced the understanding of human genetics.

The update enables users to input, view and share genomic changes, known as variants, of any type, in any region of the genome. Previously, users could view changes of a single letter of genetic code, and changes in number of copies of a gene. Now, additional variants are included: regions of repeats - STRs, regions of the genome that have been inverted or inserted, and chromosome variants including regions inherited in an atypical way - uniparental disomy.

Variants can also be grouped, reflecting the complexity of rare disease genetics. DECIPHER is one of the largest, most comprehensive resources of its kind in the world.

The majority of rare diseases are caused by genetic changes, but many of those changes are unique to an individual, or extremely rare in a population. Everyone has millions of points of genetic differences between themselves and the reference human genome sequence, so finding the one that may be causing a particular symptom is difficult. By bringing data together, DECIPHER aims to make the links between genetics and symptoms, and helps clinicians to interpret their meaning.

Consultant clinical geneticist at Addenbrooke’s Hospital and Honorary Faculty at the Wellcome Sanger Institute, Dr Helen Firth, said: “After the human genome was sequenced in 2004, we created DECIPHER to put that data to use. Our aim remains the same as when we first launched - to understand the significance of genetic changes in health and disease. DECIPHER today continues to bring emerging knowledge of human genetics and genomics

to the forefront of clinical practice."

Linking genetic variants to a patient's symptoms can not only aid research into the underlying causes of disease, but may also directly help patients by providing a molecular diagnosis for their condition. A diagnosis could enable access to treatments, support services, clinical trials and the opportunity to meet others affected by the same condition.

"The DECIPHER database has long been an essential, trusted source of information about the rarest of losses and gains in the human genome, giving hope of a diagnosis, understanding, matchmaking, improved care management and, for some, even treatments to families and individuals affected by such changes. The database's expansion to include all types of variant in all regions of the genome extends that beacon of hope to all those affected by rare disease. It is a huge step forward and one that is greatly welcomed by the patient community," said Dr Beverly Searle, CEO, Unique – the Rare Chromosome & Gene Disorder Support Group.

Since its launch in 2004, details from over 36,000 patients have been added to the database by over 250 contributing centres across the world. The data includes 158,660 phenotype observations, 38,092 copy number variants and 8,585 sequence variants. The database links to other international resources so information can be cross-referenced.

DECIPHER enables a flexible approach to data-sharing. Each genetics centre maintains control of its own patient data or shares the data with trusted parties in a collaborative group, until patient consent is given to allow data, without identifying details, to become freely viewable within genome browsers. Privacy is extremely important, and while information is shared, only the minimum amount of essential information is made available. No additional information about an individual is open to researchers, and open data sharing is agreed by the patients who sign up.

"DECIPHER is a hugely valued resource to genetic health professionals worldwide, providing a very important open-access information resource. As health professionals try to interpret and make sense of the many different ways our DNA can be altered, and the effects of this, it becomes critical to have reliable and trusted resources. DECIPHER links health professionals all around the world working in the field of rare disease seeking information on a given patient's rare variant, and in doing so directly improves diagnosis rates and patient care. DECIPHER continues to grow and develop, now adding in the capacity to share all types of genetic variation," said professor Sue White, deputy medical director, Victorian Clinical Genetics Services (VCGS), and consultant clinical geneticist, VCGS, Murdoch Children's Research Institute.

Professor Matthew Hurles, head of human genetics at the Wellcome Sanger Institute added: "The first step in finding a cure is finding what the underlying cause of a disease is. Everything is critically dependant on that. From that point onward you can narrow in on the particular biology of the disease and what kind of drugs might be needed. Finding the cause

of disease in all patients requires comprehensive consideration of all forms of genetic variation, and this latest update to DECIPHER enables exactly this."