Weill Cornell Medicine

The Bloom Syndrome Registry

Supporting the Bloom Syndrome Community

Chris Cunniff, MD
Associate Director, Bloom Syndrome Registry

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Bloom Syndrome Registry

Long term natural history study of Bloom syndrome

Demographic, clinical and laboratory testing information

Over 1,000 samples from about 163 individuals and family members

Collaborations initiated with national and international clinicians and researchers

BSR Registrants

294 registrants

137 known deceased

96 lost to follow up (no contact in the last 5 years)

How to join the BSR

- Provide consent (including assent for those under age 17)
- Complete an intake form and discuss it with Dr. Cunniff or Kucine if necessary
- Data is entered into a confidential database at WCMC
- Provide annual updates electronically
- Future direction – annual DNA collection via saliva or other tissue

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ORIGINAL ARTICLE

Health supervision for people with Bloom syndrome

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ARTICLE

Age of first cancer diagnosis and survival in Bloom syndrome

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Gene changes (variants) that cause Bloom syndrome

- 74 variants identified in 181 people in the BSR
- Common variants include founder variants in several population groups
- Most variants cause no protein to be made
- No known correlation of variants with outcomes

Tumor Whole Genome Sequencing

- DNA collected from 10 tumors
- DNA from blood or saliva collected from each person
- Compare WGS results from tumor and blood/saliva
- Analyzing samples for clues to tumor cause and treatment

Collaborations

Dr. Vivian Chang, University of California Los Angeles

Dr. Nathan Ellis, University of Arizona

Englander Institute for Precision Medicine, Weill Cornell Medical College

Dr. Frank Chan at the Max Planck Institute in Tubingen, Germany

TECHNICAL REPORT
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nature genetics

Check for updates

Rapid genotype imputation from sequence with reference panels

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Inexpensive genotyping methods are essential to modern genomics. Here we present QUILT, which performs diploid genotype imputation using low-coverage whole-genome sequence data. QUILT employs Gibbs sampling to partition reads into maternal and paternal sets, facilitating rapid haploid imputation using large reference panels. We show this partitioning to be accurate over many megabases, enabling highly accurate imputation close to theoretical limits and outperforming existing methods. Moreover, QUILT can impute accurately using diverse technologies, including long reads from Oxford Nanopore Technologies, and a new form of low-cost barcoded Illumina sequencing called haplotagging, with the latter showing improved accuracy at low coverages. Relative to DNA genotyping microarrays, QUILT offers improved accuracy at reduced cost, particularly for diverse populations that are traditionally underserved in modern genomic analyses, with accuracy nearly doubling at rare SNPs. Finally, QUILT can accurately impute (four-digit) human leukocyte antigen types, the first such method from low-coverage sequence data.

Future Directions

- Longitudinal sample analysis
- Exosome analysis
- Cell free DNA
- New methods of tumor study

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