LymphomaHub

HL

AACR 2017 | Poster 2448/5 – Deep exome sequencing reveals recurrent somatic mutations in Classical Hodgkin Lymphoma

Terri Penfold | Apr 07, 2017

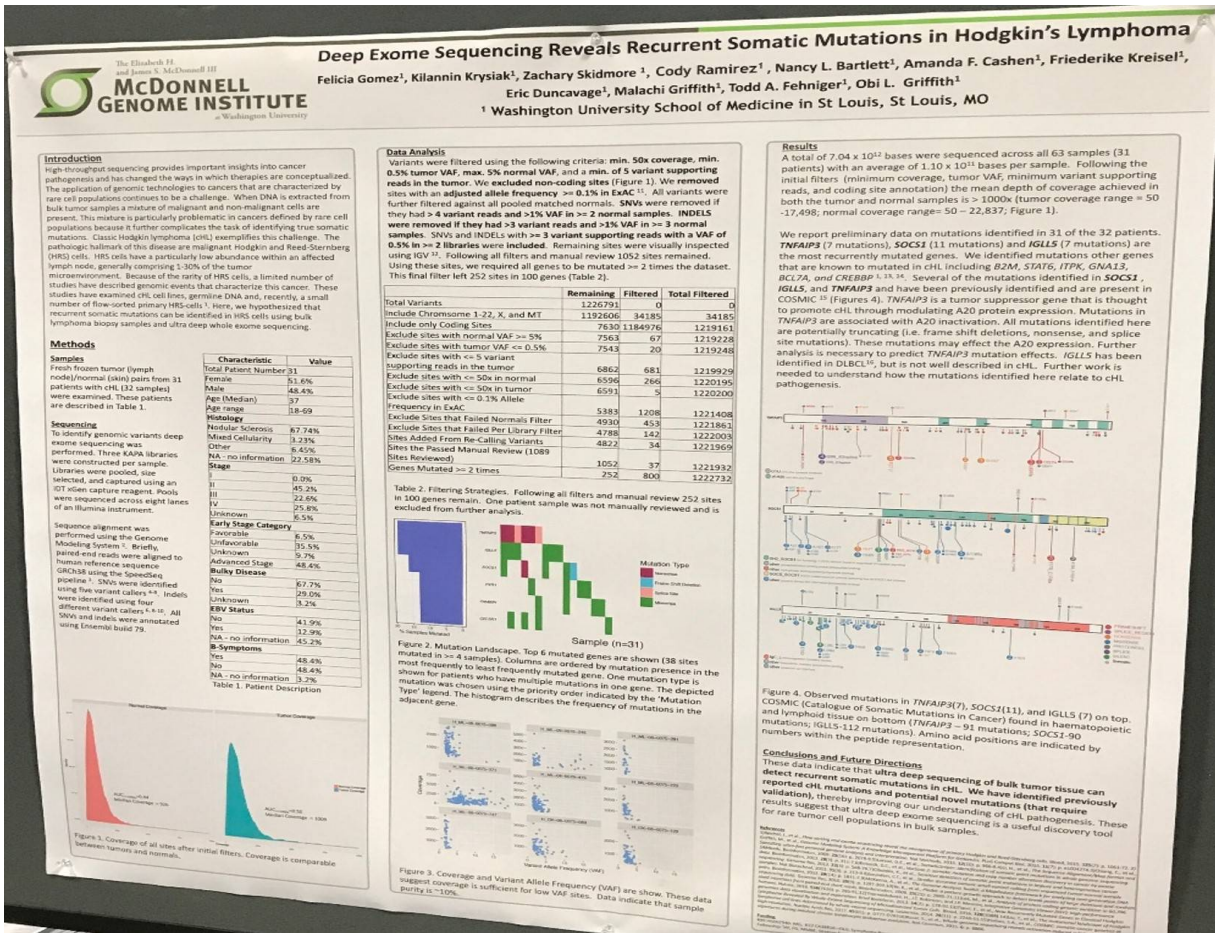
On Monday 3rd April during this year's American Association for Cancer Research (AACR) annual meeting, a poster (2448 / 5) by Felicia Gomez, from Washington University, St. Louis, MO, *et al.* titled "Deep exome sequencing reveals recurrent somatic mutations in Hodgkin's Lymphoma" was presented.

The group hypothesized that recurrent somatic mutations can be recognized in Hodgkin Reed-Sternberg (HRS) cells, taken from biopsies of bulk Hodgkin Lymphoma (HL), using ultra-deep exome sequencing.

Key Highlights:

- In total, using 63 samples from 31 patients, $7.04x10^{12}$ bases were sequenced; $1.10x10^{11}$ average bases per sample
- Mean depth of coverage achieved in both tumor and normal samples is >1,000x; tumor coverage range = 50–17,498; normal coverage range = 50–22,837
- Mutations identified in 31/32 patients
- The most currently mutated genes = *SOCS1* (11 mutations), and *TNFAIP3* and *IGLL5* (7 mutations each)
- Mutations in *TNFAIP3* were frameshift deletions, nonsense, and splice site mutations (all potentially truncating)
- Identified other mutations known to be mutated in cHL = *B2M*, *STAT6*, *ITPK*, *GNA13*, *BCL7A*, and *CREBBP*

The poster concluded by stating that recurrent mutations in cHL can be identified using ultra-deep sequencing of bulk tumor tissue. The group identified previously unreported mutations which require validation, as well as known mutations. This data improves our understanding of the pathogenesis of cHL.



Deep Exome Sequencing Reveals Recurrent Somatic Mutations in Hodgkin's Lymphoma

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Reference:

1. Gomez F. *et al.* Deep exome sequencing reveals recurrent somatic mutations in Hodgkin's Lymphoma [Poster]. In: Proceedings of the 107th Annual Meeting of the American Association for Cancer Research; 2017 Apr 1-5; Washington, DC. Philadelphia (PA): AACR; 2017. Poster nr [2448 / 5].