USE OF DIGITAL PATHOLOGY IN THE CANCER GENOME ATLAS PROJECT

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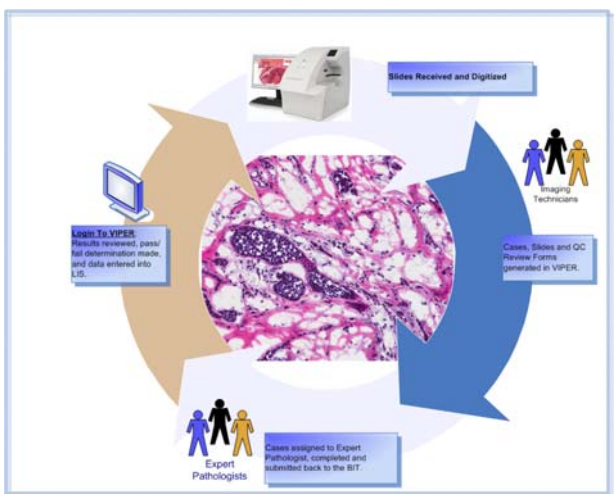
BACKGROUND

Virtual Microscopy (VM) and Digital Pathology have been an important part of day-to-day operations in the Biopathology Center (BPC) at The Research Institute at Nationwide Children's Hospital (TRINCH) since 2004. As a component of the BPC, the Biomedical Imaging Team (BIT) is responsible for imaging glass slides for various projects and cooperative groups including the Gynecological Oncology Group (GOG), The Children's Oncology Group (COG) and the Cooperative Human Tissue Network (CHTN), among others. With seven Aperio Scanscope XT digital scanners and one Hamamatsu NanoZoomer, the BIT has the capacity to convert upwards of 1,000 glass slides into digital images per day. Last year, the Biospecimen Core Resource (BCR) for The Cancer Genome Atlas Project (TCGA) began utilizing the BIT's services for digital pathology quality control of specimens received into the project.

The National Institutes of Health (NIH) established The Cancer Genome Atlas to generate comprehensive, multi-dimensional maps of the key genomic changes in major types and subtypes of cancer. This catalog serves as a powerful resource for a new generation of research aimed at developing better strategies for diagnosing, treating and preventing each type of cancer. This pioneering effort to map and analyze cancer genomes in a large-scale, systematic manner, will ultimately change the way cancer is treated. For example, TCGA data will enable both public and private sector researchers to pursue targeted therapies or combinations of therapies aimed at the specific pathways involved in a certain cancer type or subtype. This new level of insight promises to significantly shorten the time and reduce the costs involved in drug development. [1]



BIT TCGA workflow

METHODS

After tissues received by the BCR are sectioned by the BCR's histology group, the slides are scanned by the BIT using Aperio Scanscope XT and Hamamatsu NDP 2.0 whole slide imaging robots. The images are then uploaded to the Ohio Super Computer Center (OSC) where they are served to reviewing pathologists throughout the United States and Canada. The BIT utilizes its custom-designed VIPER system (Virtual Imaging for Pathology Education and Research) to distribute digital images and QC review forms to the reviewing pathologists. Upon being assigned new cases, VIPER users are notified via email of their pending reviews.

VIPER reviewer interface

VIPER TCGA review form

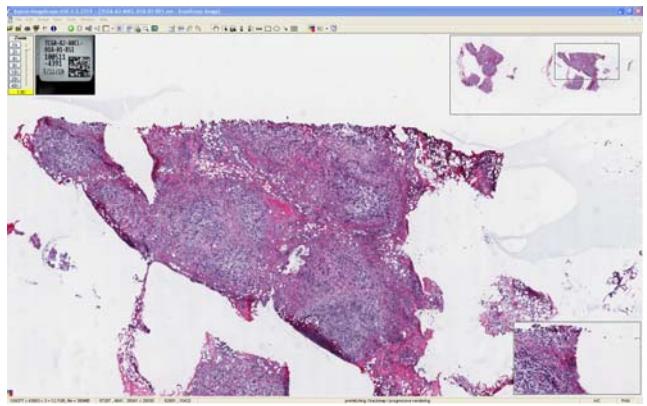
The reviewers are then able to log into the VIPER system, where they can view the whole slide images and electronic view forms simultaneously. Once the pathologist has submitted the completed review form, the case then disappears from their pending case list. After receiving completed reviews, the BIT's imaging coordinators verify whether each sample meets the required pathology metrics to support nucleic acid extraction of the case. Digital images of the samples that meet all quality control criteria throughout pathology and molecular analysis at the BCR are uploaded to the Data Coordinating Center (DCC) of TCGA.

RESULTS

Virtual microscopy and the VIPER system have been instrumental in gathering quality control pathology reviews for the BCR in an efficient manner. At this time over 7,500 slides have been scanned and digitally reviewed for this project.

CONCLUSIONS

Utilizing digital pathology eliminates the need to send glass slides to reviewers, drastically reducing turnaround times and shipping costs. Also, having pathologists complete electronic review forms allows review data to be uploaded directly to the project's lab information system, reducing human error and ensuring that samples are moved through the pipeline in an expedient manner. The use of digital pathology over traditional pathology review has clearly been beneficial to The Cancer Genome Atlas Project, as both the speed of the QC review process and overall operational efficiency has been remarkable.



Whole-slide image for TCGA

ACKNOWLEDGEMENTS

The Cancer Genome Atlas

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HAMAMATSU

Ohio Supercomputer Center

REFERENCES

1. The Cancer Genome Atlas (TCGA). Retrieved 3/17/2011, from http://ocg.cancer.gov/programs/tcga.asp.