Special session (Thu, 27 Sep, 11:15−12:15)
How do you discover new cancer genes?

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Somatic mutations in human cancer: emerging patterns from sequencing the protein kinase gene family and beyond

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The identification of somatically mutated genes in human cancer has been a major focus of cancer research since the first report of mutated HRAS some 25 years ago. It is now possible to implement large scale systematic searches for somatic mutations given the availability of the reference human genome sequence and strides made in sequencing technologies. We have recently completed resequencing the entire family of protein kinases in a series of human cancers. The patterns emerging from this work suggest that there may well be a larger number of infrequently mutated genes in human cancers than previously suspected, and that there is unlikely to be a very frequently point mutated protein kinase driving ovarian carcinogenesis. As well, the ability to have the first in-depth look at the cancer genome in various cancer types has revealed a remarkable diversity of prevalence and pattern of mutation. In addition, more targeted resequencing efforts have led to recent identification of genes important in human leukaemias. Further analyses of these data and ongoing work will be discussed.