Search for genomic predictors of nausea and vomiting

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12:00 PM to 1:00 PM
UPMC Shadyside
Hillman Cancer Center
Cooper Classroom C

Light lunch provided. Please contact Dolores Oliver (oliverdo@upmc.edu) if you plan to attend, need directions, or need more information. The Cooper Classrooms are located on the ground level of the Hillman Cancer Center, 5115 Centre Avenue, Shadyside. After entering the building walk to the left past the elevators. Facing the gift shop turn right down the hallway. Room C is the 3rd door in the lobby area on the left.

BRAIN, BEHAVIOR, AND CANCER Seminar Series
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Abstract: There have been a growing number of experimental evidences indicating that the extent and intensity of nausea and vomiting (N/V) in human subjects may have hereditary character. In particular, the genetic background has been confirmed for N/V associated with motion sickness, some forms of postoperative (and opioid induced) nausea and vomiting (PONV), migraines as well as nausea and vomiting associated with pregnancy. The details of the genetic background of hereditary nausea and vomiting remain however largely obscure, even despite recent advances in the molecular genomic techniques. In the past ten years there has been accumulating evidence that suggests nausea and vomiting are associated with multiple genetic targets along the emetic pathway (e.g. 5-HT3, NK1, muscarinic and DA2 receptors). In addition, most of the studies were related predominantly to the pharmacogenomic aspects of inadequate prophylaxis or treatment of N/V (e.g. in CINV), rather than genomic background of N/V itself.

With the exception of one genome wide association study, most of these association studies have small sample and or effect sizes, are often retrospective studies and due to focusing on only one or two previously known genes, are unable to adequately explain the individual variability observed. And there is still a fundamental lack of knowledge about the mechanisms that drive the associations, in particular in relation to other genomic pathways than described above. In addition, just only one study has focused on the relationship between motion sickness, PONV and CINV, even when most of these phenotypes might somehow be familial. The significant problem associated with research on N/V includes lack of suitable animal models for investigating of the hereditary N/V. In this respect, the significant progress has been recently made in establishing the model of hereditary N/V associated with motion sickness and PONV in musk shrew strains. The preliminary data using the next generation sequencing techniques of the brain transcriptome from musk shrew indicate that, in fact, the strains with different response to N/V may differ in various components of the brain transcriptome. The detailed analysis of these differences and its translation to the human with high incidence of familial N/V might provide the best avenue to identify genetic elements responsible for the variability in N/V.

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