events (MACE) while remaining economically sustainable. METHODS/STUDY POPULATION: This prospective, pragmatic study will enroll two-hundred patients with ACS undergoing PCI, receiving DAPT. Patients will receive point-of-care *CYP2C19* genotyping. Patients with at least one loss-of-function (LoF) allele will be recommended prasugrel. Those without LoF alleles, will be recommended to take prasugrel for 7 days then clopidogrel for 7 days, followed with platelet reactivity phenotyping. Patients with HPR >208 $P2Y_{12}$ reaction units will take prasugrel; the remainder will take clopidogrel. We will review electronic health records and contact patients at baseline, then at 1, 3, 6, and 12 months to collect data for cardiovascular and health-related quality of life (HRQoL) outcomes. RESULTS/ANTICIPATED RESULTS: Feasibility and clinical utility will be measured by the proportion of patients with a genotype or phenotype leading to a clinical recommendation of alternative therapy and whether or not recommendations were accepted by clinicians. Effectiveness will be measured by combined MACE (composite of cardiovascular death, non-fatal myocardial infarction, and non-fatal stroke), stent thrombosis, and major and minor bleeding over the study period. Cost of testing, 30-day hospital readmission, and HRQoL questionnaires will be included for pharmacoeconomic analysis from an institutional perspective. DISCUSSION/SIGNIFICANCE OF IMPACT: There are no studies investigating the clinical utility of implementing guided anti-platelet selection, combining *CYP2C19* genotyping and HPR phenotyping. We anticipate incorporating this precision medicine approach to guide $P2Y_{12}$ inhibitor selection will be feasible while improving patient outcomes.

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## Enhanced efficiency of large-scale clinical proteomic studies: when less is more

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OBJECTIVES/GOALS: Large-scale clinical proteomic studies of cancer tissues often entail complex workflows and are resource-intensive. In this study we analyzed ovarian tumors using an emerging, high-throughput proteomic technology termed SWATH. We compared SWATH with the more widely used iTRAQ workflow based on robustness, complexity, ability to detect differential protein expression, and the elucidated biological information. METHODS/STUDY POPULATION: Proteomic measurements of 103 clinically-annotated high-grade serous ovarian cancer (HGSOC) tumors previously genomically characterized by The Cancer Genome Atlas were conducted using two orthogonal mass spectrometry-based proteomic methods: iTRAQ and SWATH. The analytical differences between the two methods were compared with respect to relative protein abundances. To assess the ability to classify the tumors into subtypes based on proteomic signatures, an unbiased molecular taxonomy of HGSOC was established using protein abundance data. The 1,599 proteins quantified in both datasets were classified based on z-score-transformed protein abundances, and the emergent protein modules were characterized using weighted gene-correlation network analysis and Reactome pathway enrichment. RESULTS/ANTICIPATED RESULTS: Despite the greater than two-fold difference in the analytical depth of each proteomic method, common differentially expressed proteins in enriched pathways associated with the HGSOC Mesenchymal subtype were identified by both methods. The stability of tumor subtype classification was sensitive to the number of analyzed samples, and the statistically stable subgroups were identified by the data from both methods. Additionally, the homologous recombination deficiency-associated enriched DNA repair and chromosome organization pathways were conserved in both data sets. DISCUSSION/SIGNIFICANCE OF IMPACT: SWATH is a robust proteomic method that can be used to elucidate cancer biology. The lower number of proteins detected by SWATH compared to iTRAQ is mitigated by its streamlined workflow, increased sample throughput, and reduced sample requirement. SWATH therefore presents novel opportunities to enhance the efficiency of clinical proteomic studies.

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## Enhanced radiation therapy using chlorin-e6 conjugated gold nanoparticles

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OBJECTIVES/GOALS:

- Development of gold nanoparticles covalently linked to a photosensitizer for use to enhance radiation therapy. The particles will be thoroughly characterized structurally and mechanistically. The gold particles should enhance radiation activity by closer proximity to the photosensitizer and by increasing particle accumulation in the tumor.

METHODS/STUDY POPULATION:

- Gold nanoparticles were synthesized and coated with amine-terminated poly(ethylene) glycol, then covalently conjugated to chlorin e6, a known FDA-approved photosensitizer. The system was characterized using UV-Vis spectroscopy, transmission electron microscopy, and nanoparticle tracking analysis. The generation of reactive oxygen species was measured after X-irradiation. Enhanced cell killing was evaluated clonogenically in addition to assessment of *in vivo* efficacy and tumor pathology.

RESULTS/ANTICIPATED RESULTS:

- Conjugation of the particle to the photosensitizer was achieved, and the molecule was detected by UV-Vis spectroscopy. TEM and NTA showed no aggregation of the particles, and an increase in reactive oxygen species generation was observed. The conjugates increased cell killing during radiation treatment, whereas neither the particle alone nor the photosensitizer significantly affected clonogenic survival at the same concentrations. Breast tumors grown in immunocompetent mice showed increased necrotic tissue after a single 20 gy treatment in the presence of the conjugate.

DISCUSSION/SIGNIFICANCE OF IMPACT: Radiation therapy is widely used clinically, but dosage is limited largely to prevent injury to adjacent normal tissue. By increasing the local effect of radiation therapy, our gold conjugate has the potential to augment the effective radiation dose in the tumor, thereby reducing damage to healthy tissue and providing a more effective therapy.

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