

**Circulating tumor cells monitored over time in lung cancer patients.** *M. S. Littergen, D. Marrinucci, D. Lazar, M. Malchiodi, P. Clark, E. Huynh, K. Bethel, L. Bazhenova, J. Nieva, P. Kuhn; The Scripps Research Institute, La Jolla, CA; Scripps Clinic, La Jolla, CA; University of California, San Diego, La Jolla, CA; Billings Clinic, Billings, MT*

**Background:** Circulating tumor cell (CTC) detection and enumeration is a valuable tool for monitoring cancer patient status and outcome. While many current techniques employ immunomagnetic-enrichment based protocols focused on the importance of a particular CTC number as the indicator of patient status or outcome, we employ a cytometric, enrichment free approach using an immunofluorescent protocol to monitor CTC counts in patients with non-small cell lung cancer (NSCLC) over the course of treatment. **Methods:** Eligible patients had progressive stage IV NSCLC. The histological subtypes in the 42 cases for which the data was available included adenocarcinoma (22/42), squamous cell carcinoma (6/42), large cell undifferentiated carcinoma (3/42), and non-small cell lung carcinoma not further described, poorly differentiated, or with a mixed pattern (11/42). Blood samples were collected 3 wks, 3 mo, 6 mo, 9 mo, and 1 yr after the initial sample. CTCs were identified via immunofluorescence and cytometric analysis. Patient response to therapy was determined by RECIST every 3 months between time 0 and time 12 mo. **Results:** 80 of 109 patient samples have CTCs (73%) and all of the 52 patients tested have CTCs. 13 of 52 patients have CTC data for time 0 and 3 wks. Only 4 of these patients (30.8%) show a correlation linking CTC count change between time 0 and 3 wks and clinical assessment. 13 patients have CTC data for time 0 and 3 mo, 10 of whom show a correlation linking CTC count change between time 0 and 3 mo and clinical assessment. 7 of the 8 patients (87.5%) showing stable or partial response at 3 mo show a decrease in CTC count between time 0 and 3 mo. Five of the 6 patients (83.3%) clinically showing progressive disease at the 3 mo time point show an increase in CTC count between time 0 and 3 mo. The patients that do not show a correlation linking CTC count change between time 0 and 3 mo and clinical assessment at 3 mo show a correlation at the 6 mo time point. **Conclusions:** CTCs can be effectively enumerated in metastatic NSCLC patients, with the majority demonstrating CTCs in the setting of progressive disease. The change in CTC count at 3 mo, but not at 3 wks, correlates with radiographic response to chemotherapy. Further follow-up will determine the predictive value of CTC enumeration on survival.

**Effects of G-CSF on circulating tumor cells (CTC) and CA 27.29 in breast cancer patients.** *P. Hepp, B. Rack, A. Schneider, M. Rezaei, H. Tesch, T. Beck, U. Böling, W. Lichtenecker, M. W. Beckmann, W. Janni, SUCCESS Study Group; Heinrich Heine University, Düsseldorf, Germany; Ludwig-Maximilians-University, Munich, Germany; Charité, Berlin, Germany; Luisenkrankenhaus, Düsseldorf, Germany; Praxis Prof. Tesch, Frankfurt, Germany; Städtisches Klinikum Rosenheim, Rosenheim, Germany; Gemeinschaftspraxis Siehl & Söling, Kassel, Germany; University of Erlangen, Erlangen, Germany; SUCCESS Study Group*

**Background:** Some recent publications indicated that the use of G-CSF could be connected to an increase in CTC as well as elevated levels of tumor markers such as CA 27.29. In the SUCCESS Trial CTC and CA27.29 are examined before and after adjuvant chemotherapy (CHT) in 3754 breast cancer patients (pts). **Methods:** The SUCCESS Trial is a phase III trial comparing FEC-Docetaxel vs. EC-Doc-Gemcitabine regime and 2 vs. 5 years of treatment with zoledronate in patients with primary breast cancer (BC) (N+ or high risk). Blood samples are taken before and after CHT. CTC were assessed with the CellSearchSystem (Veridex, Warren, USA). After immunomagnetic enrichment with an anti-EpCAM-antibody, cells were labeled with anti-cytokeratin (8,18,19) and anti-CD45 antibodies to distinguish epithelial cells and leukocytes. CA27.29 has been measured with ST AIA-PACK Ca27.29 reagent using MUC-1 for AIA-600II (Tosoh Bioscience, Tessenderlo, Belgium). The cutoff for CA27.29 is 32 U/ml and >1 cell for the CTC analysis. Patients were grouped to CTC/CA27.29 raise or no raise and 1 to 6 cycles with G-CSF or no G-CSF at all. **Results:** Data on 1510 pts are available for CTC analysis. 745 pts (49%) received at least one course of G-CSF. 117 pts (8%) showed an increase in CTC after CHT. In this group 52 (3%) pts received G-CSF and 65 (4%) did not. 693 pts with stable or decreased CTC received G-CSF (46%) and 700 did not (46%). There was no significant difference ( $p=0.29$ ). The analysis of CA27.29 is based on the data of 2556 pts. 1252 pts (49%) received at least one course of G-CSF. 338 pts (13%) exceeded the threshold for CA27.29 only after CHT. In this group 209 pts (8%) received G-CSF and 129 (5%) did not. 1043 pts with stable or decreased CA27.29 received G-CSF (41%) and 1175 did not (46%). This difference was highly significant ( $p<0.0001$ ). **Conclusions:** No evidence can be provided for a significant correlation between an increase in the number of CTC and the application of G-CSF over CHT. Nevertheless the results on CA27.29 showed a highly significant correlation between the administration of G-CSF and elevated CA27.29 levels directly after CHT. This could be a possible explanation for the often observed increase of tumor markers after CHT.

**Gauging the response of circulating epithelial tumor cells (CETC) and tumor stem cell subpopulations to therapy of early-stage cancer in the individual patient.** *K. Pachmann, O. Camara, I. B. Runnebaum, K. Hoeffken; Clinic for Internal Medicine II, Jena, Germany; University Hospital Friedrich Schiller University, Jena, Germany*

**Background:** Cells released from the primary tumor persisting and recirculating in the host can lead to the formation of distant metastases. It was claimed that such cells are detectable only in a minor fraction of early-stage cancer patients but we can show that CETC are detectable and can be quantified in the peripheral blood of almost all cancer patients including early-stage solid malignancies. **Methods:** Using anticoagulated peripheral blood, red blood cell lysis as the only enrichment step, one centrifugation step, staining live cells with fluorochrome labeled anti-epithelial antigen as a search antibody, automated image analysis for detection of positive events and evaluation of exclusively surface located epithelial antigen on vital unfixed cells, CETC were detected in most patients with early stage cancer. Subsequently cells could be stained with anti-ALDH-antibody and in situ hybridized for HER2/neu amplification and quantified repeatedly during neo/adjuvant chemotherapy and during maintenance therapy with hormones or trastuzumab. **Results:** We here report the results from 497 breast cancer patients analyzed more than three times during the course of disease, 248 during neoadjuvant/adjuvant chemotherapy, 249 during trastuzumab and or hormone therapy. Different pattern of therapy response were obtained with rapidly responding CETC changes over several logs in response to chemotherapy and slow and long-lasting changes extending over several years in response to hormone therapy and trastuzumab. Stem cell like staining was seen in a minor fraction of cells (1%) in about 10% of patients. An increase in cell numbers and in the fraction of HER2/neu amplified cells was under all treatment conditions unequivocally significantly correlated to highly increased risk of relapse. **Conclusions:** CETC and subpopulation monitoring provides an invaluable tool for prompt gauging of systemic therapy in early stage solid tumors as a tool for therapy guidance and optimal personalized therapies to improve therapy results and spare unnecessary treatments.

**Preclinical testing of the PARP inhibitor ABT-888 in microsatellite unstable colorectal cancer.** *E. Vilar Sanchez, A. Chow, L. Raskin, M. D. Iniesta, B. Mukherjee, S. B. Gruber; University of Michigan, Ann Arbor, MI*

**Background:** Microsatellite instability (MSI) represents approximately 15% of colorectal cancer (CRC) cases. MSI due to hypermethylation or mutation in DNA mismatch repair genes leads to genetic instability and a mutator phenotype. Genetic instability is particularly high at repetitive sequences such as those located in MRE11, RAD50, CtIP and MBC. Each of these genes are implicated in the double strand break (DSB) repair pathway. PARP inhibitors induce single strand breaks that remain unrepaired and then will be converted to DSB during DNA replication. Our objective was to assess the preclinical activity of a novel PARP inhibitor ABT-888 in MSI cell lines deficient in the DSB repairing pathway and compare it to Microsatellite Stable (MSS) lines. **Methods:** We used the systems biology tool "Connectivity Map" to synthesize data from 5 different published studies of expression profiling of MSI CRC phenotype and to identify target compounds. We assessed the mutational status of MRE11, RAD50, CtIP and MBC in a panel of 10 CRC cell lines displaying either MSI or MSS, and measured the expression of MRE11 by quantitative RT-PCR. We tested the cytotoxic activity of single-agent ABT-888 for 6 days in MSS and MSI cell lines, stratified by mutational status. Flow cytometry was performed after 24 hours. **Results:** Systems biology studies identified PARP inhibitors as a candidate compound relevant for MSI CRC. Mutational status of MRE11 was perfectly correlated with MSI status. ABT-888 shows a preferential activity on those MSI cell lines harboring mutations in both MRE11 and RAD50 genes compared to MSS cell lines (wild-type for both genes). A significant correlation exists between MRE11 expression levels and cytotoxicity to ABT-888 at 10  $\mu$ M ( $R^2=0.915$ ,  $P<0.001$ ). Flow cytometry analyses show a G1 arrest following to the treatment with ABT-888 that is higher in MSI cell lines with mutations in MRE11 and RAD50 compared to MSS cell lines. **Conclusions:** This is the first report of the preclinical activity of a PARP inhibitor in CRC models. MSI colorectal tumors deficient in DSB repair show a higher sensitivity to PARP inhibition. Further clinical investigation of ABT-888 as a single agent or in combination with other chemotherapy drugs inducing DSB is warranted in MSI CRC with mutations in MRE11 and RAD50.

**Epidermal growth factor (EGF) gene (GERD), and esophageal adenocarcinoma.** *Kulke, R. Heist, K. Asomanin; University of Toronto, Toronto, Boston, MA; Dana-Farber Cancer Hospital, Boston, MA; Princes*

**Background:** Single nucleotide polymorphisms (SNPs) in the EGF gene (GERD), and esophageal adenocarcinoma (EAC) are associated with increased risk of EAC. The SNPs are modified by additional SNPs in the EGF gene. EGF is an established risk factor for EAC. **Methods:** EGF genotype history was collected for 309 EAC patients. Associations between genotype and EAC were analyzed using stratified regression. Genotype-stratified by GERD history and duration of GERD symptoms. **Results:** EGF genotype was associated with EAC between cases and controls (common ( $p=0.02$ ) and GERD controls. When compared to the associated with an increased risk of EAC. Stratified analyses revealed that increase in EAC risk among individuals for GERD-free individuals (see EAC was also highest for G/G more than once per week (OR GERD for longer than 15 years was a highly significant interaction of GERD ( $p<0.001$ ). **Conclusions:** EAC susceptibility through an increasing for patients with severe or at the greatest risk of EAC.

Odds of EAC stratified by EGF A61G polymorphism

	Number of cases/controls
Overall study cohort	309/275
GERD subset	150/62
GERD-free subset	159/213

EAC = esophageal adenocarcinoma; GERD = gastroesophageal reflux disease

**Detection of BRAF kinase mutations in colorectal cancer: Evidence for tumor heterogeneity.** *Litterman, M. Yancovitz, R. S. Blank, P. Lee, J. Osmani; Mount Sinai School of Medicine, New York, NY*

**Background:** Several studies have shown that BRAF mutations in polyclonal malignancies are associated with achieving durable treatment responses. However, the primary targeted therapies may select for tumor subclones. In this study we used a fluorescent-based next-generation sequencing method to include BRAF hotspot mutations in the BRAF hotspot mutation analysis. **Methods:** Paired primary and metastatic tumor samples were analyzed for BRAF mutations in DNA from 304 tumors (150 primary and 154 metastatic). We determined the presence of BRAF mutations in 18 metastatic melanomas were 18 metastatic specimens from metastases. **Results:** DNA sequencing of BRAF mutations in ovarian tumors, 1/82 (1.2%) metastatic melanomas. In contrast, the MS-PBR method in ovarian tumors, 15/82 (18%) metastatic melanomas. The presence of BRAF mutations in melanoma sample, but excluded from melanoma sample, but excluded using either methodology. BRAF mutations were also detected by MS-PBR in metastatic melanoma, but not in primary melanoma. In 19 patients with multiple primary tumors (wild-type and mutant) tumor heterogeneity was detected by mutation detection methodology within clinical tumor samples, where multiple primary tumor samples with respect to the presence of BRAF mutations suggest that failures of therapy directed against mutant BRAF may be occurring among the tumors under treatment.