

Session E. Gastrointestinal (colorectal) cancer

E07 DPYD c.1905 + 1G > A and c.2846A > T and UGT1A1*28 allelic variants as predictors of toxicity: Pharmacogenetic translational analysis from the phase III TRIBE study in metastatic colorectal cancer

C. Cremolini¹, M. Del Re², F. Loupakis³, F. Marmorino³, V. Citi², M. Palombi², F. Bergamo⁴, M. Schirripa³, D. Rossini³, E. Cortesi⁵, G. Tomasello⁶, R. Spadi⁷, A. Buonadonna⁸, D. Amoroso⁹, S. Vitello¹⁰, S. Di Donato¹¹, C. Granetto¹², M. D'Amico¹³, A. Falcone¹, R. Danesi²

¹Azienda Ospedaliero Universitaria Pisana e Università di Pisa, Pisa

²Dipartimento di Medicina Clinica e Traslazionale, Università di Pisa, Pisa

³Azienda Ospedaliero-Universitaria Pisana e Università di Pisa, Pisa

⁴Istituto Oncologico Veneto IRCCS, Padova

⁵Policlinico Umberto I, Roma

⁶Istituti Ospitalieri di Cremona, Cremona

⁷Ospedale Molinette, Torino

⁸Centro di Riferimento Oncologico Aviano, Aviano

⁹Ospedale Versilia, Lido di Camaiore (LU)

¹⁰Ospedale Sant'Elia, Caltanissetta

¹¹Ospedale Sandro Pitigliani, Prato

¹²Azienda Sanitaria Ospedaliera Santa Croce e Carle, Cuneo

¹³Ospedale Galliera, Genova

c.1905 + 1G > A and c.2846A > T. Moreover, irinotecan ADRs appear frequently in patients bearing the *UGT1A1*28* variant, associated with reduced *UGT1A1* expression. In this study, we analyse the association between *DPYD* and *UGT* variants with ADRs by 5-fluorouracil and irinotecan in subjects enrolled within the phase III TRIBE study, whose final results have been recently reported.

Methods: Out of 508 randomized patients, blood samples for pharmacogenetic analyses were available for 440 patients. DNA was extracted from 200 µl of blood and analyses of *DPYD* c.1905 + 1G > A, c.2846T > C and *UGT1A1*28* was performed by a Pyrosequencing platform (Qiagen, USA). The study was approved by the local Ethics Committee.

Results: Each of the *DPYD* c.1905 + 1GA and c.2846AT genotypes were found in 5 out of 440 subjects, with a combined frequency of 2.2%. c.1905 + 1GA and c.2846AT had the same impact on ADRs and, taken together, patients bearing these variants (N = 10) had an increased risk of G3/4 neutropenia (OR: 4.14, p = 0.043) and stomatitis (OR: 10.36, p = 0.003) as compared to wild-type patients. Five out of 10 *DPYD* mutant patients experienced a G4 ADR after the first cycle of therapy. *UGT1A1*28/*28* was found in 39/436 patients (8.9%); these patients had an increased risk of G3/4 neutropenia as compared to both *1/*1 (OR: 3.81, p < 0.001) and *1/*28 (OR: 2.28, p = 0.022) genotypes. Patients bearing *DPYD* c.1905 + 1GA, c.2846AT and *UGT1A1*28/*28* (N = 49) had an increased risk of G3/4 neutropenia (OR: 2.98, p < 0.001), febrile neutropenia (OR: 2.78, p = 0.023) and G3/4 stomatitis (OR: 6.83, p < 0.001). No significant correlation with G3/4 diarrhea was found.

Conclusions: *DPYD* c.1905 + 1GA, c.2846AT and *UGT1A1*28/*28* are associated with a higher risk of G3/4 ADRs also in the TRIBE trial, underscoring the predictive role of *DPYD* and *UGT1A1* variants across various fluoropyrimidine and irinotecan-containing schedules, and therefore their potential usefulness in treatment tailoring.

Background: Adverse drug reactions (ADRs) caused by fluoropyrimidines depend, at least in part, from DPD deficiency resulting from the loss-of-function mutations