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Description of the genetic variants identified in a cohort of patients diagnosed with localized anal squamous cell carcinoma and treated with panitumumab

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Squamous cell carcinoma is the most frequent histologic type of anal carcinoma. The standard of care since the 1970s has been a combination of 5-fluorouracil, mitomycin C, and radiotherapy. This treatment is very effective in T1/T2 tumors (achieving complete regression in 80–90% of tumors). However, in T3/T4 tumors, the 3-year relapse free survival rate is only 50%. The VITAL trial aimed to assess the efficacy and safety of panitumumab in combination with this standard treatment. In this study, 27 paraffin-embedded samples from the VITAL trial and 18 samples from patients from daily clinical practice were analyzed by whole-exome sequencing and the influence of the presence of genetic variants in the response to panitumumab was studied. Having a moderate- or high-impact genetic variant in *PIK3CA* seemed to be related to the response to panitumumab. Furthermore, copy number variants in *FGFR3*, *GRB2* and *JAK1* were also related to the response to panitumumab. These genetic alterations have also been studied in the cohort of patients from daily clinical practice (not treated with panitumumab) and they did not have a predictive value. Therefore, in this study, a collection of genetic alterations related to the response with panitumumab was described. These results could be useful for patient stratification in new anti-EGFR clinical trials.

Anal squamous cell carcinoma (ASCC) is the most frequent histologic type of anal carcinoma. An estimated 8300 new diagnoses were predicted in the United States in 2019, representing 2.5% of gastrointestinal cancers[1].

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