GENERAL SESSION 3

Alle Vortragsfolien

[GS3-01] Investigating denosumab as an add-on treatment to neoadjuvant chemotherapy and two different nab-paclitaxel schedules in a 2x2 design in primary breast cancer - First results of the GeparX study

Blohmer J-U, Link T, Kummel S, Untch M, et al.

The authors conclude that: The results of the primary endpoints and selected secondary endpoints will be presented at the meeting.

[GS3-02] Durvalumab compared to maintenance chemotherapy in patients with metastatic breast cancer: Results from phase II randomized trial SAFIR02-IMMUNO

Dalenc F, Garberis I, Filleron T, Lusque A, et al.

[GS3-03] Keynote-522 study of pembrolizumab + chemotherapy vs placebo + chemotherapy as neoadjuvant treatment, followed by pembrolizumab vs placebo as adjuvant treatment for early triple-negative breast cancer: Pathologic complete response in key subgroups

Schmid P. Barts Cancer Institute, Queen Mary University of London, London, United Kingdom.

The authors conclude that: Results suggest that adding pembrolizumab to neoadjuvant chemotherapy is beneficial for patients with the most aggressive disease and the highest unmet need.

[GS3-04] Pathologic complete response (pCR) to neoadjuvant treatment with or without atezolizumab in triple negative, early high-risk and locally advanced breast cancer. NeoTRIPaPDL1 Michelangelo randomized study

Gianni L, Huang C, Egle D, Bermejo B, et

al.

The authors conclude that: *xxxxp*CR and safety data will be presented at the meeting. Patients will continue to be followed up to allow for assessing comparative long-term event-free and overall survival analyses.

[GS3-05] Discussant

Kevin Kalinsky, MD, MS
Columbia University Irving Medical Center
New York, NY

[GS3-06] Results from the plasmaMATCH trial: A multiple parall circulating tumour DNA testing to direct targeted therapies in pati (CRUK/15/010)

Turner N, Kingston B, Kilburn L, Kernaghan S, et al.

The authors conclude that: Circulating tumour DNA testing offers accurate tumour genotyping, sufficient for routine clinical practice. This approach can be used

to identify patients with rare ***HER2*** **and** ***AKT1*** **mutations, who have clinically relevant response rates with matched targeted therapies.**

[GS3-07] **The genomic landscape of breast cancer based on ctDNA analysis: data from the plasmaMATCH trial**

Kingston B, Bye H, Hubank M, Walsh G, et al.

The authors conclude that: argeted ctDNA sequencing identified distinct genomic profiles of pre-treated advanced BC. ***ERBB2*****mutations are common in HER2 amplified advanced BC, with recurrent second novel mutations in** ***PIK3CA*** **common in HR+ BC.**Targeted ctDNA sequencing identified distinct genomic profiles of pre-treated advanced BC. ***ERBB2*****mutations are common in HER2 amplified advanced BC, with recurrent second novel mutations in** ***PIK3CA*** **common in HR+ BC.**

[GS3-08] **Multiplatform analysis of matched primary and metastatic breast tumors from the AURORA US Network**

King TA, Liu MC, McClure MB, Hinoue T, et al.

The authors conclude that: Collection of banked primary and metastatic tissue pairs identified a young MBC cohort with a high frequency of breast cancer family history and second breast primaries. Molecular characterization of luminal tumor pairs highlighted acquisition of aggressive traits including increased proliferation and loss of differentiation in the metastases. In contrast, basal-like pairs remained relatively unchanged, except for the loss of immune activation. Ongoing analyses to be presented include clonal heterogeneity and phylogeny, novel metastasis signature discovery, gene fusion, and endogenous retrovirus detection.

San Antonio - Mosaic on a pillar of streetcar station

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