BACKGROUND

- Triple negative breast cancer (TNBC) lacks the expression of both estrogen and progesterone receptors as well as human epidermal growth factor receptor 2 (HER2) overexpression.
- Advanced or metastatic A/M TNBC is a detrimental disease with limited treatment options.
- Molecular subtyping of A/M TNBC has the potential to enhance diagnostic accuracy and further enable targeted therapies, given its high degree of heterogeneity.

OBJECTIVE

The systematic literature review (SLR) aimed to identify real-world evidence for genetic alterations among A/M TNBC patients in the UK and EU4 (Germany, France, Spain, Italy).

METHODOLOGY

- Key biomedical databases were searched to identify real-world studies assessing genomic alterations among A/M TNBC patients (Table 1).
- Figure 1 presents the prespecified eligibility criteria for this SLR.
- As recommended by various HTAs, a standard methodology with two review processes for screening and data extraction was followed for this SLR.

RESULTS

- Three of the 203 screened studies provided data regarding the prevalence of genetic alteration among patients with A/M TNBC in real-world setting (Figure 2).
- Across the three included studies, a total of 399 A/M TNBC patients were analysed for genetic profiling using either digital droplet polymerase chain reaction (ddPCR), error-corrected 73-gene targeted panel (Guardant360), or AVENIO Expanded ctDNA Analysis Kit. Table 2 depicts the characteristics of the included studies.
- Patients with metastatic breast cancer diagnosed between 2000 to 2020 were identified within the GIM-14 BIOMETA study1.
  - 40% of tumors harbored at least 1 mutation in PI3K-AKT-mTOR pathway (PIK3CA, PIK3R1, AKT1, AKT2, PTEN or MTKR genes).
  - Patients with metastatic breast cancer diagnosed between January 2016 to December 2019 were sequenced by ddPCR and targeted ctDNA sequencing, for genetic profiling using either digital droplet polymerase chain reaction (ddPCR), error-corrected 73-gene targeted panel (Guardant360) or AVENIO Expanded ctDNA Analysis Kit.
  - BRCA-positive patients reported higher overall survival compared to BRCA-negative patients (median OS: 35 months vs. 16.3 months).

CONCLUSION

- The current SLR highlights the scarcity of real-world evidence on genetic alterations in A/M TNBC. Molecular subtyping exhibits a significant potential in identifying specific genetic alterations, emphasizing the need for further research and larger-scale studies.

REFERENCES