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| Clinical Utility of MOLECULAR Testing in  AML with *CEBPA* MUTATION  Diagnostic Utility  Mutations in the transcription factor CCAATT-enhancer binding protein alpha (*CEBPA*) occur in approximately 5%-10% of *de novo* AML, with approximately half of these cases carrying biallelic mutations (*CEBPA*bi)1,2.  *CEBPA* mutation is a defining genetic abnormality in AML according to both the International Concensus Classification (ICC) (AML with in-frame bZIP *CEBPA* mutations when blasts ≥10%)3 and the 5th edition of WHO classification (AML with *CEBPA* mutation when blasts ≥20%)2.  Of note, AML with *CEBPA* mutation as defined by WHO 5th edition includes both biallelic (*CEBPA*bi) as well as single in-frame mutations located in the bZIP domain (*CEBPA*bZIP)2.  *CEBPA*bi is most commonly characterised by the combination of an N-terminal frameshift mutation and a C-terminal in-frame mutation usually affecting the basic leucine zipper (bZIP) domain.  AML with *CEBPA* mutation is frequently associated with a normal karyotype and aberrant CD7 expression on the myeloblasts2.  Genes commonly co-mutated in AML with *CEBPA*mutation include *TET2*, *GATA2*, *WT1*, *FLT3-*ITD, *CSF3R* and *NRAS*4.  AML with germline *CEBPA* mutation is typically characterised by an N-terminal germline *CEBPA* mutation and a C-terminal somatic *CEBPA* mutation, although rare germline C-terminal mutations have been described5,6.  Investigation for the possibility of a germline *CEBPA* mutation is warranted in cases where *CEBPA* mutations are biallelic and/or observed at a germline variant allele frequency.  Prognostic Utility  *CEBPA*bi mutation is associated with favourable outcomes in normal karyotype, *FLT3*-ITD-negative AML7-9.  Patients with *CEBPA*bZIP have recently been shown to have a favourable prognosis similar to those with *CEBPA*bi mutations1,10.  Co-mutations in *CEBPA*bi have been reported to impact outcome such as *TET2* (inferior) and *GATA2* (favourable) however this is not consistent across all studies1,4,10,11.  BIOMARKERS OF RESPONSE TO THERAPY  *FLT3* mutations are the target of midostaurin12 (*FLT3*-ITD and TKD) (clinical trials included only TKD mutations at Asp835 and Ile836 codons), quizartinib (*FLT3*-ITD only)13 in newly diagnosed AML, and gilteritinib14 in relapsed/refractory AML.  *FLT3* testing should be repeated at relapse/progression as ~20% of patients have a change (gain or loss) in mutation status15.  *IDH1* (Arg132) and *IDH2* (both Arg140 and Arg172) mutations are the target of IDH1 and IDH2 inhibitors, respectively16.  Several mutations have been described in patients with acquired resistance to targeted inhibitors such as *FLT3* Phe691Leu (FLT3 inhibitors)17, second-site IDH1/IDH2 mutations (IDH1/IDH2 inhibitors)18, *BAX* (BCL2 inhibitors)19, and *MEN1* (menin inhibitors)20.  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