



Alignment and phylogenetic tree analysis of CCNE1 and CCNE2 cyclic protein partial gene sequences in human

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Background

CCNE cyclic protein is the limiting factor for G1 phase progression in to S phase in cell cycle associated with high genome ploidy in breast cancers. Cyclin E1 is one the most promising biomarkers in estrogen receptor positive breast cancer for response to the new standard of care drug class, CDK4/6 inhibitors. Because of its strong predictive value, cyclin E1 expression may be used in the future to triage patients into potential responders and non-responders. Importantly, cyclin E1 is highly related to cyclin E2, and both cyclin E1 and cyclin E2 are estrogen target genes that can facilitate anti-estrogen resistance and can be highly expressed in breast cancer.

Materials and Methods

The nine nucleotide and protein sequences were taken from National Center for Biotechnology Information GenBank. The alignment of nucleotide sequences was done by Multalin software. Phylogenetic tree was drawn using protein sequences by neighbor-joining method.

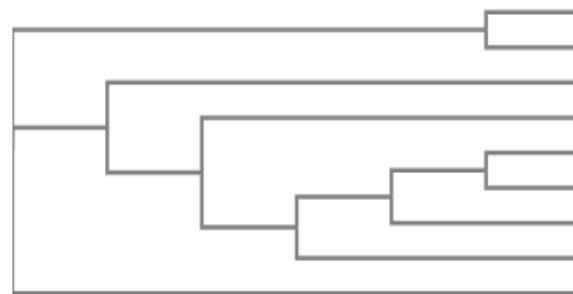
Results

Part of sequence alignment result revealed that CCNE1 and CCNE2 variants sequences are 53.3 percent similar. The phylogenetic tree shows some differences between protein sequences.

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651 660 670 680 690 700 710 720 730 740 750 760 770 780
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
NM_0012238.4 CACACCTGACACAGAGGATGATGACCGGGTTACCCAACTCAGCTGCAGGCTCGGATTATTGCACCATCCAGGGCTCC----CCGCTGCTGTACTGAGCTGGGCAATAGAGGAAAGTCTGGAA
NM_001322262.2 CACACCTGACACAGAGGATGATGACCGGGTTACCCAACTCAGCTGCAGGCTCGGATTATTGCACCATCCAGGGCTCC----CCGCTGCTGTACTGAGCTGGGCAATAGAGGAAAGTCTGGAA
XM_011527440.2 CACACCTGACACAGAGGATGATGACCGGGTTACCCAACTCAGCTGCAGGCTCGGATTATTGCACCATCCAGGGCTCC----CCGCTGCTGTACTGAGCTGGGCAATAGAGGAAAGTCTGGAA
NM_001322259.2 CACACCTGACACAGAGGATGATGACCGGGTTACCCAACTCAGCTGCAGGCTCGGATTATTGCACCATCCAGGGCTCC----CCGCTGCTGTACTGAGCTGGGCAATAGAGGAAAGTCTGGAA
NM_001322261.2 CACACCTGACACAGAGGATGATGACCGGGTTACCCAACTCAGCTGCAGGCTCGGATTATTGCACCATCCAGGGCTCC----CCGCTGCTGTACTGAGCTGGGCAATAGAGGAAAGTCTGGAA
NM_057749.3 AACACCTCACACAGAGATAGGACACAGTATTCTCCAGATT----TACAAATTACAGATTAAAAATCTTTTATTATCTCCACTTTGCTGATTTAGCTGGGGATTTCAAAAGAGTCTGGCT
XM_017013958.1 AACACCTCACACAGAGATAGGACACAGTATTCTCCAGATT----TACAAATTACAGATTAAAAATCTTTTATTATCTCCACTTTGCTGATTTAGCTGGGGATTTCAAAAGAGTCTGGCT
XM_017013959.1 AACACCTCACACAGAGATAGGACACAGTATTCTCCAGATT----TACAAATTACAGATTAAAAATCTTTTATTATCTCCACTTTGCTGATTTAGCTGGGGATTTCAAAAGAGTCTGGCT
XM_011517366.2 AACACCTCACACAGAGATAGGACACAGTATTCTCCAGATT----TACAAATTACAGATTAAAAATCTTTTATTATCTCCACTTTGCTGATTTAGCTGGGGATTTCAAAAGAGTCTGGCT
Consensus cACACCTgACACAGAGatGatgaccgGtTtAcCcaActCaacgTgCAAgcctCgGATtAtLgcAcCaTccagaggeTCC....CCgcTGCCTGAcTgAGCTGGGCAaATagAgAgGAAAGTCTGGaa

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NP_001309190.1 0.00181
 NP_001309188.1 -0.00181
 XP_011525742.1 -0.00696
 NP_001309191.1 -0.01354
 NP_477097.1 0
 XP_016869447.1 0
 XP_016869448.1 0
 XP_011515668.1 0.01005
 NP_001229.1 -0.00437

Conclusion

Some protein sequences in phylogenetic tree are near and some far from each other but their nucleotide sequences are very similar and it shows differences in the CCNE cyclic protein translation and post-translation. Although both play a role in the development of disease, cyclins E1 plays a more prominent role and is more pathogenic.

References

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