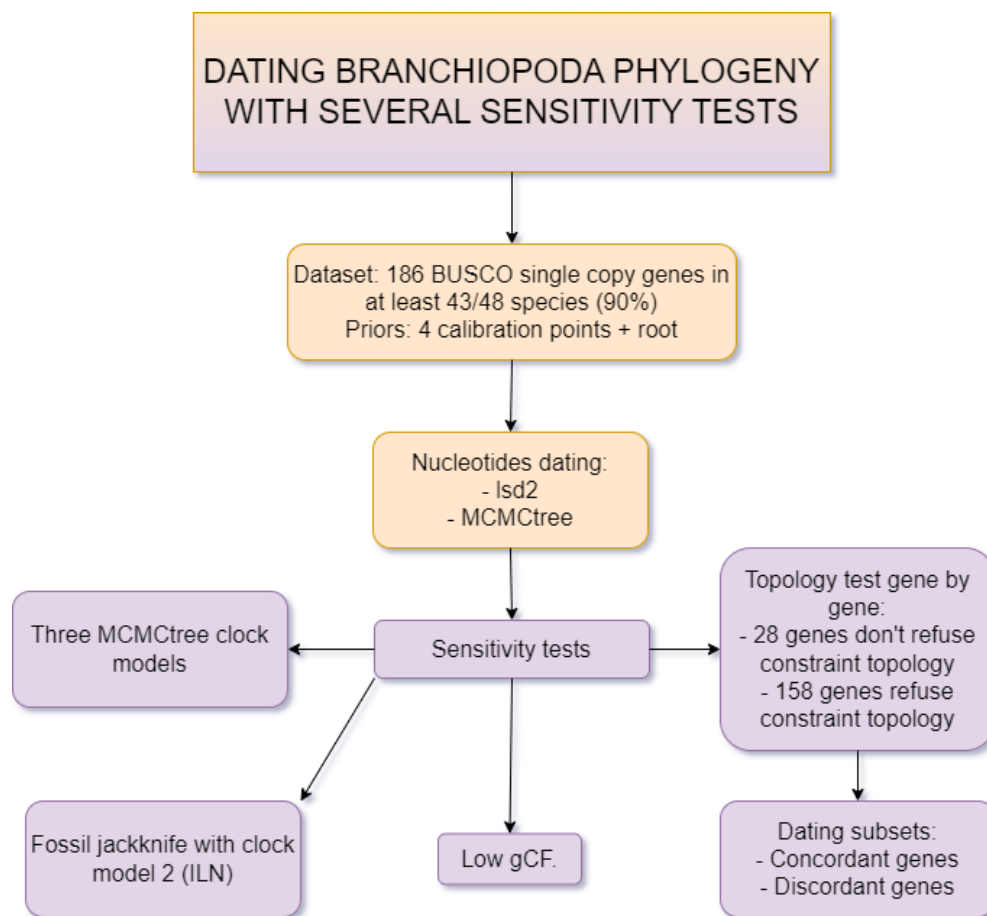


Branchiopoda Dating

Sumup

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0.1 Fatto in tesi

0.1.1 Filogenesi iqtree nucleotidi

Dataset: 186 geni BUSCO single copy in almeno 43/48 specie (90%).

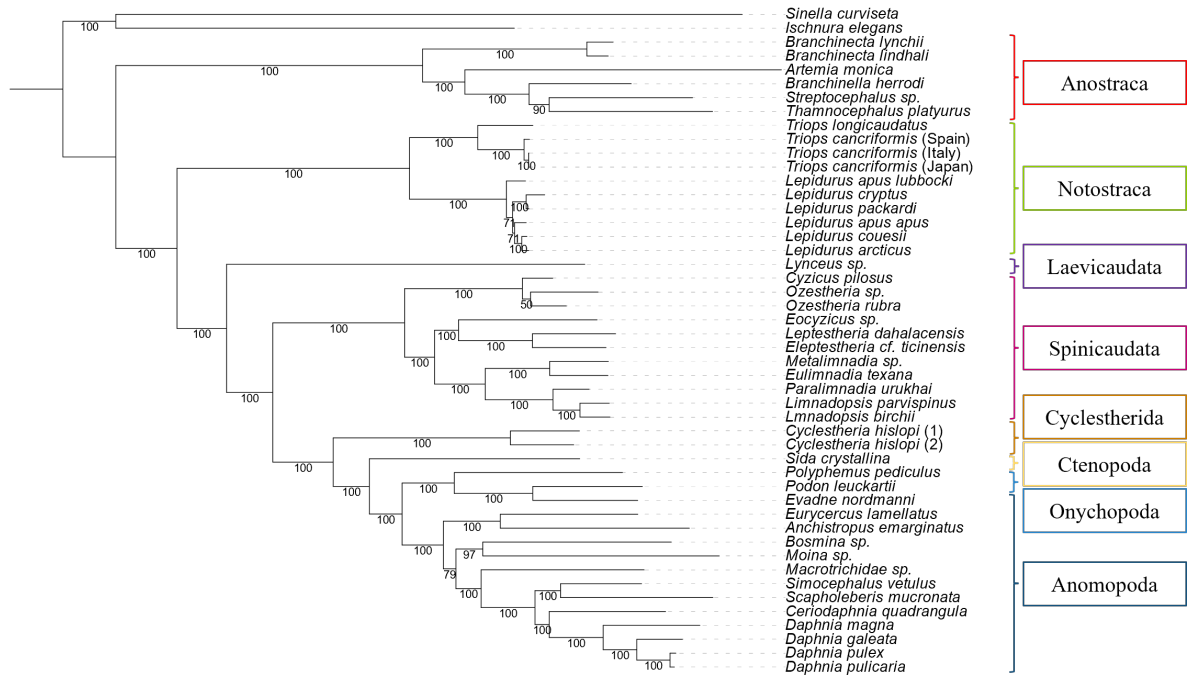


Figure 1: Maximum likelihood phylogenetic tree built on the nucleotide alignment of the 186 BUSCO genes present in at least 90% of the species (43/48) using IQ-TREE. Numbers at branches represent ultrafast bootstrap proportion.

0.1.2 Dating sui nucleotidi con lsd2 e i 3 clock model di mcmctree

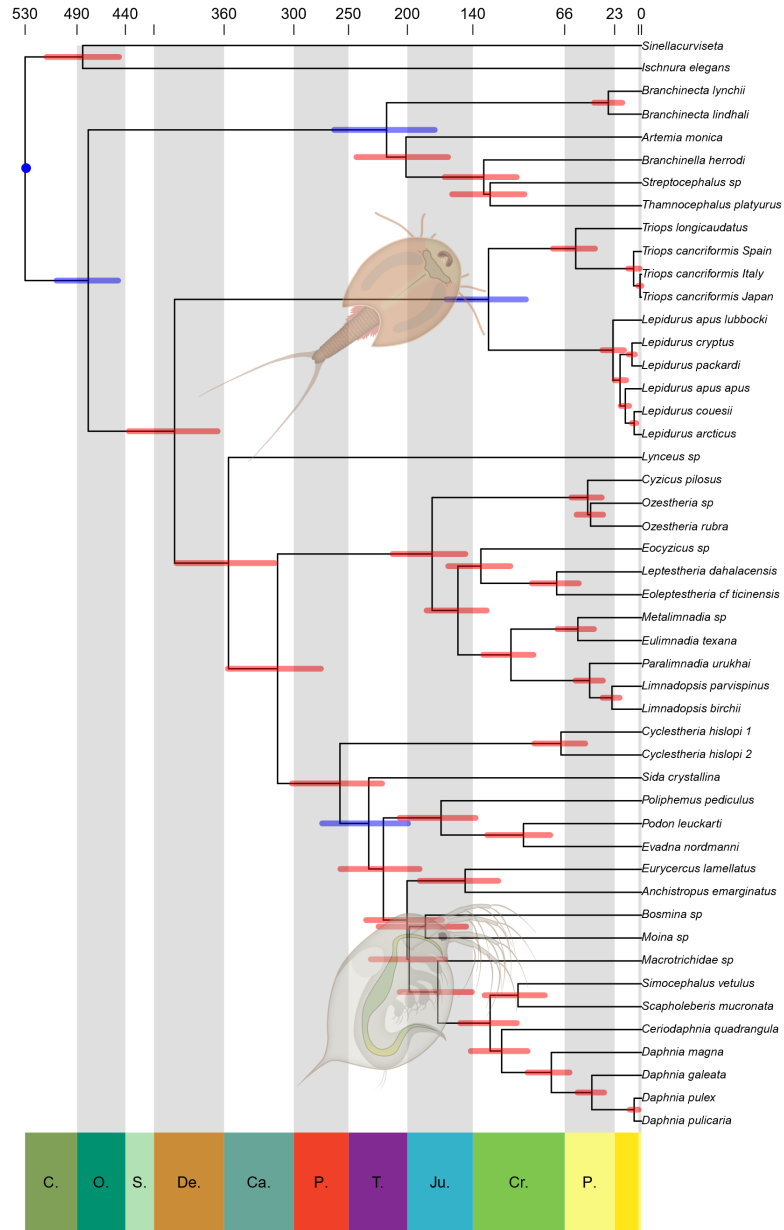


Figure 2: Tree dated with lsd2: blue bars are the prior calibrations. The two silhouettes represent the most studied groups of branchiopods, on top Notostraca and at the bottom Cladocera.

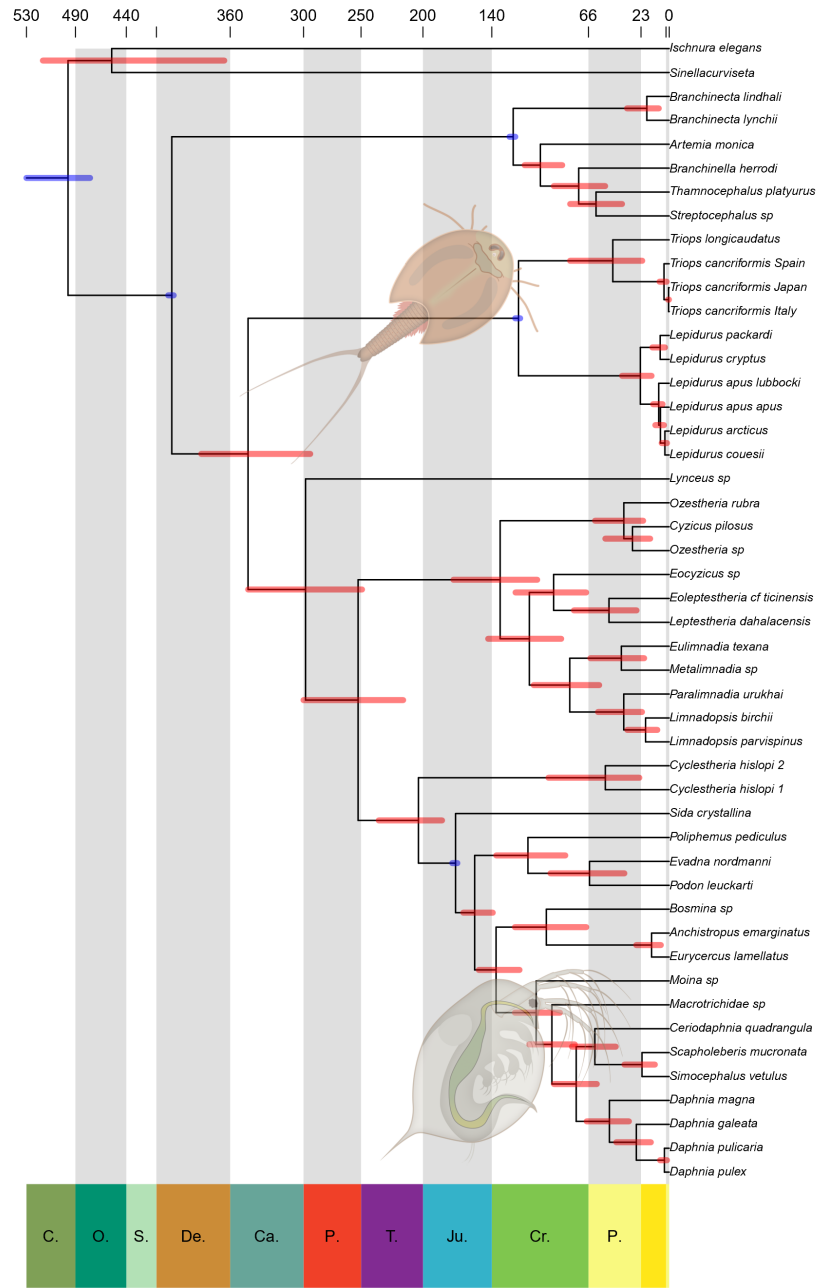


Figure 3: Tree dated with MCMCtree with correlated rates (GBM) Clock Model: blue bars are the prior calibrations. The two silhouettes represent the most studied groups of branchiopods, on top Notostraca and at the bottom Cladocera.

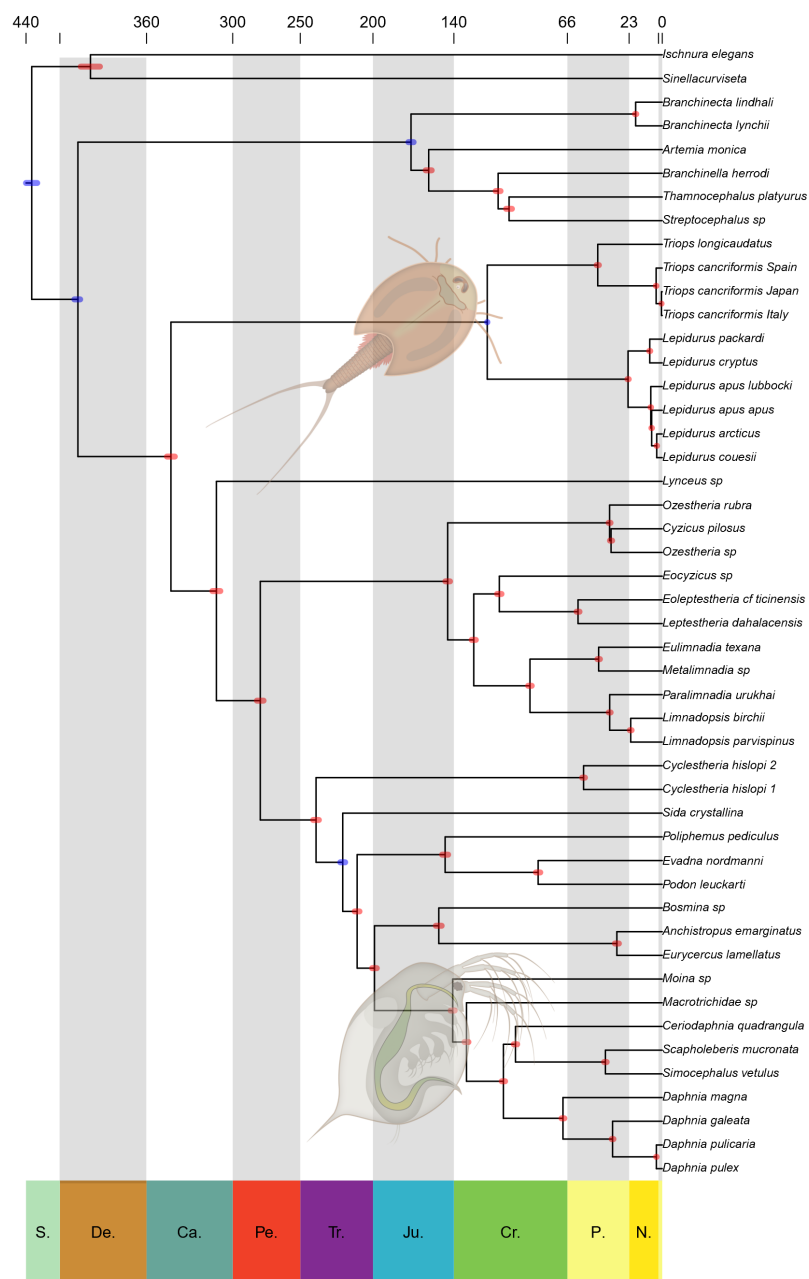


Figure 4: Tree dated with MCMCtree with global (strict) Clock Model: blue bars are the prior calibrations. The two silhouettes represent the most studied groups of branchiopods, on top Notostraca and at the bottom Cladocera.

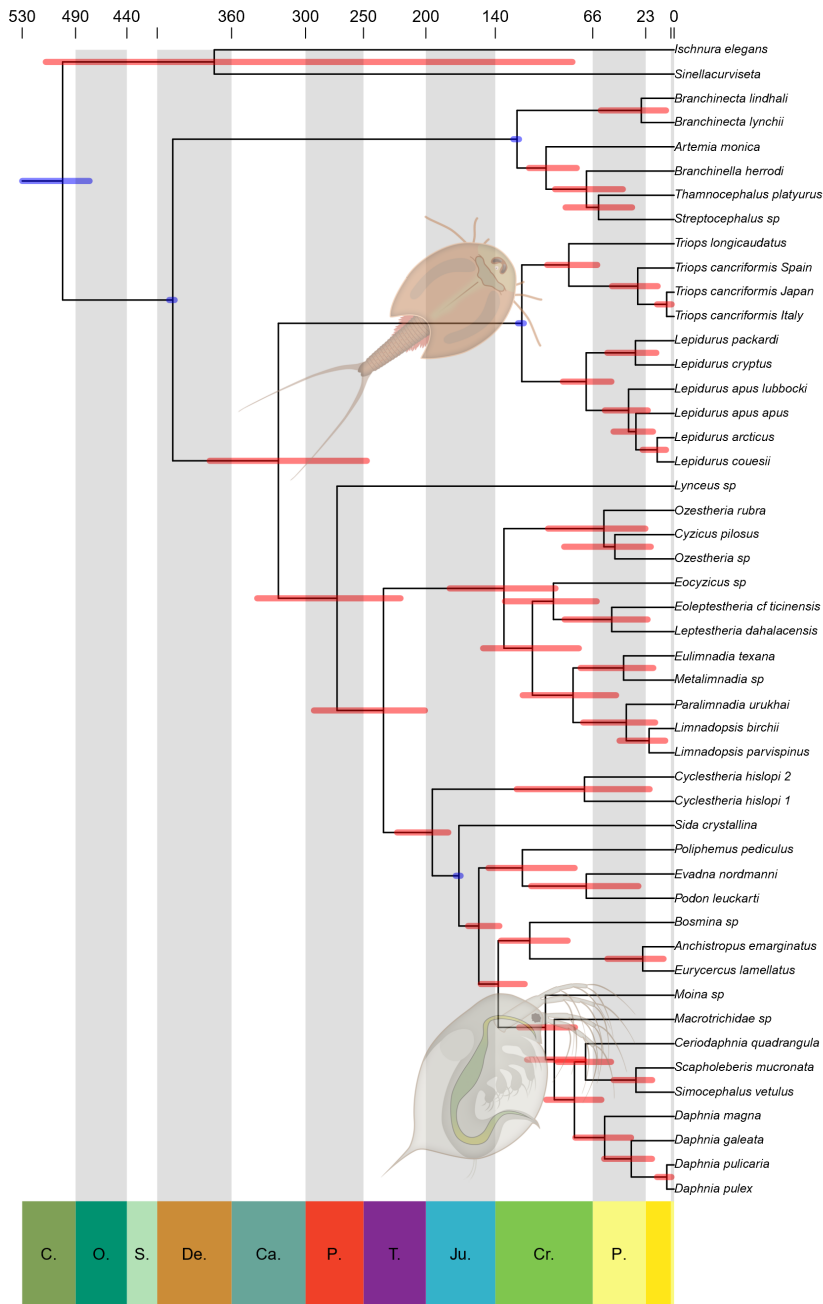


Figure 5: Tree dated with MCMCtree with ILN Clock Model: blue bars are the prior calibrations. The two silhouettes represent the most studied groups of branchiopods, on top Notostraca and at the bottom Cladocera.



Figure 6: Comparison of the dating of the major clades of Branchiopoda with 4 different methods (i.e., lsd2 and MCMCtree with GBM, strict, and ILN clock models) with confidence intervals.

0.2 Fatto dopo la laurea

0.2.1 Jackknife fossili

Jackknife dei fossili con i 186 geeni BUSCO single copy e clock model 2, ovvero l'independent rates.

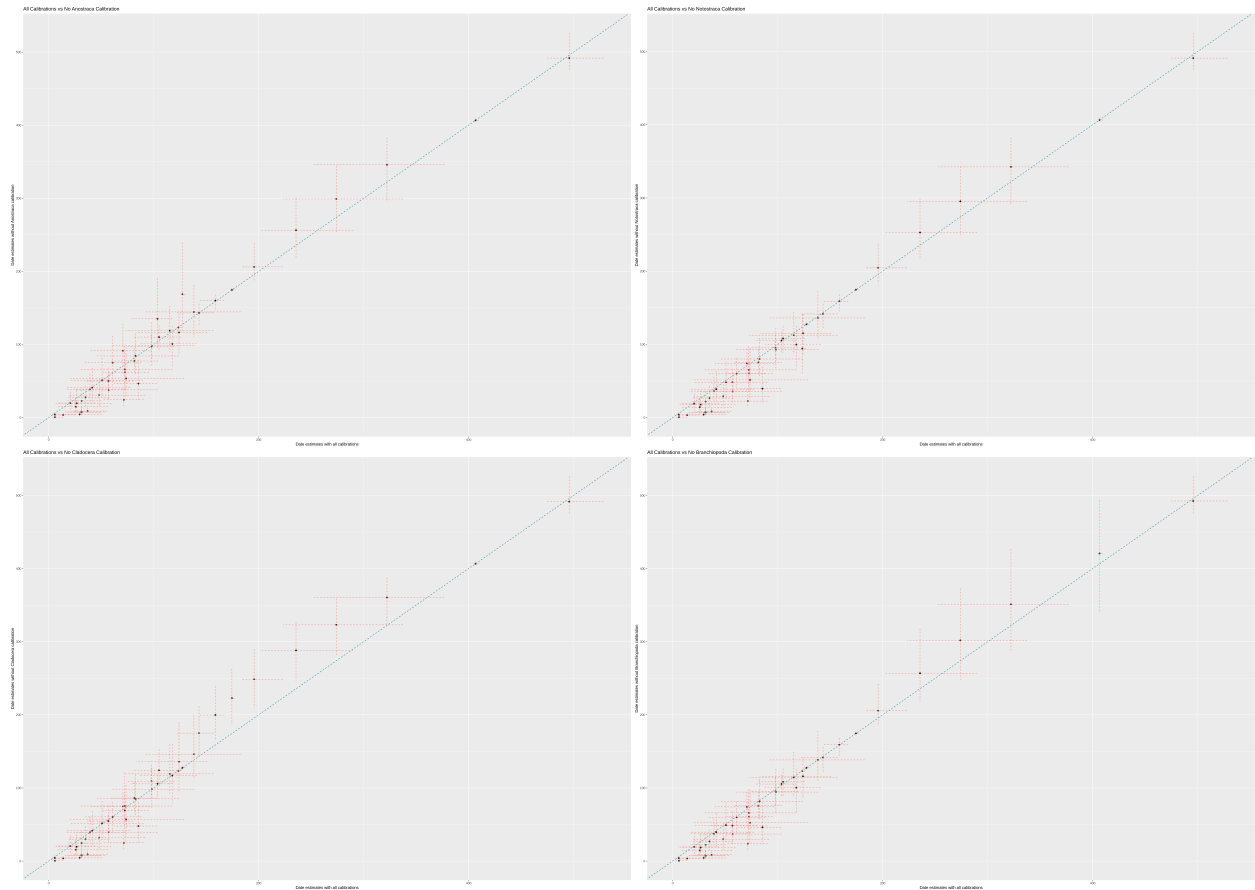


Figure 7: Dating of all nodes removing each time one node

0.2.2 gCF bassi