

佐賀県野生いのしし陽性事例 3 例目までの全ゲノム解析結果（系統樹）

89 例目農場（佐賀県：R5. 8. 31）

野生イノシシ（佐賀県：R6. 5. 30～6. 6）

88 例目農場（佐賀県：R5. 8. 30）

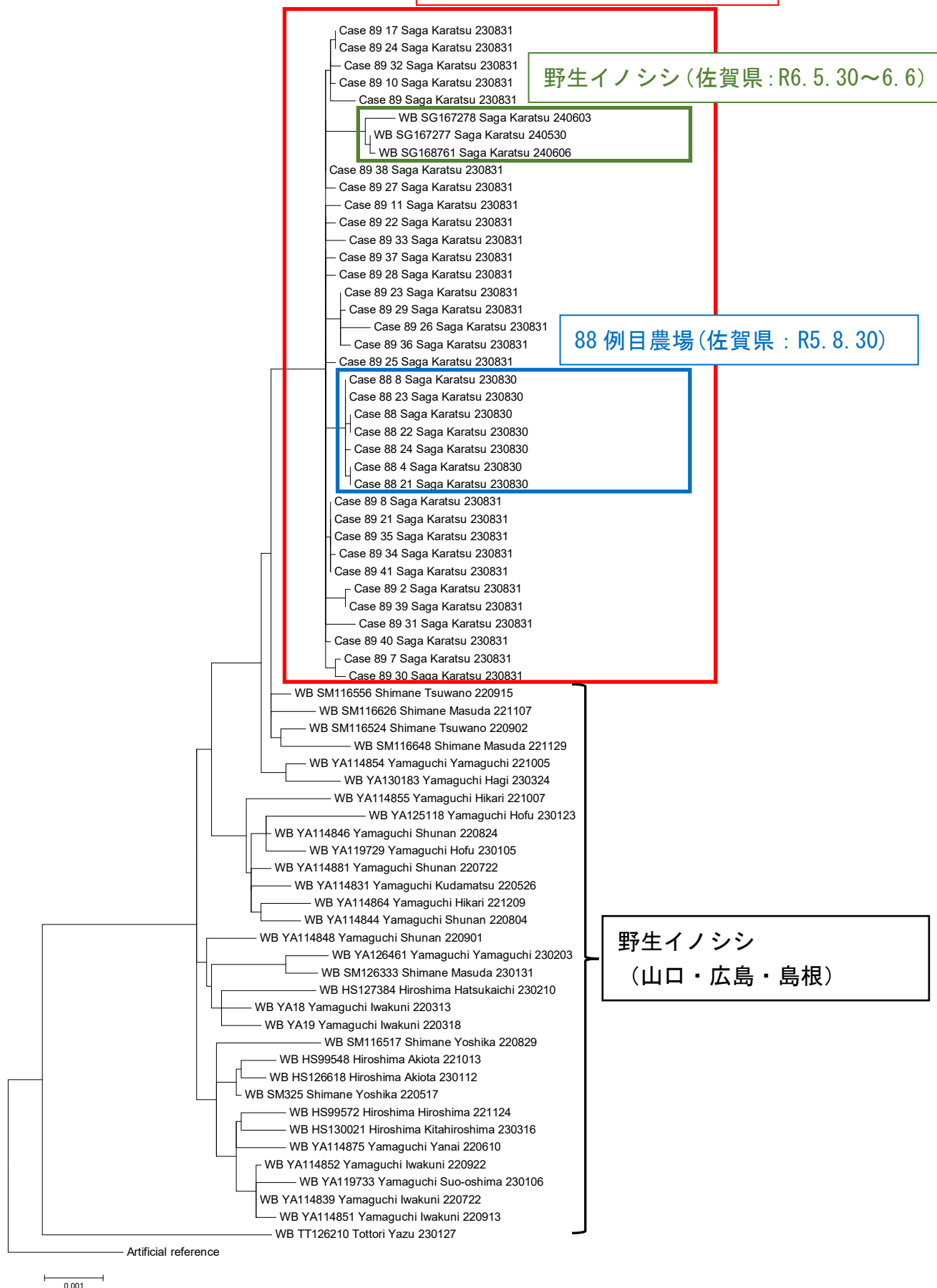
野生イノシシ
（山口・広島・島根）

Figure. Molecular Phylogenetic analysis by Maximum Likelihood method

The evolutionary history was inferred by using the Maximum Likelihood method based on the General Time Reversible model [1]. The tree with the highest log likelihood (-20703.1748) is shown. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 71 nucleotide sequences. All positions containing gaps and missing data were eliminated. There were a total of 11826 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 [2].

1. Nei M. and Kumar S. (2000). Molecular Evolution and Phylogenetics. Oxford University Press, New York.
2. Kumar S., Stecher G., and Tamura K. (2015). MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Molecular Biology and Evolution (submitted).

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