Abstract

Tooth agenesis is one of the most common congenital abnormalities

The Phenotype

Tooth agenesis is a common congenital abnormality in humans, and human dentition is a complex process that requires many biochemical interactions between tissue components. The condition is seen to affect between 3% and 10% of the U.S. Population, with more appearances in women than men (Cleveland Clinic, 2022). Congenital conditions mean that one is born with the specific trait. Tooth agenesis is the medical term for missing teeth. It affects both primary teeth (often referred to as baby teeth) and permanent teeth (also known as adult teeth). Tooth agenesis most often affects permanent teeth. Since all baby teeth develop by the age of three, dentists should note where the absence is located. Usually, all permanent teeth are present between ages of 12-14 and dentists should be aware of inappropriate tooth development (NORD, 2019). Dental agenesis is found in individuals who lack certain teeth because they do not develop. Tooth agenesis is problematic in overall oral health because it makes the physical deformation of food, or chewing, harder. In extreme cases, speaking can also become more difficult with many teeth absent, as well as cause jaw deformation and inadequate bone growth (Cleveland Clinic, 2022). Treatments for these conditions can require dentures, dental implants, orthodontic care (such as braces), or dental bridges. The reason why I am interested in this

for each forward-reverse primer. PCR products can be purifed by 2% gel electrophoresis and Nucleo-Spin Extract Kits (Liu et al., 2022). Once the strands of the PCR products are sequenced, they can be analyzed with a DNA sequencer and compared to specifc entries on official websites such as NCBI or OMIM.org. Restriction-enzyme analysis is also necessary, using the forward and reverse primers for the 5' terminal amplicon of exon 2 (Liu et al., 2022). This will help with amplifying the region of the mutation. Once the fragment is amplifed, the products, which are digestion products, can be run through a 2% gel electrophoresis. Sequencing of the gene reveals information on the specifc nucleotide transition location of the afected individuals. In other words, the information which will be obtained is how the form of tooth agenesis is genetically inherited, as well as how the specifc location of the mutation relates to the phenotype of the patient. The mutation can be identifed as a missense, frameshift, or silent mutation based on o ĀMop oq