

Abstract

Ball pythons (*Python regius*) have become increasingly popular within the exotic pet trade, driving breeders to employ selective breeding to meet the growing demand. By combining distinct mutants, known as morphs, breeders generate unique phenotypic variation to maximize the animals' economic value. Among the highly prized variations is the "Monsoon" morph, a recessive mutation characterized by a distinct, shattered side pattern and thin dorsal striping. To breed for this trait, small-scale breeders frequently rely on time-consuming, cost-intensive backcrossing with heterozygous individuals. While polymerase chain reaction (PCR)-based genetic testing services can expedite the selection of heterozygotes, such services are currently unavailable in Indonesia. Therefore, this study aims to design specific primer pairs to amplify candidate genes underlying the Monsoon mutation as a preliminary step toward developing PCR-based genetic testing for ball python morphs in Indonesia. A literature review was conducted to identify candidate genes associated with the Monsoon trait, followed by primer design and verification via *in silico* PCR simulation. Four candidate genes identified are *PMEL*, *MLANA*, *EDN3*, and *SOX10*. A total of 24 primer pairs were designed to amplify the four candidate genes. All designed primers demonstrated robust *in silico* amplification of the target exons, with predicted product sizes remaining consistent across multiple simulation software tools. These findings provide a foundational framework for establishing accessible ball python genetic testing services in Indonesia and contribute valuable data to study color formation in reptiles.

Keywords: *Ball python, morph, Monsoon, genetic testing, in silico primer design*