Artificial Transcription Factorsfor Genomic Studies and Industrial Applications

LEE Horim, JANG Young-Soon, KIM Jin-Soo and PARK Kyung-Soon*

ToolGen, Inc. Daeduk Biocommunity 461-6, Junmin-Dong, Yusung-Gu, Daejon, Korea ZIP 305-390.

We have developed a method that uses libraries of zinc finger-containing, artificial transcription factors to induce phenotypic variations in yeast and cells. The modular structure and diverse DNA-binding specificities of zinc finger domains make them ideal building blocks for artificial transcription factors. By linking multiple zinc finger domains together, we constructed more than 10⁵ zinc finger proteins with diverse DNA-binding specificities and fused each of them to either a transcriptional activation or repression domain. The resulting transcriptional regulatory proteins were expressed individually in cells, and the transformed cells were screened for drug resistance, thermotolerance, osmotolerance, and growth inhibition. Novel gene associated with drug resistance was identified by microarray analysis of mutant phenotype. Our results show that artificial transcription factors are powerful tools for functional genomics and phenotypic engineering.