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Science news

Zincing towards genome engineering

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'Zinc finger proteins' (ZFPs) have long been hailed as excellent candidates for site-specific genome engineering because of their ability to target DNA. A team from the Indian Institute of Technology Delhi has now designed a novel online database of natural and engineered ZFPs¹ that can be used by genome engineers to modify DNA sequences — a boon for gene therapy.

ZFPs are important since the knowledge of their target DNA-binding sequences is crucial for the development of chimeric proteins leading to site-specific gene correction. Custom-designed zinc finger nucleases (ZFNs) are fast becoming powerful tools in gene targeting which entails replacing a gene within a genome by another sequence. ZFN-mediated gene targeting provides molecular biologists with the ability to modify plant and mammalian genomes at a specific site.

The team led by Durai Sundar had earlier developed a method to rapidly select and improve the DNA sequence specificity of the 'three-finger' ZFPs. They designed a novel computational approach for re-programming ZFPs towards predetermined DNA-binding specificities².

The work led to the development of the **database** called ZifBASE, an extensive collection of natural and engineered ZFP. The database has been highly accessed since it was made public in 2009.

"Zinc finger technology has enormous applications in health waiting to be explored. The impact will be big", says Dorai Sundar.

Sundar's work enables rapid design of the desired ZFPs needed for targeting and modifying a specific locus within any genome. "It is critical to identify all possible ZF motif designs to enable rapid assembly of ZFPs. This will reduce the experimental time and speed up custom development of designs," he says.

Sundar and his team tried to find if it was possible to custom-design ZFPs that could identify DNA regions which specifically recognized each of the 64 possible DNA triplets. Development of a 'zinc-genetic code' would be a key step towards the construction of artificial DNA binding proteins that recognize a target sequence within a genome.

The team made a breakthrough earlier in zinc finger technology by developing a unique bacterial one-hybrid single-reporter system³. This led to greater understanding of DNA-ZFP interactions and development of novel computational approaches for re-programming ZFPs towards customized DNA-binding specificities.

The work on ZFPs have varied applications. As of now, having found the anti-cancer mechanism of withaferin-A obtained from *Withania somnifera*, Sundar's lab is working towards increasing the levels of a prospective herbal drug using the technology.



Durai Sundar.

References

1. Molparia, B. *et al.* ZiF-Predict: a web tool for predicting DNA-binding specificity in C2H2 zinc finger proteins. *Genomics Proteomics Bioinformatics*. 8, 122-126 (2010)
2. Jayakanthan, M. *et al.* ZifBASE: a database of zinc finger proteins and associated resources. *BMC Genomics*. 10, 421 (2009)
3. Durai, S. *et al.* A bacterial one-hybrid selection system for interrogating zinc finger-DNA interactions. *Comb. Chem. High T. Scr.* 9, 301-311 (2006)

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