

Towards a pan-genome atlas of transcription factor DNA-binding specificity in *Ciona intestinalis*

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要旨：

Gene Regulatory Networks (GRNs) consist in the direct links between the *cis*-regulatory sequences driving the expression of transcription factor genes and the transcription factors (TFs) that bind to and regulate them. GRNs play a crucial role in development and evolution. *Ciona intestinalis* is emerging as a powerful model to decipher GRNs, owing to powerful functional genomics, detailed atlases of gene expression, and a reasonably small repertoire of around 500 TFs. In most cases, however, the DNA-binding specificity of individual TFs is unknown. To overcome this limitation, we have initiated a project aiming at the expression in *E. coli* of milligram amounts of soluble recombinant DNA-Binding domains (DNA-BD) followed by the *in vitro* characterization their DNA binding specificity by SELEX (Systematic Evolution of Ligands by EXponential enrichment). After extensive and multiple optimizations of expression parameters in *E. coli*, a consensus production and purification protocol was established and used to express a first set of 460 DNA-BD TF at a rate of 48 proteins/week. Over 280 of these proteins were expressed in soluble form and could be purified in milligram amount. The *in vitro* characterization of their DNA specificity by automated and high throughput (HTP) SELEX in 96-well format is underway and preliminary results suggest that we successfully established the HTP SELEX pipeline.

ホヤという動物を使って，何百種類もの転写調節因子（配列特異的にDNAに結合して遺伝子の転写調節をするタンパク質）の結合DNA配列を片っ端から決定しようという試みを紹介していただきます。

要旨は英語ですが，講演は日本語です。みんなの先輩です。気軽にいろいろ質問



しましょう。

学部・学年などに関わらず興味のある方は是非お越しく下さい。 お問い合わせは藤原（tatataa@kochi-u.ac.jp）まで。