Systems Biology Research Symposium
Oral Presentation Session

Grand Ballroom
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7:00-8:30pm

Dissecting Hierarchical Regulatory Network of Estrogen-Dependent Breast Cancer through an Integrative Genomic Analysis

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A global level profiling of *in vivo* protein-DNA interactions using ChIP-based technologies has evolved rapidly in recent years, the emerging technology ChIP-seq has shown many advantages in terms of resolutions, accuracy, and cost. In this study, we have combined ChIP-seq and computational approaches to dissect regulatory networks for estrogen-dependent breast cancer. Although many studies including ours have genome-widely identified thousands of ERα binding sites and revealed a few transcription factor (TF) partners with ERα, such as AP1, FOXA1, MYC, SP1, little has been explored about complex regulatory networks. Our integrated genomic analysis reveals hierarchical regulatory networks existing for MCF7 and tamoxifen-resistant MCF7 (MCF7-T) cells. The fact that only 20 common genes showing differential expression after E2-induced and few common TF partners between MCF7 and MCF7-T strongly suggests they underlie completely different estrogen-mediated mechanisms. Our results not only confirmed estrogen-mediated gene repression path requiring ERα binding sites concluded from other studies, but also revealed a new estrogen-mediated up-regulated path requiring XBP1. Our data provide additional resources of ERα binding sites and regulated genes, thus may guide further study for underlying mechanisms in breast cancer.