Henrik Devitt Moller et al., Biol syst Open Access 2016, 5:2 (Suppl)
http://dx.doi.org/10.4172/2329-6577.C1.005

Extrachromosomal circular DNA: A key player in creation of copy number variation

Henrik Devitt Moller[1], **Camilla Eggert Larsen**[1], **Lance Parsons**[2], **David Botstein**[3] and **Birgitte Regenberg**[1]
[1]University of Copenhagen, Denmark
[2]Princeton University, USA
[3]Calico Life Sciences LLC, USA

Numerous human cancers are caused by copy-number variations (CNVs) of proto-oncogenes. Yet, detecting chromosomal CNVs before they reach establishment in large cell populations is a major challenge. By screening for a potential deletion-byproduct of CNVs, the so-called extrachromosomal circular DNA (eccDNA), we reasoned that we might elucidate some of the early ongoing processes in genomic rearrangements. We developed a highly sensitive eccDNA purification method, Circle-Seq that relies on removal of all linear DNA and next-generation sequencing of circular DNA. More than a thousand eccDNAs larger than 1 kb were recorded in the eukaryotic model *Saccharomyces cerevisiae* (yeast) increasing the number of known eccDNAs in eukaryotes more than a hundred fold. Now we present hundreds of eccDNA profiles from a distant related yeast subspecies. A number of eccDNAs are found to be identical between the two yeast strains, advocating for conserved hotspots for DNA circularization and potential genomic reintegration. We reveal that CNVs in the form of eccDNAs are common in *S. cerevisiae* and we hypothesize that eccDNAs could be important players in genetic variation and evolution of eukaryotic genomes.

Biography

Henrik Devitt Moller has completed his PhD at the University of Copenhagen, Denmark in 2015 and continued his work on extrachromosomal circular DNA as Post doctorate in the Regenberg Laboratory. He has published 8 papers in peer-reviewed journals.

hdmoller@bio.ku.dk

Notes: