tbg translational biodiversity genomics

LOEWE Exzellente Forschung für Hessens Zukunft

Comparative genomics of ‘solar-powered’ sea slugs

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Pictures of sea slugs: Gregor Christa, Patrick Krug, Elise Laetz, Victoria Moris, Heike Wägele

Introduction:

‘Solar-powered’ sea slugs. Fiction or reality? *Plakobranchus ocellatus* (van Hasselt 1824) belongs to a small group of marine, heterobranch slugs, called Sacoglossa, of which certain species have the ability to incorporate and maintain the chloroplasts of its food algae (e.g., Hirose 2005, Christa et al. 2013). These ‘stolen’ plastids (kleptoplasts) are then stored in a functional state in the digestive gland cells of the slugs and presumably allow them to endure weeks (short-term retention (StR)) or months (long-term retention (LtR)) of starvation (e.g., Wägele & Martin 2013, Christa et al. 2014, de Vries et al. 2015). How do they keep the chloroplasts active which continuously produce starch? No one knows! But up to now, this spectacular phenomenon termed ‘functional kleptoplasty’ is unique among animals.

Materials & Methods:

Genomic DNA of *P. ocellatus* was extracted exclusively from brain tissue of approximately 50 adult individuals to avoid contamination with ingested food algae and bacterial contamination from digestive lumen or epidermis. Paired-end sequencing of Illumina short-insert-size libraries and synthetic long reads was performed on an Illumina HiSeq 2500 platform. For PacBio SMRT Sequencing we prepared >30 kb libraries using the SMRTbell® Express Template Preparation Kit.

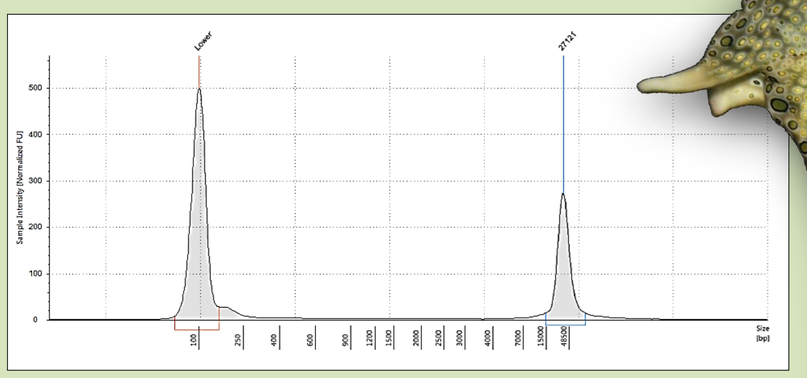
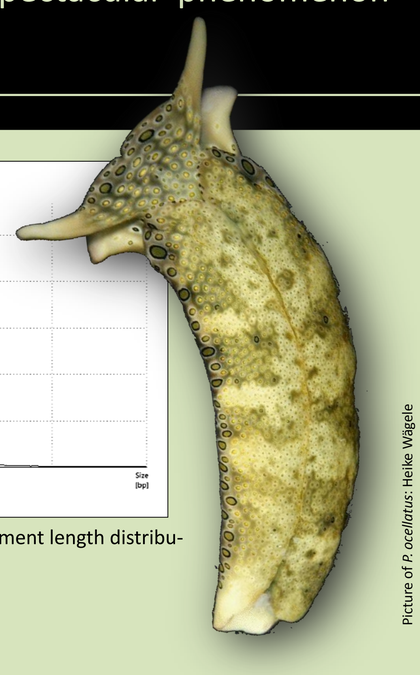


Fig. 1: Tapestation electropherogram (Agilent 2200) showing the fragment length distribution of the SMRTbell® Express library preparation.



Picture of *P. ocellatus*: Heike Wägele

Comparative statistics of DNA reads:

Elysia chlorotica - Genome size 575 Mb estimated by k-mer approach (Data and picture taken from Cai et al. 2019):

Platform	Insert size (bp)	Read length (bp)	Raw data	
			Total bases (Gb)	Sequencing coverage (X)
Illumina short reads	170; 500; 800	100	102.5	178.27
Illumina mate pairs	2,500; 5,000; 10,000	49; 90	194.24	337.81
PacBio RS platform	**6,000**	**~ 1,700 (N50)**	**9.45**	**16.43**

Plakobranchus ocellatus - Genome size 1.3 Gb estimated by flow cytometry (own data):

Platform	Insert size (bp)	Read length (bp)	Raw data	
			Total bases (Gb)	Sequencing coverage (X)
Illumina short reads	350; 550	125	76.9	59
Illumina TSLR	-	150	0.7	0.5
PacBio Sequel	-	**~ 9,000 (N50)**	**3.1**	**2.4**

Comparative assembly statistics:

Elysia chlorotica based on Illumina & PacBio data:

Assembly statistics		BUSCO assessment		
Assembly size (Mb)	Contig N50 (kb)	Complete BUSCOs (%)	Fragmented BUSCOs (%)	Missing BUSCOs (%)
557	28.5	93.3	1.4	5.3

Plakobranchus ocellatus only based on Illumina data:

Assembly statistics		BUSCO assessment		
Assembly size (Mb)	Contig N50 (kb)	Complete BUSCOs (%)	Fragmented BUSCOs (%)	Missing BUSCOs (%)
1,479	4.9	92.6	21.8	13.1

Photograph of *E. chlorotica* (image courtesy of Patrick Krug)

Problems:

- High molecular weight (HMW) DNA extractions from snails & slugs
- N50 subread length of 9 kb is much lower than expected from the prepared 30 kb SMRTbell library (**Fig. 1**)

Aims:

Comparative genomics between *E. chlorotica* and *P. ocellatus* will give us the unique chance to gain new insights into underlying genomic mechanisms related to kleptoplasty. It will further provide a valuable genomic resource for future genome-wide comparative analyses to organisms with similar life styles, i.e. those stealing useful parts out of their prey and incorporating, instead of digesting them.

References:

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