

INNOVATIVE GENOMIC LIBRARY PREPARATION METHODS FOR PLANT GENOTYPING OF LARGE POPULATIONS

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The great advancement of sequencing technologies over the last 20 years now enables the analysis of a genome at just few hundred euros. However, the cost of genomic library preparation can easily exceed the cost of sequencing in the case of small genomes and/or low coverage whole genome sequencing (lcWGS). This becomes a problem if hundred or thousand individuals must be sequenced, as occurs in plant population studies. New low-cost library prep kits have recently been released to overcome this limitation but the performance of these approaches for genotyping analysis have not been investigated yet. We tested and optimized the production of genomic libraries using two approaches, the Twist 96-Plex Library Prep Kit (formerly iGenomX Riptide Kit) and plexWell LP384 Library Preparation Kit (SeqWell), based on distinct approaches, namely random priming and tagmentation respectively, both associated with a genome complexity reduction step. The two different kits were evaluated on their capability to circumvent time/reagent-consuming steps and to process simultaneously large set of samples. Technical parameters, i.e. library size and type of random primers were tuned in order to optimize the library production from common bean (*P. vulgaris*) samples. Libraries generated with the two approaches were sequenced and results were evaluated starting from different amount of data in terms of genotyping efficiency, namely the number of genotypable bases and variants identified. Results were compared with those of traditional approaches, commonly utilized for population genotyping: double digest restriction-site associated DNA (ddRAD) and lc-WGS. The new library prep methods demonstrated to be cost- and time-

effective, but the number and density of genotyped markers achievable with each approach is different, so this must be considered in relation to the study objective and analysis setup. The new approaches investigated can represent important tools for extending plant genotyping and genome-wide association studies, that combine genotypic and phenotypic characterization of large accession collections.