Draft template for Applications in Plant Sciences - Review Article
Short Title for Running Head: Surname of the first author, followed, as appropriate, with the surname of a sole co-author, or et al. (if there are three or more authors) - 2 or 3 descriptive words

Next-generation sequencing techniques for evolutionary studies in the plant sciences[1]

[no more than 125 characters; after a species name, include family name in parentheses]

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Number of words: YYYY *[6500 or fewer, covering Introduction to Discussion sections].*

ABSTRACT

The abstract should capture the interest of the general plant sciences community as well as be informative to specialists in the immediate field. The abstract is 200 words or less, written in an unstructured format. The abstract must contain the premise of the review (why it is important) as well as the overall conclusions, including implications for future investigators.

Avoid references; if essential, cite parenthetically with journal name, volume number, pages, and year.

Key words: bioinformatics; Illumina; next-generation sequencing; RNA-seq

[List 3 to 6 key words here in alphabetical order, separated by semicolons.]

INTRODUCTION

This section should outline why the review is necessary and timely, as well as its overall importance so that readers in all areas of the plant sciences can understand the context in which it was conducted. Enough background information should be given, either in text or supplemented as figures or tables, so readers are equipped to understand and appreciate any new insights detailed later in the article. Authors must also provide details as to how the review was conducted, including any information necessary for readers to readily access the protocols or applications being analyzed; this information can be placed within the text or in a table. If appropriate, definitions of important terms can be provided in a separate box ancillary to the main text.

[The Introduction is then followed by one or more sections with customized headings that are appropriate for the topic of review. See the Instructions for Authors for heading formats.]

CUSTOM HEADING

Beginning with this section and continuing on to subsequent sections, authors should organize their review, as appropriate for the material or question at hand.

DISCUSSION

In this final section, the author(s) should clearly state the main conclusions that have been reached as a result of the review, including any conceptual or empirical advances that propel forward our current understanding. This section should also include a concise description of future research needs for other investigators.

LITERATURE CITED *[no more than 85]*

GOUDET, J. 1995. FSTAT: A computer program to calculate *F* statistics, version 1.2. *Journal of Heredity* 86: 485–486.

STEBBINS, G. L. 1974. Flowering plants: Evolution above the species level. Belknap Press, Cambridge, Massachusetts, USA.

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TURNER, B. L., AND R. M. KING. 1977. Chromosome numbers in the Compositae. VIII. Mexican and Central American species. *Southwestern Naturalist* 9: 27–39.

WHITE, T. J., T. D. BRUNS, S. B. LEE, AND J. W. TAYLOR. 1990. Amplification and direct sequencing

of fungal ribosomal RNA genes for phylogenetics. *In* M. A. Innis, D. H. Gelfand, J. J.

Sninsky, and T. J. White [eds.], PCR protocols: A guide to methods and applications, 315–

322. Academic Press, San Diego, California, USA.

Tables

Tables are recommended as appropriate. For instructions on formatting tables, please see the

Instructions for Authors.

Table 1. Available next-generation sequencing approaches for use in the plant sciences (adapted

from Metzker, 2010).

Approach	Read length (bases)	Gb per run[1]	Run time (days)	Pros	Cons
Illumina	75 or 100	18	4	Most widely used platform	Low multiplexing ability for some samples
454	330	0.45	0.35	Fast run times; longer reads	High error rates and reagent costs
SOLiD 3	50	30	7	Inherent error correction	Long run times

[1] Refers to a fragment run and not a mate-pair run.

Figure and Legend

[Figures should be uploaded as a separate file(s); the legend should be included in the text file.]