

Accepted Manuscript

Next-generation sequencing as a tool for the molecular characterisation and risk assessment of Genetically Modified Plants: added value or not?

Katia Pauwels, Sigrid C.J. De Keersmaecker, Adinda De Schrijver, Patrick du Jardin, Nancy H.C. Roosens, Philippe Herman



PII: S0924-2244(15)00176-4

DOI: [10.1016/j.tifs.2015.07.009](https://doi.org/10.1016/j.tifs.2015.07.009)

Reference: TIFS 1688

To appear in: *Trends in Food Science & Technology*

Received Date: 10 January 2015

Revised Date: 19 June 2015

Accepted Date: 14 July 2015

Please cite this article as: Pauwels, K., De Keersmaecker, S.C.J., De Schrijver, A., du Jardin, P., Roosens, N.H.C., Herman, P., Next-generation sequencing as a tool for the molecular characterisation and risk assessment of Genetically Modified Plants: added value or not?, *Trends in Food Science & Technology* (2015), doi: 10.1016/j.tifs.2015.07.009.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.

1 Next-generation sequencing as a tool for the molecular characterisation and risk 2 assessment of Genetically Modified Plants: added value or not?

3 Katia Pauwels ¹ †*, Sigrid C. J. De Keersmaecker ² †*, Adinda De Schrijver ¹, Patrick du Jardin ³, Nancy H.C.
4 Roosens ²£ and Philippe Herman ¹£

5
6
7 ¹ Scientific Institute of Public Health, Biosafety and Biotechnology Unit, J. Wytsmanstraat 14, B-1050 Brussels,
8 Belgium. E-mail: Adinda.DeSchrijver@wiv-isp.be, Philippe.Herman@wiv-isp.be

9 ² Scientific Institute of Public Health, Platform of Biotechnology and Molecular Biology, J. Wytsmanstraat 14,
10 B-1050 Brussels, Belgium. E-mail: Sigrid.DeKeersmaecker@wiv-isp.be, Nancy.roosens@wiv-isp.be

11 ³ University of Liège, Gembloux Agro-Bio Tech, Unit of Plant Biology, Passage des Déportés, B-5030
12 Gembloux, Belgium. E-mail : Patrick.DuJardin@ulg.ac.be

13
14 † equally shared first author

15 £ equally shared last author

16 * Corresponding authors:

17 Katia Pauwels, Scientific Institute of Public Health, Biosafety and Biotechnology Unit, J. Wytsmanstraat 14, B-
18 1050 Brussels, Belgium, E-mail: Katia.Pauwels@wiv-isp.be, phone : +32 2 642 54 24, fax: +32 2 642 52 92.

19 Sigrid De Keersmaecker, Scientific Institute of Public Health, Platform of Biotechnology and Molecular
20 Biology, J. Wytsmanstraat 14, B-1050 Brussels, Belgium. E-mail: Sigrid.DeKeersmaecker@wiv-isp.be, phone
21 +32 2 642 52 57, fax : +32 2 642 52 92

23 Abstract

24 Background

25 Legislations and international organizations provide a framework to ensure proper risk assessment of
26 **Genetically Modified Organisms** (GMO). With regard to the deliberate release of GMO as food or feed,
27 applications for Genetically Modified Plants (GMP) typically contain data for the molecular characterisation at
28 the nucleic acid level based on Southern blot and polymerase chain reaction analysis in combination with Sanger
29 sequencing. Along with the diverse range of applications of **next-generation sequencing** (NGS) in genomic
30 research, some recent research projects and product developers explored the use of NGS as an alternative tool for
31 meeting the data requirements for the molecular characterisation of GMPs in view of their risk assessment.

32 Scope and Approach

33 By means of a literature survey and information collected through the organisation of an international workshop,
34 we investigated whether NGS can replace and/or complement the currently used techniques for **molecular**
35 **characterisation** of GMP taking into account the possibilities and current bottlenecks of NGS technologies and
36 recent developments in molecular breeding.

37 Key Findings and Conclusions

38 We conclude that although NGS might present clear advantages for product developers, NGS currently does not
39 always offer a significant added value with respect to the **risk assessment** of GMPs. However, the approaches
40 used so far may soon be further challenged by the fast evolution in NGS technologies and also by the recent
41 developments in molecular breeding of plants. We postulate that setting up a common workflow for the
42 generation of relevant and interpretable data by NGS would facilitate a scientifically sound assessment of
43 GMPs.

Download English Version:

<https://daneshyari.com/en/article/10894754>

Download Persian Version:

<https://daneshyari.com/article/10894754>

[Daneshyari.com](https://daneshyari.com)