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Application Note

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| Subject Section  The Genetic Map Comparator: a quick and easy way to visualize your genetic maps  Yan Holtz1, Jacques David1, Vincent Ranwez1\*  1*1Montpellier SupAgro, UMR AGAP, 34060 Montpellier, France*  \*To whom correspondence should be addressed.  Associate Editor: XXXXXXX  Received on XXXXX; revised on XXXXX; accepted on XXXXX  Abstract  **Motivation:** Genomic selection strongly relies on genetic map to accelerate breeding programs. Thanks to high throughput sequencing high density maps are now available for numerous species. Comparing several maps require dedicated tools able to summarize the key characteristics of high density maps and to pinpoint their differences and similarities.  **Results:** We developed GeneMap Comparator a web based application allowing to easily compare different maps by depicting their key statistics and the relative position of their common markers.  **Availability:** The genetic map comparator is available online: <http://www.agap-sunshine.inra.fr/holtz-apps/GenMap-Comparator/>. Source code is freely available on GitHub for non-commercial use only. (<https://github.com/holtzy/GenMap-Comparator>).  **Contact:** ranwez@supagro.fr  **Supplementary information**: Supplementary data are available at *Bioinformatics* online. |

# Introduction

Why comparing genetic maps?

What tools are available yet?

In this study, we investigated the genetic basis of WSSMV resistance in 2 RILs population of durum

Why a new one was needed?

- Permet de comparer des cartes plus denses (NGS). Exemple: map chart deviant illisible avec >100 marqueurs par chromosomes ( avérifier)

- Permet des comparaisons inter-chromosomiques.

- Utilisation sur le WEB -> 0 installation.

- Utilisation des outils de visualisation interactive actuels !

# Technology and installation

R, shiny. Web interface or easy local installation It is a shiny application available online. No installation needed. Works on every device. An example dataset is available.

# Key functionalities

Several sheet: Basic statistics / genetic map comparison with parallele representation / interchromosomal analyses / rough map. It is possible to export figures to pdf or other format with publication quality.

# Case study

In this study, we investigated the genetic basis of WSSMV resistance in 2 RILs population of durum wheat. Two elite cultivars (Silur and Lloyd) were crossed with Dic2, a dicoccum that

Fig. 1: Parallele comparison of 4 genetic maps.

A representation of the third sheet of the application. Each vertical black line illustrates the selected chromosome of the 4 populations, with a point for each marker. Numbers on the left side specifies positions in cM. Names of markers are available on hover. Common markers between 2 adjacent maps are represented by a purple line.

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*Conflict of Interest:* none declared.

References