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transPLANT

Trans-national Infrastructure for Plant Genomic Science

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MS22

Initial analysis of synteny, rearrangement and duplication

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РР	Restricted to other programme participants (including the Commission Services)		
RE	Restricted to a group specified by the consortium (including the Commission Services)		
CO	Confidential, only for members of the consortium (including the Commission Services)		



Contributors

Kai Christian Bader, Dan Bolser, Manuel Spannagl, Hadi Quesneville

Introduction

This milestone is about synteny, duplication and rearrangement data, integrated into the transPLANT portal via GUIs and tabular visualisation interfaces, and into data mining tools.

To analyse syntenic relationships, rearrangements and intragenomic duplications HMGU enhances the CrowsNest tool (http://mips.helmholtz-muenchen.de/plant/crowsNest/index.jsp). CrowsNest is a Comparative Viewer that uses a dynamic graphical interface to visualize and investigate genome-wide synteny between two or more plant genomes. CrowsNest is specifically designed to visualize synteny at macro and micro levels. It allows to intuitively explore rearrangements, inversions, deletions at different resolutions, to transfer knowledge about function and conservation between several plant species and to derive evolutionary information.

Methods

To facilitate direct access to CrowsNest views for searches with single gene identifiers from species included in CrowsNest, the tool functionalities were extended. Search indexes were computed and extracted for all genes in syntenic regions between pairwise species combination within CrowsNest (*e.g.* between genes in barley and Brachypodium).

These index dumps were formatted according to the common format proposed for the integrated transPLANT search engine hosted on transplantdb.eu (EU). From there, searches for a particular gene name will yield relevant results from several transPLANT partners including direct links to corresponding Crownest synteny views through the URL.

Results (if applicable, interactions with other workpackages)

Data from Crownest were provided in tab-delimited format with columns matching the transPLANT integrated search schema (v0.2), developed by the transPLANT search working group (WP6).

Each 'record' in CrowsNest is stored in the transPLANT index twice, once for each sequence feature with an appropriate db_id, name, description, and URL. For completeness and consistency, one 'xref' is added to each entry, linking it to the other entry in the pair (although technically this is not needed).

Here is an explicit example, mapping a pair onto the integrated search schema:

Record 1 entry type = sequence feature database_name = CrowsNest db id = Os03g0297400 to Sb01g038160.1 name = Homology between Os03g0297400 and Sb01g038160.1 in CrowsNest description = Homology between Os03g0297400 (Oryza sativa) and Sb01g038160.1 (Sorghum_bicolor) in CrowsNest url = <u>http://seacow.helmholtz-muenchen.de/cgi-</u> bin/mips cviewer/mips cgmviewer.pl?size=normal&viewer type=pp&viewer level=4&ref genome=Sorghum bicolor&tar genome =Oryza sativa&tar chr nr=3&ref chr nr=1&tar start=10450000&tar end=10460000&ref start=61740000&ref end=61760000&sh ow ruler=1&lock scaling=0&synteny type=homology species = Oryza sativa xref = sequence feature: Sb01g038160.1 to Os03g0297400feature type = homology sequence id = 3start position = 37281407end position = 37283439Record 2 entry type = sequence feature database name = CrowsNest db id = Sb01g038160.1 to Os03g0297400 name = Homology between Sb01g038160.1 and Os03g0297400 in CrowsNest







description = Homology between Sb01g038160.1 (Sorghum bicolor) and Os03g0297400 (Oryza sativa) in CrowsNest url = http://seacow.helmholtz-muenchen.de/cgibin/mips_cviewer/mips_cgmviewer.pl?size=normal&viewer_type=pp&viewer_level=4&ref_genome=Oryza_sativa&tar_genome=So rghum_bicolor&tar_chr_nr=1&ref_chr_nr=3&tar_start=61740000&tar_end=61760000&ref_start=10450000&ref_end=10460000&sh ow_ruler=1&lock_scaling=0&synteny_type=homology species = Sorghum bicolor xref = sequence feature: Os03g0297400 to Sb01g038160.1 feature_type = homology sequence_id = 1 start_position = 61747553 end_position = 61751061

The Figure 1 illustrates the search for the syntenic region between rice and sorgho containing two homologous genes.

CURRENT SEARCH	transPLANT search Resource registry Site search		
Found 2 results	Search		
FILTER BY DATABASE:			
 CrowsNest (2) 	Os03g0297400 to Sb01g038160.1 Search		
FILTER BY DATA TYPE:	Search results		
• sequence feature (2)	Sb01g038160.1 to Os03g0297400		
	Sb01g038160.1 to Os03g0297400 Homology between Sb01g038160.1 and Os03g0297400 in CrowsNest Homology between Sb01g038160.1 (Sorghum bicolor) and Os03g0297400 (Oryza satiya) in CrowsNest		
• Oryza sativa (1)			
 Sorghum bicolor (1) 	Os03g0297400 to Sb01g038160.1		
	Os03g0297400 to Sb01g038160.1 Homology between Os03g0297400 and Sb01g038160.1 in Crows Homology between Os03g0297400 (Oryza sativa) and Sb01g038160.1 (Sorghum_bicolor) in Crows	Nest sNest	
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1. Search example for a synteni	c region containing two homologous genes into the integrated search nortal		

Publications