

## REFERENCES

- Altenhoff, A. M., & Dessimoz, C. (2009). Phylogenetic and functional assessment of orthologs inference projects and methods. *PLoS Computational Biology*, 5(1), e1000262.
- Altschul, S., Gish, W., Miller, W., Myers, E., & Lipman, D. (1990). Basic local alignment search tool. *Journal of Molecular Biology*, 215 (3): 403–410.
- Bennetzen, J. L. (2000). Comparative sequence analysis of plant nuclear genomes: microcolinearity and its many exceptions. *The Plant Cell*, 12(7), 1021-9.
- Berglund, A.-C., Sjölund, E., Ostlund, G., & Sonnhammer, E. L. L. (2008). InParanoid 6: eukaryotic ortholog clusters with inparalogs. *Nucleic Acids Research*, 36(Database issue), D263-6.
- Chen, F., Mackey, A. J., Vermunt, J. K., & Roos, D. S. (2007). Assessing performance of orthology detection strategies applied to eukaryotic genomes. *PLoS One*, 2(4), e383.
- Choi, H.-K., Mun, J.-H., Kim, D.-J., Zhu, H., Baek, J.-M., Mudge, J., Roe, B., et al. (2004). Estimating genome conservation between crop and model legume species. *Proceedings of the National Academy of Sciences of the United States of America*, 101(43), 15289-94.
- Hillier, L. W., Miller, R. D., Baird, S. E., Chinwalla, A., Fulton, L. a, Koboldt, D. C., & Waterston, R. H. (2007). Comparison of *C. elegans* and *C. briggsae* genome sequences reveals extensive conservation of chromosome organization and synteny. *PLoS Biology*, 5(7), e167.
- Hulsen, T., Huynen, M. A., de Vlieg, J., & Groenen, P. M. A. (2006). Benchmarking ortholog identification methods using functional genomics data. *Genome Biology*, 7(4), R31.
- Klein, P. E., Klein, R. R., Vrebalov, J., & Mullet, J. E. (2003). Sequence-based alignment of sorghum chromosome 3 and rice chromosome 1 reveals extensive conservation of gene order and one major chromosomal rearrangement. *The Plant Journal: for cell and molecular biology*, 34(5), 605-21.
- Krzywinski, M., Schein, J., Birol, I., Connors, J., Gascoyne, R., Horsman, D., Jones, S. J., et al. (2009). Circos: an information aesthetic for comparative genomics. *Genome Research*, 19(9), 1639-45.
- Ku, H. M., Liu, J., Doganlar, S., & Tanksley, S. D. (2001). Exploitation of Arabidopsis-tomato synteny to construct a high-resolution map of the ovate-containing region in tomato chromosome 2. *Genome / National Research Council Canada = Génom / Conseil national de recherches Canada*, 44(3), 470-5.
- Kumar, S., Mohan, A., Balyan, H. S., & Gupta, P. K. (2009). Orthology between genomes of Brachypodium, wheat and rice. *BMC Research Notes*, 2, 93.

McClean, P. E., Mamidi, S., McConnell, M., Chikara, S., & Lee, R. (2010). Synteny mapping between common bean and soybean reveals extensive blocks of shared loci. *BMC Genomics*, *11*, 184.

Murat, F., Xu, J.-H., Tannier, E., Abrouk, M., Guilhot, N., Pont, C., Messing, J., et al. (2010). Ancestral grass karyotype reconstruction unravels new mechanisms of genome shuffling as a source of plant evolution. *Genome Research*, *20*(11), 1545-57.

Ng, M.-P., Vergara, I. a, Frech, C., Chen, Q., Zeng, X., Pei, J., & Chen, N. (2009). OrthoClusterDB: an online platform for synteny blocks. *BMC Bioinformatics*, *10*, 192.

O'Brien, K. P., Remm, M., & Sonnhammer, E. L. L. (2005). InParanoid: a comprehensive database of eukaryotic orthologs. *Nucleic Acids Research*, *33*(Database issue), D476-80.

Ostlund, G., Schmitt, T., Forslund, K., Köstler, T., Messina, D. N., Roopra, S., Frings, O., et al. (2010). InParanoid 7: new algorithms and tools for eukaryotic orthology analysis. *Nucleic Acids Research*, *38*(Database issue), D196-203.

Paterson, a H., Bowers, J. E., Burow, M. D., Draye, X., Elsik, C. G., Jiang, C. X., Katsar, C. S., et al. (2000). Comparative genomics of plant chromosomes. *The Plant Cell*, *12*(9), 1523-40.

Remm, M., Storm, C. E., & Sonnhammer, E. L. (2001). Automatic clustering of orthologs and in-paralogs from pairwise species comparisons. *Journal of Molecular Biology*, *314*(5), 1041-52.

R Development Core Team (2008). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0, URL: <http://www.R-project.org>.

Salse, J., Abrouk, M., Bolot, S., Guilhot, N., Courcelle, E., Faraut, T., Waugh, R., et al. (2009). Reconstruction of monocotyledonous proto-chromosomes reveals faster evolution in plants than in animals. *Proceedings of the National Academy of Sciences of the United States of America*, *106*(35), 14908-13.

Salse, J., Abrouk, M., Murat, F., Quraishi, U. M., & Feuillet, C. (2009). Improved criteria and comparative genomics tool provide new insights into grass paleogenomics. *Briefings in Bioinformatics*, *10*(6), 619-30.

Salse, J., Bolot, S., Throude, M., Jouffe, V., Piegu, B., Quraishi, U. M., Calcagno, T., et al. (2008). Identification and characterization of shared duplications between rice and wheat provide new insight into grass genome evolution. *The Plant Cell*, *20*(1), 11-24.

Salse, J., Piegu, B., Cooke, R., & Delseny, M. (2002). Synteny between *Arabidopsis thaliana* and rice at the genome level: a tool to identify conservation in the ongoing rice genome sequencing project. *Nucleic Acids Research*, *30*(11), 2316-2328.

Salse, J., Piégu, B., Cooke, R., & Delseny, M. (2004). New in silico insight into the synteny between rice (*Oryza sativa* L.) and maize (*Zea mays* L.) highlights reshuffling and

identifies new duplications in the rice genome. *The Plant Journal : for cell and molecular biology*, 38(3), 396-409.

Schmidt, R. (2002). Plant genome evolution: lessons from comparative genomics at the DNA level. *Plant Molecular Biology*, 48(1-2), 21-37.

Shultz, J. L., Ray, J. D., & Lightfoot, D. a. (2007). A sequence based synteny map between soybean and *Arabidopsis thaliana*. *BMC Genomics*, 8, 8.

Throude, M., Bolot, S., Bosio, M., Pont, C., Sarda, X., Quraishi, U. M., Bourgis, F., et al. (2009). Structure and expression analysis of rice paleo duplications. *Nucleic Acids Research*, 37(4), 1248-59.

Timms, L., Jimenez, R., Chase, M., Lavelle, D., McHale, L., Kozik, A., Lai, Z., et al. (2006). Analyses of synteny between *Arabidopsis thaliana* and species in the Asteraceae reveal a complex network of small syntenic segments and major chromosomal rearrangements. *Genetics*, 173(4), 2227-35.

Vergara, I. a, & Chen, N. (2010). Large synteny blocks revealed between *Caenorhabditis elegans* and *Caenorhabditis briggsae* genomes using OrthoCluster. *BMC Genomics*, 11, 516.

Vergara, I. A., & Chen, N. (2009). Using OrthoCluster for the detection of synteny blocks among multiple genomes. *Current protocols in bioinformatics*, Chapter 6, Unit 6.10 6.10.10-18.

Wootton, J.C. & Federhen, S. (1993). Statistics of local complexity in amino acid sequences and sequence databases. *Comput. Chem.* 17:149-163.

Zeng, X., Pei, J., Vergara, I. A., Nesbitt, M. J., Wang, K., & Chen, N. (2008). OrthoCluster: a new tool for mining synteny blocks and applications in comparative genomics. *Proceedings of the 11th International Conference on Extending Database Technology (EDBT'08), Nantes, France, March 25-30.*

Zhu, H., Kim, D.-jin, Baek, J.-min, Choi, H.-kyu, Ellis, L. C., Küester, H., McCombie, W. R., et al. (2003). Syntenic relationships between *Medicago truncatula* and *Arabidopsis* reveal extensive divergence of genome organization. *Plant Physiology*, 131(3), 1018-26.