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Sommario/riassunto	<p>Fungi of the order Pucciniales cause rust diseases on many plants including important crops and trees widely used in agriculture, forestry and bioenergy programs; these encompass gymnosperms and angiosperms, monocots and dicots, perennial and annual plant species. These fungi are obligate biotrophs and -except for a few cases- cannot be cultivated outside their hosts in a laboratory. For this reason, standard functional and molecular genetic approaches to study these pathogens are very challenging and the means to study their biology, i. e. how they infect, develop and reproduce on plant hosts, are rather limited, even though they rank among the most devastating pathogens. Among fungal plant pathogens, rust fungi display the most complex lifecycles with up to five different spore forms and for many rust fungi, unrelated alternate hosts on which sexual and clonal reproduction are achieved. The genomics revolution and particularly the application of new generation sequencing technologies have greatly changed the way we now address biological studies and has in particular accelerated and made feasible, molecular studies on non-model species, such as rust fungi. The goal of this research topic is to gather articles that present recent advances in the understanding of rust fungi biology, their complex lifecycles and obligate biotrophic interactions with their hosts, through the means of genomics. This includes genome sequencing and/or resequencing of isolates, RNA-Seq or large-scale transcriptome analyses, genome-scale detailed annotation of gene families, and</p>

comparative analyses among the various rust fungi and, where feasible, with other obligate biotrophs or fungi displaying distinct trophic modes. This Research Topic provides a great opportunity to provide an up-to-date account of rust fungus biology through the lens of genomics, including state-of-the-art technologies developed to achieve this knowledge.

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