Nicomics, a user friendly bioinformatic server for high quality Nicotiana reference genomes

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Nicotiana tabacum and Nicotiana benthamiana are widely used models in plant biology research. However, genomic studies of these species have lagged. Recently, we report the chromosome-level reference genome assemblies for N. benthamiana and N. tabacum with an estimated 99.5% and 99.8% completeness, respectively [1]. Sensitive transcription start and termination site sequencing methods were developed and used for accurate gene annotation in N. tabacum. Comparative analyses revealed evidence for the parental origins and chromosome structural changes, leading to hybrid genome formation of each species. Interestingly, the antiviral silencing genes RDR1, RDR6, DCL2, DCL3, and AGO2 were lost from one or both subgenomes in N. benthamiana, while both homeologs were kept in N. tabacum. Furthermore, the N. benthamiana genome encodes fewer immune receptors and signaling components than that of N. tabacum. These findings uncover possible reasons underlying the hypersusceptible nature of N. benthamiana. We developed the user-friendly Nicomics web server (http://lifenglab.hzau.edu.cn/Nicomics/) to facilitate better use of Nicotiana genomic resources as well as gene structure and expression analyses. Updates on the Nicomics server will be discussed to accommodate other recently published high quality nicotiana genomes [2-7].

References

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