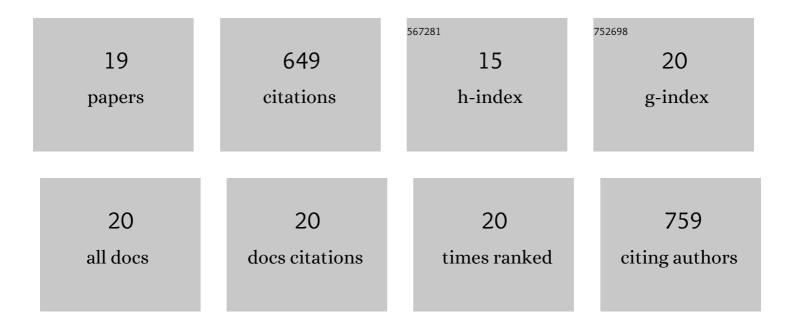
## Jian Huang

List of Publications by Year in descending order

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| #  | Article  | IF  | CITATIONS |
|----|--|-----|-----------|
| 1  | Genome-Wide Identification of WRKY Transcription Factors in Chinese jujube (Ziziphus jujuba Mill.)<br>and Their Involvement in Fruit Developing, Ripening, and Abiotic Stress. Genes, 2019, 10, 360.             | 2.4 | 26        |
| 2  | Genetic diversity of Ziziphus mauritiana germplasm based on SSR markers and ploidy level estimation.<br>Planta, 2019, 249, 1875-1887.  | 3.2 | 16        |
| 3  | Transcript analyses of ethylene pathway genes during ripening of Chinese jujube fruit. Journal of<br>Plant Physiology, 2018, 224-225, 1-10.  | 3.5 | 26        |
| 4  | Soil propagule bank of ectomycorrhizal fungi associated with Masson pine (Pinus massoniana) grown<br>in a manganese mine wasteland. PLoS ONE, 2018, 13, e0198628.  | 2.5 | 7         |
| 5  | The ectomycorrhizal fungal communities associated with Quercus liaotungensis in different habitats across northern China. Mycorrhiza, 2017, 27, 441-449.   | 2.8 | 16        |
| 6  | Diversity and community structure of ectomycorrhizal fungi associated with Larix chinensis across the alpine treeline ecotone of Taibai Mountain. Mycorrhiza, 2017, 27, 487-497.                                 | 2.8 | 22        |
| 7  | Comparative Analysis of the Complete Chloroplast Genome of Four Known Ziziphus Species. Genes, 2017, 8, 340.   | 2.4 | 35        |
| 8  | The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. PLoS Genetics, 2016, 12, e1006433.  | 3.5 | 136       |
| 9  | Transcriptomic Analysis Reveals the Metabolic Mechanism of L-Ascorbic Acid in Ziziphus jujuba Mill<br>Frontiers in Plant Science, 2016, 7, 122.  | 3.6 | 19        |
| 10 | Biochemical Responses of Ten Ectomycorrhizal Fungal Isolates to Manganese. Water, Air, and Soil<br>Pollution, 2016, 227, 1.  | 2.4 | 8         |
| 11 | Construction of a high-density genetic map of Ziziphus jujuba Mill. using genotyping by sequencing technology. Tree Genetics and Genomes, 2016, 12, 1.   | 1.6 | 42        |
| 12 | Ectomycorrhizal fungal communities associated with Populus simonii and Pinus tabuliformis in the hilly-gully region of the Loess Plateau, China. Scientific Reports, 2016, 6, 24336.                             | 3.3 | 33        |
| 13 | Soil Propagule Banks of Ectomycorrhizal Fungi Along Forest Development Stages After Mining.<br>Microbial Ecology, 2015, 69, 768-777.   | 2.8 | 21        |
| 14 | Genetic diversity and population structure of sour jujube, Ziziphus acidojujuba. Tree Genetics and<br>Genomes, 2015, 11, 1.  | 1.6 | 24        |
| 15 | Inoculation of ectomycorrhizal fungi contributes to the survival of tree seedlings in a copper mine tailing. Journal of Forest Research, 2015, 20, 493-500.  | 1.4 | 35        |
| 16 | Identification of appropriate reference genes for RT-qPCR analysis in Ziziphus jujuba Mill Scientia<br>Horticulturae, 2015, 197, 166-169.  | 3.6 | 29        |
| 17 | Development of Chloroplast Microsatellite Markers and Analysis of Chloroplast Diversity in Chinese<br>Jujube (Ziziphus jujuba Mill.) and Wild Jujube (Ziziphus acidojujuba Mill.). PLoS ONE, 2015, 10, e0134519. | 2.5 | 57        |
| 18 | Ectomycorrhizal fungal communities associated with Masson pine (Pinus massoniana) and white oak<br>(Quercus fabri) in a manganese mining region in Hunan Province, China. Fungal Ecology, 2014, 9, 1-10.         | 1.6 | 48        |

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|----|---|-----|-----------|
| 19 | Ectomycorrhizal fungal communities associated with Masson pine (Pinus massoniana Lamb.) in Pb–Zn<br>mine sites of central south China. Mycorrhiza, 2012, 22, 589-602. | 2.8 | 48        |