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Transcriptomic signature of Fusarium toxin in chickpea unveiling wilt pathogenicity pathways and marker discovery

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14 **1. Introduction**

Chickpea is the second most important food legume in terms of gross production and acreage 15 and is grown in over fifty countries of the world representing all the continents [1]. It is a self-16 17 pollinated, diploid (2n=2x=16), cool season pulse crop with a moderate genome size of 740 Mb. It is not only an excellent source of nutritive dietary protein for mass of undernourished people 18 throughout the developing world, but also plays an important role in improving soil health, 19 fertility and sustainability of agro-ecosystems [2]. The global chickpea production is about 13.1 20 Mt from an area of 13.54 Mha with India being the largest producer contributing about 67.3% of 21 the total world production (FAOSTAT 2013) [3]. Chickpea yield is severely curtailed by several 22 abiotic (drought, heat, cold and salinity) and biotic (Ascochyta blight, fusarium wilt, dry root rot 23

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