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CORRECTION

Correction to: Survey of root knot nematodes and RMi resistance to Meloidogyne incognita in soybean from Khyber Pakhtunkhwa, Pakistan

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- We acknowledge that in the published work (1), Table 5 and Fig. 2 and the entire text of their captions came from the published previous manuscript (2) and were used without citation of the previous manuscript (2). Along with that the following text, with and without rephrasing, also taken from the published previous manuscript (2) without citation;

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Results in manuscript (1): In the current study, 200 bp band was amplified in Mi resistant homozygous genotype, 200 and/or 192 bp bands in hybrid Mi resistant genotypes and 192 bp band in Mi susceptible genotypes except NARC-1 (did not show amplification) with Satt _358 markers. In case of susceptible cultivars Satt_132 can amplify 236 bp, 246 bp, 248 bp, 250 bp or 252 bp bands. In susceptible soybean cultivars Satt_492 is accounted to amplify 232 bp band. **Results in manuscript (2):** Satt _358 exhibits 200 bp amplified band in Mi resistant homozygous genotype, 200/192 bp bands in heterozygous Mi resistant genotypes and 192 bp band in Mi susceptible genotypes. Satt_132 is reported to amplify characteristic 238 bp band in Mi resistant cultivars whereas in susceptible cultivars it could be 236, 246, 248, 250 or 252 bp band. Satt_492 is reported to amplify 232 bp bands.

Discussion in manuscript (1): Microsatellite marker technique was applied to screen indigenous soybean germplasm against RMi resistance. SSR markers Satt-358 and Satt-132 have been reported to identify resistant genotypes. Bo et al. (2004) and Li et al. (2001) used six SSR markers flanking the G248 A-1 locus on LG-O to track the inheritance of this locus in different soybean lines. **Discussion in manuscript (2):** In the present study microsatellite marker technique was utilized to screen indigenous soybean germ plasm for RMiresistance. SSR markers Satt_358 and Satt_132 have been

reported to identify resistant genotypes whereas Sat_492 has been found to be less effective. Bo et al. and Li et al. used six SSR markers flanking the G248 A-1 locus on LG-O to track the inheritance of this locus in different soybean lines.

Discussion in manuscript (1): Co-descent analysis of markers and phenotype showed that Mi resistant cultivars possessed a 200 bp band at Satt-358 (Fig. 2a) and a 238 bp at Satt-132 against southern RKN. **Discussion in manuscript (2):** Co-descent analysis of markers and phenotype (pathogenicity) showed that Mi-resistant cultivars possess a 200 bp band at Satt_358 and a 238 bp at Sat_132 against southern root-knot nematode (Meloidogyne incognita).

Discussion in manuscript (1): Therefore, the tight linkage of both Satt-358 and Satt-132 to the diagnostic marker G248A-1 on LG-O in studied soybean cultivars indicated that selection for the Mi resistant allele employing these markers should be highly effective in identifying Mi resistant plants/genotypes.

• Initially this experiment was performed at NNRC from 2005 to 2009 for PhD research by the first author of this manuscript then later it was repeated at small scale, to include biochemical analysis, at NNRC in 2016. Meanwhile, the first author had graduated in 2012 and got a new affiliation with the University of Sargodha sub campus Bhakkar – Pakistan as a faculty.

1. Ramzan, M., Ahmed, R.Z., Khanum, T.A. et al. Survey of root knot nematodes and *RMi* resistance to *Meloidogyne incognita* in soybean from Khyber Pakhtunkhwa, Pakistan. *Eur J Plant Pathol* (2019). https://doi.org/10.1007/s10658-019-01740-z
2. Ramzan M, Ahmad R, Kauser N, Shah AA, Saba R, Hussain I, Fayyaz S, Khan S (2017). Confirmation of root-knot nematode resistant gene Rmi1 using SSR markers. Adv. Life Sci. 4(2): 55–59.