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Characterization of wheat (*Triticum aestivum* L.) mutants for improved agronomic traits and disease resistance

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Induced mutation holds promise as a strategy for creating new variations. In this study, we analysed mutant lines of cultivar HD 3086 selected for its extensive cultivation in India, at both morphological and molecular levels. A total of 150 M_4 mutant lines exhibited improved yield attributes, enhanced disease resistance and other agronomically important traits. Evaluation of mutant lines against leaf rust race 77-9 and stripe rust race 238S119 identified four and six highly resistant lines, respectively. SNP genotyping of rust-resistant mutants using 35K Axiom array revealed polymorphism rates ranging from 7.1 to 11.9% compared to the parent line, HD3086. Several induced point mutations were observed that may underlie key genes involved in disease resistance. The identified mutant lines, particularly the rust-resistant ones, have strong potential as valuable donors in breeding programs and as a resource for fundamental genetic studies in the future.

Keywords: biotic stress, leaf rust, mutation, stripe rust, *Triticum aestivum*

Supplementary Table 1 — Genes associated with altered SNPs in rust resistant lines and their expression in transcripts per million (tpm) as observed in wheat expression database (http://www.rust-expression.com/)

S. No	Gene ID	SNP ID	Gene description	tpm	S.No.	Gene ID	SNP ID	Gene description	tpm
1	TraesCS2A02G000700	AX-94959059	Histone deacetylase subunit SAP30/SAP30-like	6.64	38	TraesCS5B02G320900	AX-95215709	Damage-control phosphatase ARMT1-like	4.76
2	TraesCS2A02G014300	AX-94968218	CBS domain	16.02	39	TraesCS5B02G321800	AX-94621773	ClpA/B family	6.9
3	TraesCS2A02G046500	AX-95177447	Peptidase S10, serine carboxypeptidase	5.09	40	TraesCS5B02G323900	AX-94745227	ER lumen protein retaining receptor	6.36
4	TraesCS2A02G079500	AX-94738192	Dehydrogenase, E1 component	1.26	41	TraesCS5B02G391200	AX-94496362	GNAT domain	2.19
5	TraesCS2A02G088000	AX-94998685	Importin-beta, N-terminal domain	1.2	42	TraesCS5B02G410400	AX-94916379	Nucleotide-diphospho-sugar transferases	3.57
6	TraesCS2A02G197300	AX-94849076	Major facilitator, sugar transporter-like	2.79	43	TraesCS5B02G450400	AX-94576415	Small GTP-binding protein domain	7.17
7	TraesCS2A02G280400	AX-94842946	RIN4, pathogenic type III effector avirulence factor	12.2	44	TraesCS5B02G485600	AX-94649358	FYVE zinc finger	2.76
8	TraesCS2A02G280700	AX-94796049	Fatty acid desaturase, type 2	3.21	45	TraesCS5B02G514400	AX-94693063	Ulp1 protease family, C-terminal catalytic	5.13
9	TraesCS2A02G327000	AX-94738148	PB1 domain	6.76	46	TraesCS5D02G235200	AX-95201440	Protein of unknown function DUF1666	8.72
10	TraesCS2A02G367700	AX-94929514	Caleosin-related	2.17	47	TraesCS6A02G334000	AX-94840398	SCP2 sterol-binding domain	8.21
11	TraesCS2A02G474300	AX-94732891	CRIB domain	7.58	48	TraesCS6A02G344000	AX-94754601	Saccharopine dehydrogenase, NADP binding	1.85
12	TraesCS3A02G512400	AX-94652687	Pyridoxal phosphate-dependent decarboxylase	0.78	49	TraesCS6A02G371300	AX-94513497	Protein of unknown function DUF3531	7.26
13	TraesCS3D02G543400	AX-94928882	Zinc finger, PHD-type	5.56	50	TraesCS6A02G402500	AX-94614034	Peptidase C12	0.54
14	TraesCS4B02G307500	AX-94421709	Aminoacyl-tRNA synthetase, class Ia	7.77	51	TraesCS6B02G002800	AX-94672442	Mss4-like superfamily	439.2
15	TraesCS4B02G327800	AX-94498360	Cytochrome b245, heavy chain	5.23	52	TraesCS6B02G041200	AX-94796211	Peptidase S8/S53 domain	8.8

16	TraesCS4B02G351900	AX-94593455	Glycosyl transferase, family 48	5.85	53	TraesCS6B02G272700	AX-94776164	Mechanosensitive ion channel MscS-like	4.96
17	TraesCS5A02G012600	AX-94422102	CSC1/OSCA1-like, 7TM region	3.02	54	TraesCS6B02G310600	AX-94686993	Mitochondrial carrier protein	203.4
18	TraesCS5A02G015600	AX-94909932	Mechanosensitive ion channel MscS	15.53	55	TraesCS6B02G316000	AX-95079927	Cellulose synthase	2.56
19	TraesCS5A02G053100	AX-94432807	Homocysteine-binding domain	13.88	56	TraesCS6D02G003200	AX-94405661	Amino acid transporter	3.77
20	TraesCS5A02G056400	AX-94525913	Aldo-keto reductase	5.02	57	TraesCS6D02G012200	AX-94981795	Oxidoreductase FAD/NAD(P)-binding	700.7
21	TraesCS5A02G060600	AX-94403987	EF-hand domain	26.24	58	TraesCS6D02G041600	AX-95242491	Transketolase-like	6.98
22	TraesCS5A02G083600	AX-94986114	Ion channel regulatory protein, UNC-93	2.74	59	TraesCS6D02G054900	AX-95178786	Plant peroxidase	111.9
23	TraesCS5A02G220600	AX-94957897	Tetraspanin/Peripherin	22.6	60	TraesCS6D02G226000	AX-94418575	Domain of unknown function DUF676	22.44
24	TraesCS5A02G222100	AX-94675521	Pentatricopeptide repeat	0.51	61	TraesCS6D02G371200	AX-95016894	Alcohol dehydrogenase, zinc-type	40.52
25	TraesCS5A02G233200	AX-95220729	Potassium transporter	0.67	62	TraesCS7A02G342100	AX-94641332	Nuclear protein DGCR14/ESS-2	2.43
26	TraesCS5A02G251200	AX-94465470	Phosphatidylinositol 3-/4-kinase, catalytic domain	2.57	63	TraesCS7A02G344500	AX-94433472	Ribosomal protein L22e	24.06
27	TraesCS5A02G296300	AX-94564432	DNA repair RAD52-like protein	13.34	64	TraesCS7A02G344700	AX-94546940	Small-subunit processome, Utp14	1.41
28	TraesCS5A02G300400	AX-94418429	Cysteine synthase/cystathionine beta-synthase	54.83	65	TraesCS7A02G345500	AX-94426455	Heavy metal-associated domain, HMA	1.07
29	TraesCS5A02G306900	AX-94570208	Alpha/beta hydrolase fold-1	15.01	66	TraesCS7A02G350100	AX-94430527	Spermidine/spermine synthases	27.09
30	TraesCS5A02G322700	AX-94553874	Glycoside hydrolase family 9	2.1	67	TraesCS7B02G055600	AX-94474203	Bromo adjacent homology (BAH) domain	1.12
31	TraesCS5A02G404400	AX-94636029	Protein of unknown function DUF616	2.43	68	TraesCS7B02G115900	AX-94383404	Aspartic peptidase A1 family	4.12
32	TraesCS5B02G022300	AX-94476767	Carbon-nitrogen hydrolase	13.67	69	TraesCS7B02G130600	AX-94553373	D-isomer specific 2-hydroxyacid dehydrogenase	15.17
33	TraesCS5B02G227200	AX-94500078	Zinc finger, RING-CH-type	27.81	70	TraesCS7B02G144400	AX-95248046	Short-chain dehydrogenase/reductase SDR	3.08
34	TraesCS5B02G233500	AX-94389734	RlpA-like domain superfamily	0.34	71	TraesCS7B02G302300	AX-94968148	Protein N-terminal asparagine amidohydrolase	4.1
35	TraesCS5B02G255100	AX-95112943	Tetratricopeptide-like helical domain superfamily	2.08	72	TraesCS7B02G393900	AX-95209306	ELM2 domain	2.27
36	TraesCS5B02G288700	AX-94664259	Palmitoyltransferase, DHHC domain	13.49	73	TraesCS7D02G421500	AX-94851711	NIF system FeS cluster assembly, NifU	15.45
37	TraesCS5B02G320500	AX-95107370	Signal transduction response regulator	5.68	74	TraesCS7D02G526000	AX-94616626	Bromodomain	5.79