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Genetic basis of resistance to leaf rust in tetraploid wheats

Francesca Desiderio[1], Davide Guerra[1], Anna Maria Mastrangelo[2], Diego Rubiales[3], Marina Pasquini[4], Rosanna Simeone[5], Antonio Blanco[5], Luigi Cattivelli[1], Giampiero Valè[1]

[1] C. R. A., Genomics Research Centre, Fiorenzuola d'Arda, Italy
[2] C. R. A., Cereal Research Centre, Foggia, Italy
[3] CSIC, Córdoba, Spain
[4] C. R. A., Cereal Quality Research Unit , Rome, Italy
[5] University of Bari "Aldo Moro", DEASBC Bari, Italy

Abstract. Leaf rust, caused by *Puccinia triticina* Eriks., is one of the major constraints to durum wheat production. It is globally distributed with different race structures that continuously evolve and form novel virulent races. Growing resistant cultivars represent the most effective way of controlling rust diseases in wheat. In this paper we report a summary about the leaf rust genes (*Lr*), the quantitative trait loci (QTLs) and significant regions detected in tetraploid wheats.

Keywords. *Puccinia triticina* – Tetraploid wheats – Genetic resistance – Mapping.

Base génétique de la résistance à la rouille brune chez les blés tétraploïdes

Résumé. *La rouille brune, causée par Puccinia triticina Eriks., est l'un des principaux obstacles à la production de blé dur. Ce pathogène est distribué à l'échelle mondiale et présente des structures de races différentes qui évoluent continuellement et forment de nouvelles races virulentes. Cultiver des variétés résistantes représente le moyen le plus efficace de lutte contre les maladies de la rouille du blé. Dans cet article, nous allons parcourir les gènes de la rouille brune (Lr), les loci des caractères quantitatifs (QTLs) et les régions significatives détectées dans les blés tétraploïdes.*

Mots-clés. *Puccinia triticina – Blés tétraploïdes – Résistance génétique – Cartographie.*

Leaf rust, caused by *Puccinia recondita* Rob. ex. Desm. f.sp. tritici Eriks. & E. Henn. (syn. *P. triticina*), is an important disease in durum wheat that causes significant reduction in grain yield and quality in most wheat growing areas (Samborsky, 1985). The level of damage inflicted by leaf rust varies with the growth stage of plants at the initial infection and environmental conditions (Kolmer *et al.*, 2007). The use of resistant cultivars is the most effective way to control this disease and the constant search for novel resistance genes is essential to cope with the dynamic and rapidly evolving pathogen populations (Kolmer, 2005; Bolton *et al.*,2008). Sources for the identification of new resistance genes frequently include the wild relatives of crop plants and germplasm from the center of diversity of the cultivated species, and wild emmer (*T. turgidum* ssp. *dicoccoides*) has represented an useful source of genes for resistance to pathogens, including leaf rust, in wheat (Marais *et al.*, 2005; Dyck 1994; Xie *et al.*, 2012). Similarly, also *T. turgidum* ssp. *dicoccum*, one of the earliest domesticated wheat derived from wild emmer (Kilian *et al.*, 2009) acted as a donor of genes for resistance to leaf rust (Piarulli *et al.*, 2012; Liu *et al.*, 2005; McIntosh *et al.*, 1995).

Knowledge of genetic nature of the resistance to infective diseases, the genes at the basis of this character, as well as their inheritance and interaction, is essential for breeding for resistance.

Usually, the identification of genes/quantitative trait loci (QTLs) for resistance to fungal pathogens has been carried out through linkage mapping, but association mapping also revealed to be a useful tool for finding significant associations between molecular markers and the resistance to

leaf rust in durum wheat. As shown in Table 1, 15 different genes and 4 QTLs have been identified in durum wheat using linkage mapping, and different types of closely linked molecular markers have been found. Leaf rust resistance (*Lr)* genes were detected along all chromosomes except for 2A, 3A, 4A, 4B and 5A, while the QTLs regions were identified on chromosomes 1B, 2B and 7B.

More recently, the use of association mapping with durum wheat germplasm collections has been introduced to discover new useful allelic variants through genome-wide scan. Association mapping has several advantages over biparental mapping, including increased mapping resolution and reduced research time by utilizing historic recombination rather than developing new mapping populations, and the ability to detect a greater number of alleles at a particular locus (Yu and Buckler, 2006). A high number of molecular markers associated to the resistant phenotype were recently identified through association mapping in a collection of 164 elite cultivars of durum wheat analyzed with 25 different *P.triticina* isolates (Maccaferri *et al*. 2010), as reported in Table 1.

Information on genetic loci for resistance to leaf rust, closely linked molecular markers and the genotype source of the resistance (as reported in Table 1) is an important prerequisite for marker assisted selection (MAS) programs. With respect to traditional breeding, the use of genetic markers for MAS can greatly shorten the duration of a breeding program, increase the selection efficiency, and limit the phenotypic assessment, which is often laborious and time-consuming. Many efforts have been made internationally to incorporate modern selection technologies into breeding programs. An example of this is the WHEAT CAP project (http:// maswheat.ucdavis.edu/), which is aimed at preparing MAS protocols to incorporate valuable genes for many traits of interest into the best wheat breeding lines (Borrelli *et al.* 2009). For instance, more than 160 leaf (*Lr*), stem (*Sr*) and stripe (*Yr*) rust resistance genes have been found and characterized in common hexaploid wheat, tetraploid durum wheat, and many diploid wild wheat species (Todorovska *et al.* 2009). Nevertheless, the knowledge of the gene sequences linked to the resistance is still lacking, even if it is of great importance, as this allows the design of perfect molecular markers that are not subject to the risk of recombination between the marker and the R gene. Three genes for leaf-rust resistance that confer race-specific resistance have been isolated in bread wheat: *Lr1* and *Lr10*, which originated from common wheat, and *Lr21*, which originated from *Triticum tauschii* (Cloutier *et al.* 2007; Feuillet *et al.* 2003; Huang *et al.* 2003). With the rapid progress of “omics” technologies, great efforts should be aimed at the isolation and cloning of genes and QTL for resistance to leaf rust also in durum wheat, to understand the genetic and molecular mechanisms of resistance and to use this information for the release of cultivars characterized by high and durable resistance.

Table 1. Leaf rust resistance genes (*Lr*), QTLs (*QLr*) and significant regions detected using linkage mapping (LM) and association mapping (AM, marker-wise significant of P ≤ 0.01) approaches on durum wheat. Information on durum wheat genotypes, chromosome location (Chr.) and closely linked markers are also provided.

	Donor genotypes	Chr.	Closely linked markers	Method	References
Lr3a	Storlom	6BL	AFLP: Xmwg798; cDNA marker:TaR16; UBC849540	LM	Herrera-Foessel et al., 2007; Danna CH et al., 2002; Khan RR et al., 2005
Lr10	Altar, Russello	1A	Xsfr1, Xsfrp1	LM	Schachermayr et al., 1997
Lr14a	Lloreta INIA, Somateria	7B	Xwmc273, Xgwm344	LM	Herrera-Foessel et al., 2008a
Lr19	UC1112, UC1113, Ammar9 and Azeghar2	7A	Xwg420, Xmwg2062, SSR-Gb	LM	Zhang et al., 2005; Kassem et al 2011

	Donor genotypes	Chr.	Closely linked markers	Method	References
Lr23	Altar84; W-7974	2BS	Xksu904	LM	Nelson et al., 1997;Faris et al., 1999
Lr26	Cando2/Veery; KS91WGRC14	1BL	IB-267, iag95	LM	Mago et al., 2002; Friebe et al., 1993
Lr27	Benimichi C2004, Jupare C2001	3B	XksuG53	LM	Huerta-Espino J et al., 2009; Nelson et al., 1997
Lr31	Benimichi C2004, Jupare C2001	3B	XksuG10	LM	Huerta-Espino J et al., 2009; Nelson et al., 1997
Lr47	-	7AS	PS10	LM	Dubcovsky et al., 1998
Lr50	TA870, TA 145, TA874, TA 870, TA895 (*T. armeniacum*)	2B	Xgwm382,Xgdm87	LM	Brown-Guerdira et al., 2003
Lr53	98M71 and 479 (*T. dicoccoides*)	6BS	PSR167	LM	Marais et al., 2003,2005;
Lr61	Guayacan 2, Guayacan INIA	6BS	AFLP: P81/M70269/P87/ M75131; SSR: Xwmc487	LM	Herrera-Foessel et al., 2008b
Lr64	8404 (*T. dicoccoides*)	6AL	Xbarc104, Xgwm427	LM	Kolmer JA 2008 Personal communication
LrWo	Wollaroi AUS99174	5BS	Xgwm234; wPT-1420	LM	Singh et al. 2010
QLr	Sachem	7BL	Xgwm146	LM	Singh et al., 2013
QLr	Sachem	1BL	wPt-3579	LM	Singh et al., 2013
QLr	Strongfield	2B	wPt-3632	LM	Singh et al., 2013
QLr. ubo-7B.2	Creso/Colosseo	7BL	Xgwm344.2 and DaRT 378059	LM	Marone et al., 2009; Maccaferri et al., 2008
-	164 elite durum wheat accessions	1A	Xgpw2276, Xwmc24, Xwmc469, Xcfa2129	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	1B	Xwmc500.1, Xgwm124, Xbarc188, Xwmc44, Xbarc80, Xgwm140, Xcfd251.1	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	2A	Xbarc212, Ppd-A1, Xcfa2201, Xgwm1198.2,Xgwm1198.3, Xwmc552.1	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	2B	Xbarc2318, Xwmc770, Xgwm410.1, Xgwm148, Xbarc183.1, Xbarc40, Xbarc101.1, Xwmc175, Xgwm846.2	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	3A	Xwmc388.2, Xwmc264, Xcfa2193	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	3B	Xgwm685, Xbarc84, Xgwm299	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	4A	Xgwm894, Xbarc155, Xwmc313	AM	Maccaferri et al., 2010

	Donor genotypes	Chr.	Closely linked markers	Method	References
-	164 elite durum wheat accessions	4B	Xbarc193, Xwmc524, Xgwm856, Xgwm6	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	5A	Xwmc489.1, Xbarc303, Xwmc705, Xwmc805, Xgwm1570, Xgwm410.2	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	5B	Xgwm335, Xcfa2121, Xwmc640.1	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	6A	Xgwm1009, Xksum98	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	6B	Xwmc486, Xgwm1682	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	7A	Xgwm233, Xgwm1187, Xwmc488	AM	Maccaferri et al., 2010
-	164 elite durum wheat accessions	7B	Xwmc323, Xgwm1184, Xgwm333, Xwmc396	AM	Maccaferri et al., 2010

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