研究论文

普通小麦(Taestivum)ph1b、ph2a、ph2b基因系与黑麦(Secale cereale)的杂交及回交研究

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利用中国春ph1b、ph2a、ph2b基因系及对照中国春分别与甘肃黑麦杂交,结实率分别为94.0%、87.9%、9 3.8%和90.8%,其F_1减数分裂中期 I 染色体配对交叉数分别为9.748、2.968、5.000和1.376,ph1b、ph2a、ph2b基因 ▶ PDF(480KB) 诱导小麦与黑麦F_1部分同源染色体配对顺序是ph1b>ph2b>ph2a。用中国春回交F_1取得了成功,回交结实率分别 为1.06%、0.73%、2.52%和11.40%。利用ph1b、ph2b基因可以将黑麦中有益基因直接遗传转移给小麦,ph2a在导 入黑麦有益基因方面不宜利用,或其效果不及ph1b、ph2b,回交结实率与染色体配对有关。

关键词 ph基因系,黑麦,部分同源染色体配对,染色体交叉数,回交 分类号

Study on Crosses and Backcrosses of Common Wheat(Triticum aestivum)M utants ph1b, ph2a, ph2b with Rye (Secale cereale)

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Abstract 'Gan Su' rye was crossed with 'Chinese Spring' mutants ph1b, ph2a, ph2b andwith 'Chinese Spring' as the control. The seed sets were 94.0% \$7.9% 93.8% and 90.8%, respectively, indicating no significant difference amo ng them. Chiasma fre-quencies of the F_1 hybrids at meiotic metaphase I were 9.784, 2.968, 5.000 and 1.376, respectivel y. The order of the ability of inducing homoeologous pairing by theph genes in wheat x rye F_1 hybrids at meiotic metapha se I is ph1b>ph2b>ph2a.Backcrosses of F_1 hybrids to Chinese Spring were successful and the backcrossesseed sets were 1.06%, 0.73%, 2.52% and 11.40%, respectively, indicating therewas significant difference between the ph derivatives and the control. So, directgenetic transfer of desirable genes from rye to wheat by ph1b, ph2b genes is available, but it is impos sible by ph2a gene. Seed sets of backcrossing to the F 1hybrids are related to the homoeologous pairing at meiotic metapha se I.

Key words ph lines S. cereale Homoeologous pairing Chiasma frequency Backcross DOI:

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