

研究论文

小麦RIL群体中GMP含量的动态累积和净遗传增量的变化规律

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摘要 以普通小麦京771和Pm97034及其175个重组自交系RIL (F₂:8) 后代群体为材料, 研究了籽粒灌浆期(花后12 d、17 d、22 d、27 d和32 d) GMP含量的动态累积规律和各个时期GMP的净遗传效应。结果表明, 多数RIL后代家系GMP含量的变化趋势与两亲的变化趋势相一致, 呈现“低-高-低-高-高”的规律, 即籽粒灌浆初期GMP的累积量较低, 后逐渐升高, 但在花后22 d左右又开始下降, 出现一个明显的低谷期, 然后逐渐上升, 成熟期达到最高。不同亚基组合对GMP含量累积的影响不尽相同, (1,17+18,5+10)、(N,17+18,5+10)、(1,14+15,5+10)和(N,14+15,5+10)组合的后代家系虽然在整个籽粒灌浆期GMP含量的累积变化各不相同, 但均于花后27 d到32 d迅速上升, 籽粒成熟期达到最高。若从GMP最后的累积量看, 这4个组合是利于GMP含量累积的组合, 而5+10亚基较其他亚基对GMP的累积更为有利。不同发育阶段GMP含量条件遗传分析表明, 控制GMP性状的基因在整个籽粒灌浆期都有表达, 大多数后代家系该基因表达在花后17 d左右最为活跃, 花后22 d左右为低谷期, 各阶段基因净表达量的变化与GMP观测值的变化基本一致。

关键词 [普通小麦](#) [GMP含量](#) [净遗传增量](#)

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Dynamic Changes of GMP Content and Net Genetic Variation in Wheat RIL Population

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Abstract The experiment was conducted using 175 recombinant inbred lines (RILs) derived from a cross between common wheat Jing 771 and Pm97034. The results indicated that the GMP content in most RILs was accumulated at low level in early stage of grain filling, then ascended gradually, but descended at about 22 days after anthesis, then ascended continually up to maturity, which was the same as that in their parents. The effects of different subunit combinations on the dynamic changes of GMP content were different. The GMP content in the RILs with (1,17+18,5+10), (N,17+18,5+10), (1,14+15,5+10), (N,14+15,5+10) subunit combinations were quickly accumulated from 27 days to 32 days after anthesis, and up to the highest value at maturity. The four subunits combinations especially the 5+10 subunits were favorable to GMP accumulation. The results of conditional genetic variance components showed that the GMP quantitative genes were expressed from filling to mature, and most active at 17 days after anthesis, while inactive at about 22 days after flowering. The dynamic changes of the GMP net genetic variation were similar to that of GMP content accumulation.

Key words [Common wheat](#) [GMP content](#) [Net genetic variation](#)

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