

Close relationship between the *HinfI* and *DpnA* DNA-methyltransferase

R. Lauster

Max-Planck-Institut für Molekulare Genetik, Ihnestr. 73, D-1000 Berlin 33, FRG
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The amino acid sequences of some thirty different DNA methyltransferases (Mtases) have been established during the last several years. Their comparison revealed a close relationship among all the cytosine (5C) specific enzymes (1). In contrast high divergence is found between the adenine specific Mtases. Only the five Mtases *dam*, *damT4*, *DpnII*, *EcoRV* and *damT2* proved to be closely related (2,3). Table I shows, that the sequence of the GANTC recognizing *HinfI* Mtase, which was recently published (4), does not only exhibit some identities to the isomethylomeric enzyme *HhaII* (5), but to a much larger extent similarities to the GATC methylating enzyme *DpnA* (5,6). In the alignment 42% of the positions are occupied by identical amino acids. The comparison thus defines a third group of closely related Mtases. It also supports the previous observation that recognition of different target sequences may well be achieved by Mtases whose core structure is conserved (1,2).

Table 1

| | | |
|-------|--|-----------------------------|
| DpnA | MTKPYYNKMKMLVHSDTFKFLSKMKPESMDMIFADPPYFLSNGG | ISNSGGQVVSVDKGDWDKISSFFEEKH |
| HinfI | NMKENINDFLNTILKGDGCKIEKLTIPNESIDLIFADPPYFMQTGKLLRTNGDEFGVDDWDEWDFNDVFEYD | |
| DpnA | EFNRKWIRLAKEVLKPNGTVMVIGSLHNIYSVGMALQEGFKILNNTWQKTNPAPNLSCRYFTHSTETILW | |
| HinfI | SFCELWLKCKRILKSTGSIWVIGSFQNIYRIGYIMQNLDWFILNDVWNNKTNPVPNVGGTRFCNAHETMLW | |
| DpnA | ARKNDKKARHYNYDLMKELNDGKQMKDVTGSLTKKVEK | WAGK HPTQKPEYLLERILASTKEGDY |
| HinfI | CSCK KKNKFTFNKTKMKHLNQEQRSVWLSLCTGKERIKDEEGKKAHSTQKPESLLYKVLSSSKPNDV | |
| DpnA | ILDPPVFGSGTTGVAKRLGRRFIGIDAEKEYLKIARKRLEAENETN | |
| HinfI | VLDPPFGTGTGAVAKALGRNYIGIEREQYIDVAEKRLREIKPNPNDIELLSLEIKPPKVPKMTLIEADFL | |
| HinfI | RVGQTLFDKNENAICIVTQDGNVKNDEETLSIHKMSAKYLNKTNNGWDYFYLFRRNNFITLDSLRYEYTNQ | |

Table 1: Alignment of the two DNA Mtase sequences *DpnA* (5) and *HinfI* (4). The alignment was performed by hand. The number of gaps/inserts was kept to a minimum. Conserved amino acids are indicated by vertical lines. The two boxes indicate regions, which are conserved in all adenine specific Mtases (7).

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