8), 6.00 (d, J = 2.5 Hz, 1H, H-6), 5.30 (dd, J = 4 and 12 Hz, 1H, H-2), 4.00 (s, 3H, 1 × OMe), 3.95 (s, 3H, 1 × OMe), 2.60 (m, 2H, H-3); MS (m/e); 300 (M^+), 299, 285, 282, 133, 134, 107, 192, 193, 166, 181 and 209.

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RECORD OF MARINE PALEOCENE SEQUENCE NEAR SANU, JAISALMER, WESTERN RAJASTHAN

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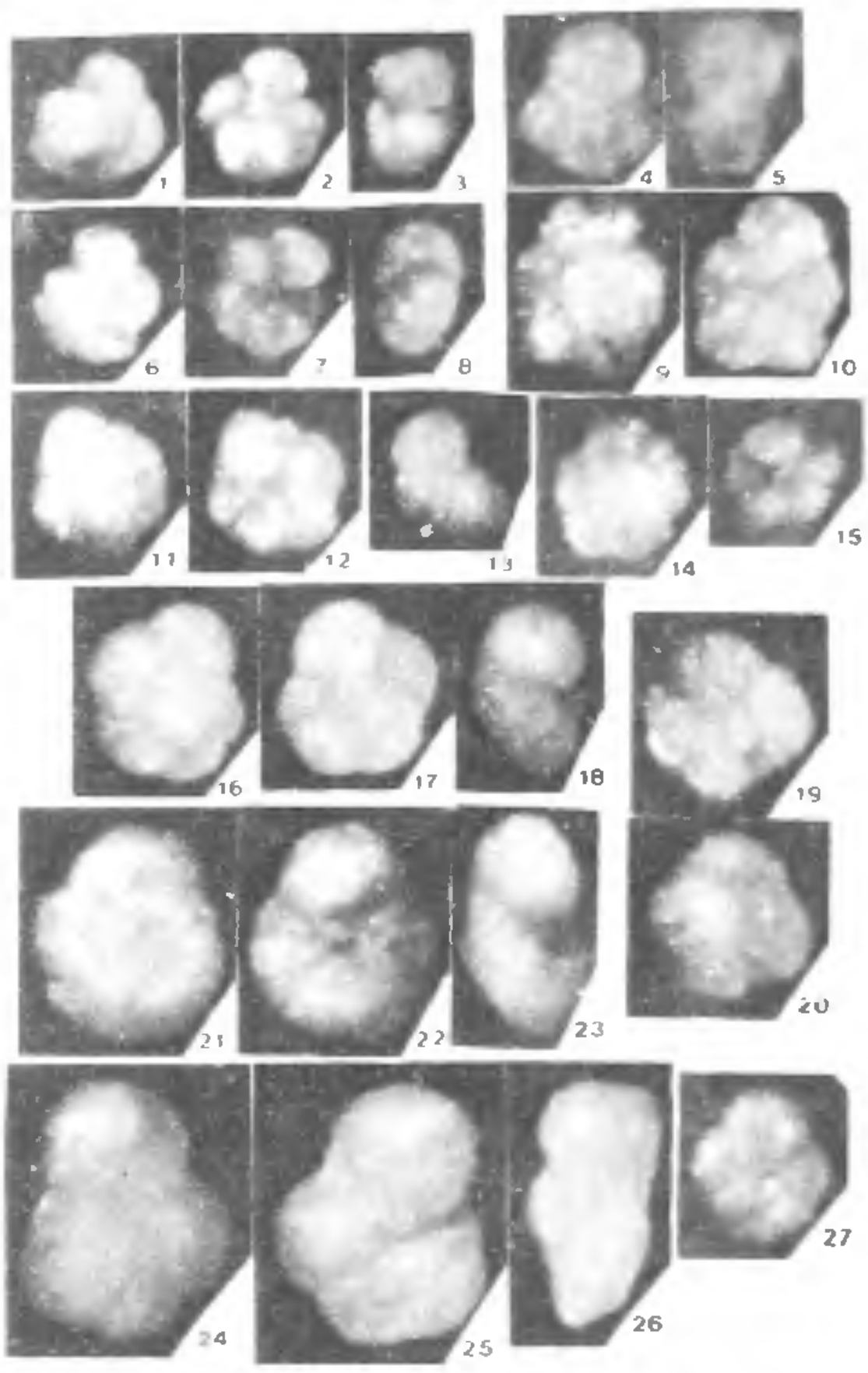
THE study of planktonic foraminifers from the core samples near Sanu, Jaisalmer has provided the evidence for the presence of almost complete Paleocene succession in Jaisalmer basin, western Rajasthan. The Paleocene sequence comprises of sandstone, Fuller's



Figures 1–27. 1–3. *Subbotina spiralis.* **1.** Spiral view **2.** Umbilical view **3.** Edge view. **4–5.** *Subbotina pseudobulloides.* **4.** Spiral view **5.** Edge view. **6–8.** *Subbotina praecursoria.* **6.** Spiral view **7.** Umbilical view **8.** Edge view. **9–10.** *Morozovella Uncinata.* **9.** Spiral view **10.** Umbilical view. **11–13.** *Morozovella pusilla.* **11.** Spiral view **12.** Umbilical view **13.** Edge view. **14–15.** *Subbotina edita.* **14.** Spiral view **15.** Umbilical view. **16–18.** *Subbotina inconstans.* **16.** Spiral view **17.** Umbilical view **18.** Edge view. **19–20.** *Globigerina daubjergensis.* **19.** Umbilical view **20.** Spiral view. **21–23.** *Morozovella velascoensis.* **21.** Spiral view **22.** Umbilical view **23.** Edge view. **24–26.** *Planorotalites pseudomendardii.* **24.** Spiral view **25.** Umbilical view **26.** Edge view. **27.** *Morozovella angulata* (Umbilical view) (figures 1–8, 11–27 × 114, 9, 10 × 182)

earth, marl, chalk and limestone, typically exposed near Sanu village (70° 39′6″ : 27° 14′ 30″), 45 km NW of Jaisalmer, along the arcuate ridge extending from Parewar (70° 44′ 26″ : 27° 15′ 55″) to Mohammed-Ki-Dhani (70° 29′ 49″ : 27° 7′ 17″). The basal transgressive sandstone, lies unconformably over the Cretaceous sands of Habur Formation and is overlain by alternating horizons of Fuller's earth and marl. The succeeding chalk and chalky limestone form a distinct unit, rich in planktonic assemblages and marked by the occurrence of nautiloids. Hard coralline-nummulitic limestone above the chalk unit constitutes the uppermost unit of Paleocene sequence.

The planktonic foraminiferal study carried out on 26 m run of core samples, from the top of ridge has helped us in establishing P_{1b} to P_5 zones[1], (figure 28). Recognition of P_{1b} to P_2 zones has established the presence of Danian which was considered to be missing in both surface and subsurface in the Jaisalmer basin[2]. The presence of Thanetian is marked by the recognition of P_3 to P_5 zones. Singh[3] identified P_4 and P_5 zones in the Karathar well sections and considered the time of initial Paleocene transgression in Jaisalmer basin as early part of late Paleocene. In Indian ocean the earliest Paleocene is not generally encountered and is represented by the hiatus at Cretaceous/Tertiary boundary. The earliest Danian planktonic foraminiferal zone recognised from Cauvery and Kutch basins is the P_{1d} (*Subbotina praecursoria*) zone[4]. $P_{1b\&c}$ (*Subbotina pseudobulloides*) zone marking the earlier, Danian was recognised in Assam[5]. The presence of $P_{1b\&c}$ zone, characterised by the associations of *S. pseudobulloides, S. edita* and *Gl. daubjergensis* (figures 1–27), is significant, as it provides the record of Early Danian in Western India too.

Sanu Formation was designated by Das Gupta[2] for the sandstone unit devoid of fossils who, regarded it to be continental deposits of Paleocene age. The sand-

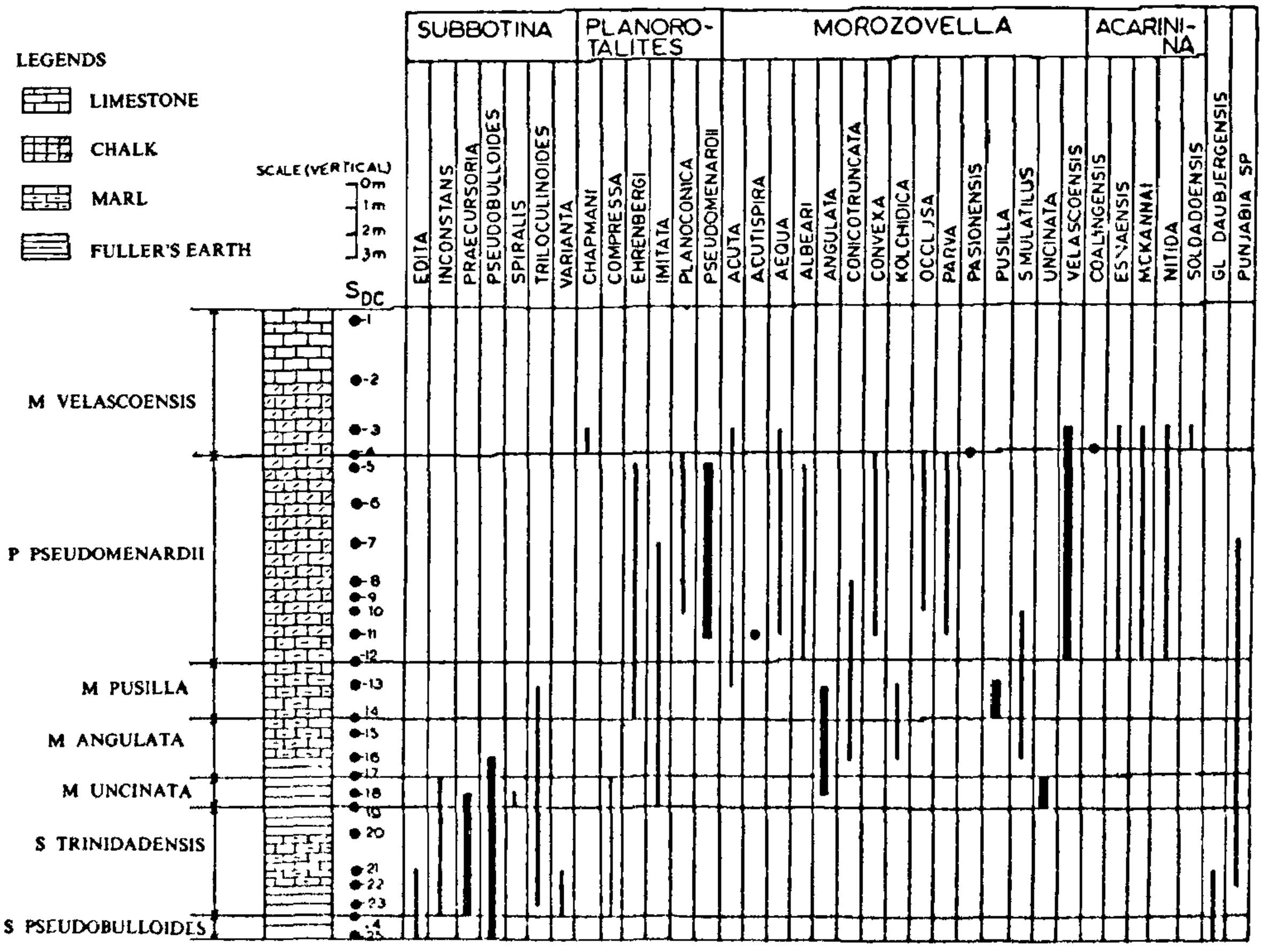


Figure 28. Biozonation and distribution of planktonic foraminifers in Paleocene of Jaisalmer basin.

stone unit above Habur Formation is regarded here as integral part of Paleocene transgression in Jaisalmer basin. The definition of Sanu Formation as proposed by Das Gupta[2] is emended here to include basal transgressive sandstones, Fuller's earth, marl, chalk, chalky limestone and coralline limestone interbedding.

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CROSSABILITY BETWEEN TRITICALE × WHEAT AND REVERSION PATTERNS IN EARLY SEGREGATING GENERATIONS

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TRITICALE (× Tritosecale wittmack) a cereal crop owns the distinction of being the creation of the plant breeders rather than natural processes of evolution. It is an intergeneric hybrid between wheat (*Triticum* species) and rye (*Secale cereale*) and may be used as food, feed and forage. The present day triticales have many draw backs. In the present study investigation was conducted to find out the extent of crossing between triticale × wheat and reversion of early segregating generations to the parental types.

Four hexaploid ($2n = 42$) triticale strains namely, UPT 72142, UPT 75233, UPT 78267 and PR 673 were crossed during *rabi* 1980–81 with the bread wheat (*Triticum aestivum* L.) varieties HD 2009 and UP 262. Triticale was used as female parent while wheat was used as male parent. The total number of seeds set and total number of florets pollinated were counted and the extent of crossability was calculated as follows:

$$\text{Crossability}\,(\%) = \frac{\text{Number of seeds set}}{\text{Number of florets pollinated}} \times 100$$

$B_1(F_1 \times \text{Triticale})$, $B_2(F_1 \times \text{wheat})$ and F_2 generations were raised during *rabi* 1982–83, to study the reversion to the parental types. On the basis of the morphological features, plants were classified as having resemblance to either of the parent in each cross.

The crossability between triticale (female parent) and wheat (male parent) varied from 1.6% to 18.2% with an average crossability of 8.16% (table 1). Cross UPT 75233 × HD 2009 exhibited the highest crossability of 18.2% while the lowest crossability of 1.6% was observed in the cross PR 673 × UP 262. The seed setting in different crosses was thus influenced by genotypes of the parents.

Studies on the genetical control of crossability between hexaploid wheat and rye have shown the existence of the two recessive genes Kr_1 and Kr_2, controlling the high crossability[1]. The dominant Kr_1 reduced crossability to a greater degree than did Kr_2. These genes have been located on chromosome 5B and 5A respectively, of the wheat genome[2]. The dominant alleles of the gene manifest the inhibition of pollen tube growth both in style and near the wall and prevent

Table 1 *Crossability between triticale × bread wheat varieties*

Triticale (female parent)	Wheat (male parent)	No of spikes pollinated	No. of florets pollinated	No of seeds set	Crossability percentage
UPT 72142	HD 2009	25	20 × 25 = 500	68	13 60
	UP 262	25	20 × 25 = 500	56	11 20
UPT 75233	HD 2009	25	18 × 25 = 450	82	18 20
	UP 262	25	18 × 25 = 450	30	6 67
UPT 78267	HD 2009	25	18 × 25 = 450	25	5 56
	UP 262	25	18 × 25 = 450	20	4 45
PR 673	HD 2009	25	25 × 25 = 625	25	4 00
	UP 262	25	25 × 25 = 625	10	1 60
Average		25	506 25	39 5	8 16